

- F-PLACE1003611//EST//0.00015:318:59//Hs.28788:R66896
 F-PLACE1003618//Human Line-1 repeat mRNA with 2 open reading frames//1.3e-122:737:87//Hs.23094:M19503
 F-PLACE1003625//ESTs//1.6e-16:103:96//Hs.111223:N51105
 F-PLACE1003638//ESTs//0.60:305:57//Hs.19104:W07762
- 5 F-PLACE1003669//ESTs, Weakly similar to 3-7 gene product [H.sapiens]//0.021:445:58//Hs.158275:AI365413
 F-PLACE1003704//Human mRNA for KIAA0301 gene, partial cds//0.014:622:56//Hs.76730:AB002299
 F-PLACE1003709//Homo sapiens protein kinase (BUB1) mRNA, complete cds//1.4e-133:669:95//Hs.98658:AF053305
- 10 F-PLACE1003711//ESTs//2.2e-14:178:77//Hs.114831:T57101
 F-PLACE1003723//Homo sapiens mRNA for T lymphocyte specific adaptor protein//8.5e-09:393:60//Hs.103527:AJ000553
 F-PLACE1003738//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//1.8e-53:260:99//Hs.102928:AI346344
- 15 F-PLACE1003760//ESTs//5.1e-08:334:63//Hs.43675:AA805648
 F-PLACE1003762//ESTs//1.0:59:83//Hs.29863:W28963
 F-PLACE1003768//Human knpi repeat mma (cdna clone pcd-kpni-4), 3' end//2.7e-40:608:68//Hs.139107:K00629
 F-PLACE1003771//ESTs//6.6e-10:226:65//Hs.15776:T91944
 F-PLACE1003783
- 20 F-PLACE1003784//Homo sapiens mRNA for KIAA0765 protein, partial cds//1.0:457:57//Hs.62318:AB018308
 F-PLACE1003795//Human homologue of yeast sec7 mRNA, complete cds//0.85:314:60//Hs.1050:M85169
 F-PLACE1003833//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.00059:201:68//Hs.40806:AA018786
 F-PLACE1003850//ESTs//0.0088:220:61//Hs.145504:AI254165
 F-PLACE1003858//EST//0.77:137:61//Hs.146935:AI188124
 F-PLACE1003864//ESTs//0.11:225:59//Hs.160910:AI370359
- 25 F-PLACE1003870//EST//7.2e-18:283:69//Hs.135497:AI091257
 F-PLACE1003885//H.sapiens PAP mRNA//2.4e-75:759:72//Hs.49007:X76770
 F-PLACE1003886
- 30 F-PLACE1003888//Human mRNA for phospholipase C, complete cds//8.4e-55:702:67//Hs.153322:D42108
 F-PLACE1003892//ESTs//2.4e-13:258:67//Hs.28039:H24050
 F-PLACE1003900//ESTs//3.5e-14:271:66//Hs.28589:AI004944
- 35 F-PLACE1003903//CTP synthetase//1.6e-49:528:71//Hs.84112:X52142
 F-PLACE1003915//ESTs, Highly similar to ARGINYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR [Saccharomyces cerevisiae]//1.2e-49:251:98//Hs.65831:F03069
 F-PLACE1003923//Interferon, alpha 16//0.48:278:60//Hs.56303:M28585
- 40 F-PLACE1003932//EST//0.00060:221:63//Hs.163044:AA707537
 F-PLACE1003936//ESTs//0.86:211:62//Hs.150751:AI123536
 F-PLACE1003968//Human 5'-AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds//2.0e-47:522:71//Hs.3136:U42412
- 45 F-PLACE1004103//ESTs//8.6e-35:226:89//Hs.78973:AI026812
 F-PLACE1004104//ESTs//1.0:179:61//Hs.163935:AA506940
 F-PLACE1004114//ESTs//1.3e-52:323:89//Hs.35156:AA148516
 F-PLACE1004118//Spleen focus forming virus (SFFV) proviral integration oncogene spi1//0.85:164:64//Hs.153045:X52056
- 50 F-PLACE1004128//Guanine nucleotide binding protein (G protein), beta polypeptide 1//3.1e-41:422:74//Hs.3620:X04526
 F-PLACE1004149//ESTs, Weakly similar to F48F7.1 [C.elegans]//8.2e-82:418:96//Hs.156161:AI333779
 F-PLACE1004156//ESTs//0.10:166:63//Hs.133279:AI053552
 F-PLACE1004161//Human mRNA for KIAA0200 gene, complete cds//0.85:269:64//Hs.76986:D83785
 F-PLACE1004183//EST//1.3e-40:224:94//Hs.156603:AI343666
- 55 F-PLACE1004197//ESTs//2.8e-91:441:98//Hs.97269:AA292201
 F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds//1.3e-145:695:98//Hs.24640:AF069493
 F-PLACE1004242//ESTs//0.99:213:60//Hs.117311:AA699722
 F-PLACE1004256//EST//0.019:364:58//Hs.122395:AA789273
 F-PLACE1004257//ESTs//0.77:154:64//Hs.112582:AA608689
- 60 F-PLACE1004258//ESTs, Weakly similar to vanilloid receptor subtype 1 [R.norvegicus]//1.1e-98:479:97//Hs.31718:N29128
 F-PLACE1004270//Homo sapiens CAGF9 mRNA, partial cds//0.00010:369:63//Hs.110826:U80736

- F-PLACE1004274//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.085:573:56//Hs.154139:AB007914
- F-PLACE1004277//Homo sapiens two pore domain K⁺ channel (TASK-2) mRNA, complete cds//2.0e-157:756:97//Hs.127007:AF084830
- 5 F-PLACE1004284//ESTs//3.6e-71:344:99//Hs.145870:AI271884
- F-PLACE1004289//ESTs//2.6e-57:370:85//Hs.16740:AA586576
- F-PLACE1004302//FACTOR VIII INTRON 22 PROTEIN//0.032:513:59//Hs.83363:M34677
- F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//9.3e-152:797:94//Hs.11171:Y11588
- F-PLACE1004336
- 10 F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//1.9e-140:688:97//Hs.16232:AF100153
- F-PLACE1004376//ESTs, Weakly similar to F27D4.4 [C.elegans]//3.9e-109:521:98//Hs.14079:AA306552
- F-PLACE1004384//Human HsLIM15 mRNA for HsLIM15, complete cds//2.0e-49:466:76//Hs.37181:D64108
- F-PLACE1004388
- 15 F-PLACE1004405//EST//0.010:191:64//Hs.147600:AI217871
- F-PLACE1004425//ESTs//2.1e-20:124:80//Hs.94195:W03579
- F-PLACE1004428//H.sapiens mRNA for Branched chain Acyl-CoA Oxidase//1.0:552:58//Hs.9795:X95190
- F-PLACE1004437//Human NAD⁺-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds//9.9e-131:536:99//Hs.155410:U49283
- 20 F-PLACE1004451//ESTs//5.9e-18:203:73//Hs.156097:AI348867
- F-PLACE1004460
- F-PLACE1004467//ESTs//8.0e-17:345:66//Hs.112993:AA824363
- F-PLACE1004471//EST//9.3e-69:463:84//Hs.116391:AA644085
- F-PLACE1004473//ESTs//0.93:358:58//Hs.33263:AA724416
- 25 F-PLACE1004491//EST//2.5e-58:285:99//Hs.97603:AA398163
- F-PLACE1004506//CD81 ANTIGEN//7.2e-06:228:63//Hs.54457:M33680
- F-PLACE1004510//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds//2.5e-147:699:97//Hs.122752:AF026445
- F-PLACE1004516//EST//1.0e-26:343:71//Hs.142595:N24150
- 30 F-PLACE1004518
- F-PLACE1004548//EST//0.84:193:62//Hs.99583:AA461314
- F-PLACE1004550//ESTs, Weakly similar to No definition line found [C.elegans]//4.0e-120:627:94//Hs.107387:AA058854
- F-PLACE1004564//EST//1.0:240:62//Hs.16824:T91371
- 35 F-PLACE1004629//Centromere protein B (80kD)//0.0015:242:64//Hs.85004:X05299
- F-PLACE1004645
- F-PLACE1004646//Retinal pigment epithelium-specific protein (65kD)//1.4e-12:386:63//Hs.2133:U18991
- F-PLACE1004658//ESTs//0.52:273:61//Hs.97252:AA291590
- F-PLACE1004664
- 40 F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene//1.5e-66:357:95//Hs.77705:U07563
- F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//1.4e-110:625:91//Hs.80019:AF035806
- F-PLACE1004681//EST//0.00092:303:61//Hs.149560:AI281589
- 45 F-PLACE1004686//ESTs//3.0e-31:186:76//Hs.139130:AA704561
- F-PLACE1004691//Homo sapiens clone 23963 mRNA sequence//0.54:242:61//Hs.48483:AF007131
- F-PLACE1004693//ESTs, Weakly similar to pot. ORF III [H.sapiens]//0.56:96:71//Hs.125740:AA884845
- F-PLACE1004716//ESTs//2.0e-79:388:98//Hs.150999:AI306542
- F-PLACE1004722//ESTs//7.5e-06:105:72//Hs.128796:AA485891
- 50 F-PLACE1004736//ESTs//1.7e-27:203:86//Hs.119593:AA700148
- F-PLACE1004740//ESTs//1.0e-25:174:89//Hs.29696:AA910680
- F-PLACE1004743
- F-PLACE1004751//ESTs, Highly similar to CMP-N-ACETYLNEURAMINATE-BETA-1,4-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE [Rattus norvegicus]//2.0e-41:260:90//Hs.6863:W52470
- 55 F-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds//1.7e-172:828:97//Hs.104715:AF084367
- F-PLACE1004777//Human myosin IXb mRNA, complete cds//1.0e-29:556:63//Hs.159629:U42391
- F-PLACE1004793
- F-PLACE1004804

- F-PLACE1004813//EST//2.8e-42:296.83//Hs.155725:AI310340
 F-PLACE1004814//ESTs. Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus laevis]//2.4e-78:415.95//Hs.80965:AA493284
- 5 F-PLACE1004815//Human mRNA for KIAA0364 gene, complete cds//4.3e-14:294.69//Hs.22111:AB002362
 F-PLACE1004824//ESTs//0.0072:128.69//Hs.164062:AA934047
 F-PLACE1004827//ESTs//0.78:38.100//Hs.18925:V30943
 F-PLACE1004836//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.78:338.57//Hs.8546:U97669
 F-PLACE1004838
 F-PLACE1004840//Protein phosphatase 1, catalytic subunit, beta isoform//0.89:200.66//Hs.21537:X80910
- 10 F-PLACE1004868
 F-PLACE1004885//ESTs//0.41:181.61//Hs.116796:AA633772
 F-PLACE1004900
 F-PLACE1004902//ESTs//4.7e-72:367.96//Hs.54971:AI424382
 F-PLACE1004913//ESTs//0.031:166.63//Hs.130110:AA904929
- 15 F-PLACE1004918//Human tumor susceptibility protein (TSG101) mRNA, complete cds//4.1e-24:402.64//Hs.118910:U82130
 F-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//9.7e-86:519.88//Hs.17839:AF099936
 F-PLACE1004934//ESTs//7.2e-43:231.78//Hs.133503:AA628592
- 20 F-PLACE1004937//ESTs//0.97:80.68//Hs.144264:C00851
 F-PLACE1004969
 F-PLACE1004972//Human retinoic acid- and interferon-inducible 58K protein RI58 mRNA, complete cds//0.031:235.60//Hs.27610:U34605
 F-PLACE1004979//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-43:331.83//Hs.153468:
- 25 AB011147
 F-PLACE1004982//ESTs//0.020:148.63//Hs.129377:AI218520
 F-PLACE1004985//ESTs//7.9e-05:372.61//Hs.87606:AA242831
 F-PLACE1005026//ESTs//4.6e-29:212.89//Hs.137451:AA351459
 F-PLACE1005027//ESTs//6.5e-91:455.97//Hs.30890:H15159
- 30 F-PLACE1005046//ESTs//3.7e-56:250.96//Hs.152730:AI308943
 F-PLACE1005052//EST//1.8e-36:370.73//Hs.123424:AA813594
 F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds//6.2e-161:761.98//Hs.14687:AB011148
 F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//3.0e-11:757.56//Hs.122967:AF059569
- 35 F-PLACE1005077//EST//0.79:283.591//Hs.89276:AA283899
 F-PLACE1005085//ESTs//3.5e-18:231.72//Hs.142654:AA324740
 F-PLACE1005086//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.9e-49:401.80//Hs.153468:AB011147
- 40 F-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds//8.2e-20:194.80//Hs.75437:L40401
 F-PLACE1005102//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//8.9e-18:538.62//Hs.104640:AF000561
 F-PLACE1005108//Treacher Collins syndrome susceptibility protein//0.73:405.57//Hs.73166:U76366
 F-PLACE1005111//ESTs//0.66:191.63//Hs.106446:N93227
- 45 F-PLACE1005128//Breakpoint cluster region protein BCR//5.6e-08:291.63//Hs.2557:Y00661
 F-PLACE1005146//ESTs. Weakly similar to hypothetical protein II [H.sapiens]//4.8e-12:360.63//Hs.142177:H11741
 F-PLACE1005162//Human mRNA for KIAA0118 gene, partial cds//3.9e-49:563.72//Hs.154326:D42087
 F-PLACE1005176//Homo sapiens mRNA for KIAA0641 protein, complete cds//0.82:259.60//Hs.128316:AB014541
- 50 F-PLACE1005181//ESTs. Weakly similar to No definition line found [C.elegans]//4.4e-126:583.99//Hs.25347:AI138605
 F-PLACE1005187//ESTs//6.2e-34:222.90//Hs.124265:N70417
 F-PLACE1005206//EST//0.089:167.62//Hs.140487:AA767009
- 55 F-PLACE1005232//ESTs. Weakly similar to synapse-associated protein sap47-1 [D.melanogaster]//0.56:192.60//Hs.47334:W72370
 F-PLACE1005243
 F-PLACE1005261//ESTs//0.52:245.58//Hs.6682:T76941

- F-PLACE1005266//Kallmann syndrome 1 sequence//7.8e-06:484:60//Hs.89591:M97252
 F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds//5.1e-150:706:98//Hs.118087:AB011182
 F-PLACE1005287//ESTs//8.1e-107:501:99//Hs.145703:AA447947
 5 F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//4.4e-37:597:66//Hs.101642:X60673
 F-PLACE1005308//High-mobility group (nonhistone chromosomal) protein 2//0.83:239:62//Hs.80684:X62534
 F-PLACE1005313
 10 F-PLACE1005327//ESTs, Weakly similar to No definition line found [C.elegans]//6.0e-81:459:91//Hs.146177:R51650
 F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569//3.7e-66:412:88//Hs.134031:AC004794
 F-PLACE1005335//Homo sapiens mRNA for KIAA0754 protein, partial cds//0.96:510:56//Hs.159183:AB018297
 F-PLACE1005373
 F-PLACE1005374//ESTs//7.5e-77:437:91//Hs.143266:AI141348
 15 F-PLACE1005409//ESTs//2.4e-05:267:63//Hs.163307:AA856751
 F-PLACE1005453//ESTs//0.12:333:58//Hs.134672:AI087951
 F-PLACE1005467//HOMEBOX/POU DOMAIN PROTEIN RDC-1//0.0043:148:67//Hs.74095:L20433
 F-PLACE1005471//ESTs//3.4e-24:135:97//Hs.49275:N66925
 F-PLACE1005477//Human Line-1 repeat mRNA with 2 open reading frames//3.5e-126:744:87//Hs.23094:M19503
 20 F-PLACE1005480//ESTs//3.7e-26:184:70//Hs.113198:N39323
 F-PLACE1005481//EST//0.27:153:64//Hs.120066:AA707973
 F-PLACE1005494//ESTs//2.4e-50:257:98//Hs.159003:AA633029
 F-PLACE1005502//ESTs//0.15:408:57//Hs.45106:AA504105
 F-PLACE1005526//ESTs//3.2e-61:305:98//Hs.122574:AA767647
 25 F-PLACE1005528//ESTs//9.9e-32:249:78//Hs.142531:N91572
 F-PLACE1005530//ESTs//1.0e-94:491:95//Hs.131731:AI339335
 F-PLACE1005550//ESTs//0.084:290:58//Hs.157775:AI359385
 F-PLACE1005554//EST//0.38:213:58//Hs.102749:N64144
 F-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR [Saccharomyces cerevisiae]//4.5e-51:258:97//Hs.7736:V81261
 30 F-PLACE1005574//ESTs//3.2e-09:236:66//Hs.146884:AI160278
 F-PLACE1005584//Fragile X mental retardation 2//1.2e-05:151:69//Hs.54472:U48436
 F-PLACE1005595//ESTs//2.1e-98:512:95//Hs.118552:W74594
 F-PLACE1005603//EST//1.0:90:66//Hs.111204:AA211851
 35 F-PLACE1005611//ESTs, Weakly similar to B0035.14 [C.elegans]//3.5e-32:197:92//Hs.8241:AA283057
 F-PLACE1005623//ESTs//3.0e-30:191:92//Hs.77570:N48234
 F-PLACE1005630//ESTs//2.3e-32:175:97//Hs.122278:AA781867
 F-PLACE1005639//ESTs//0.88:218:58//Hs.117389:AA701991
 F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//2.1e-151:721:98//Hs.8765:AF083255
 40 F-PLACE1005656//Ribonucleotide reductase M2 polypeptide//3.9e-53:480:74//Hs.75319:X59618
 F-PLACE1005666//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.086:223:59//Hs.27349:AB007917
 F-PLACE1005698//Human membrane-associated lectin type-C mRNA//6.1e-65:374:85//Hs.23759:M98457
 45 F-PLACE1005727//ESTs//8.7e-65:330:96//Hs.127027:AA935437
 F-PLACE1005730//ESTs//2.9e-14:270:67//Hs.28589:AI004944
 F-PLACE1005739//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//0.75:289:59//Hs.75111:D87258
 F-PLACE1005755//Insulin-like growth factor binding protein 2//3.6e-05:377:62//Hs.162:X16302
 50 F-PLACE1005763//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN [Rattus norvegicus]//5.7e-49:252:88//Hs.24309:AI125696
 F-PLACE1005799//ESTs//5.2e-13:392:58//Hs.110530:AA191493
 F-PLACE1005802
 F-PLACE1005803
 55 F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//4.5e-128:636:96//Hs.125315:AF027156
 F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//8.4e-156:739:98//Hs.11183:AF065482

- F-PLACE1005828/ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.1e-42:327.81//Hs.138404:R70986
- F-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)//0.038:436.58//Hs.75770:L41870
- F-PLACE1005845/ESTs//4.8e-50:309.89//Hs.107149:AI379497
- 5 F-PLACE1005850/ESTs//7.1e-40:253.79//Hs.158096:AA186905
- F-PLACE1005851/ESTs//7.6e-93:483.95//Hs.135608:AA732242
- F-PLACE1005876/ESTs//0.97:282.60//Hs.98664:AI381487
- F-PLACE1005884/ESTs//0.070:276.60//Hs.106057:AI031552
- F-PLACE1005890/ESTs//1.5e-91:500.93//Hs.136993:AA843300
- 10 F-PLACE1005898
- F-PLACE1005921
- F-PLACE1005923/ESTs//0.50:308.58//Hs.52489:R61504
- F-PLACE1005925/ESTs//0.024:93.68//Hs.149868:AI288274
- F-PLACE1005932//TYROSINE-PROTEIN KINASE RECEPTOR EPH PRECURSOR//0.97:342.57//Hs.89839: M18391
- 15 F-PLACE1005934/ESTs//8.6e-10:74.93//Hs.25092:AA922142
- F-PLACE1005936/DNA excision repair protein ERCC5//1.0:144.63//Hs.48576:X69978
- F-PLACE1005951//B94 PROTEIN//0.00025:371.61//Hs.75522:M92357
- F-PLACE1005953/ESTs//2.8e-06:290.61//Hs.140996:R73468
- 20 F-PLACE1005955/ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.15:136.66//Hs.107747:AI357868
- F-PLACE1005966/Human zinc finger/leucine zipper protein (AF10) mRNA, complete cds//1.0:215.63//Hs.7885: U13948
- F-PLACE1005968
- F-PLACE1005990
- 25 F-PLACE1006002//Putative mismatch repair/binding protein hMSH3//1.9e-48:312.77//Hs.42674:U61981
- F-PLACE1006003/EST//0.00018:171.67//Hs.138862:W73256
- F-PLACE1006011
- F-PLACE1006017/ESTs//3.1e-21:159.88//Hs.142173:AA757743
- F-PLACE1006037//Homo sapiens mRNA for KIAA0789 protein, complete cds//0.021:202.64//Hs.158319: AB018332
- 30 F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine//1.1e-148:719.97//Hs.98782:X99906
- F-PLACE1006076/EST//0.29:92.64//Hs.161536:N80395
- F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds//4.1e-147:679.99//Hs.4976: AF039023
- 35 F-PLACE1006129
- F-PLACE1006139
- F-PLACE1006143//Human mRNA for KIAA0355 gene, complete cds//9.3e-43:357.79//Hs.153014:AB002353
- F-PLACE1006157/ESTs, Weakly similar to ETX1 (alternatively spliced) [H.sapiens]//2.9e-12:119.84//Hs.23153: R92857
- 40 F-PLACE1006159/ESTs//2.3e-87:443.96//Hs.23740:H17868
- F-PLACE1006164/ESTs//0.099:223.60//Hs.8108:AA902721
- F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//1.1e-68:333.92//Hs.152894:AC005239
- F-PLACE1006170/ESTs//0.081:171.67//Hs.135187:AI074005
- F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//1.2e-150:694.99//Hs.30464:AF091433
- 45 F-PLACE1006195/ESTs//8.9e-14:229.70//Hs.141470:N49608
- F-PLACE1006196/ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog//3.5e-59:369.88//Hs. 135623:AA134719
- F-PLACE1006205
- F-PLACE1006223/ESTs, Weakly similar to TERATOCARCINOMA-DERIVED GROWTH FACTOR 1 [H.sapiens] //0.0089:166.63//Hs.127179:AI279486
- 50 F-PLACE1006225
- F-PLACE1006236/EST//0.060:89.69//Hs.136977:AA830668
- F-PLACE1006239/ESTs//0.028:105.66//Hs.142336:AA358185
- F-PLACE1006246/ESTs//0.060:330.60//Hs.105695:AI085802
- 55 F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//7.3e-168:791.98//Hs.31921: AB014548
- F-PLACE1006262
- F-PLACE1006288//Homo sapiens mRNA for Pex3 protein//4.8e-37:186.100//Hs.7277:AJ001625

- F-PLACE1006318
F-PLACE1006325//ESTs//3.7e-25.206.83//Hs.102319:AI246503
F-PLACE1006335//ESTs//2.0e-27.161.95//Hs.163529:AI361492
F-PLACE1006357//ESTs//0.013:268.61//Hs.105775:AA526249
5 F-PLACE1006360//ESTs//4.8e-27.146.98//Hs.100739:Z98481
F-PLACE1006368//Homo sapiens clone 24540 mRNA sequence//0.65:272.59//Hs.153529:AF070581
F-PLACE1006371//Homo sapiens jerky gene product homolog mRNA, complete cds//2.6e-07.403.61//Hs.105940:AF004715
F-PLACE1006382//EST//0.98:77.68//Hs.136933:AA814693
10 F-PLACE1006385//Homo sapiens epsin 2b mRNA, complete cds//1.6e-111:539.97//Hs.22396:AF062085
F-PLACE1006412//Human mRNA for KIAA0298 gene, complete cds//1.0e-36:424.74//Hs.21560:AB002296
F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds//4.3e-111:525.98//Hs.131846:AF069735
F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds//2.2e-24:531.65//Hs.101414:AB011129
15 F-PLACE1006445//Homo sapiens chromosome 16 zinc finger protein ZNF200 (ZNF200) mRNA, complete cds//1.0:248.60//Hs.88219:AF060866
F-PLACE1006469//Human SA mRNA for SA gene product, complete cds//0.24:210.62//Hs.89659:AC004381
F-PLACE1006470
20 F-PLACE1006482//Homo sapiens basic-leucine zipper transcription factor MafK (MAFK) mRNA, complete cds//5.0e-46:520.71//Hs.131953:AF059194
F-PLACE1006488//ESTs//6.2e-47:239.97//Hs.158161:AA312511
F-PLACE1006492//ESTs//0.82:37.100//Hs.160417:AA488493
F-PLACE1006506//HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2//0.98:505.56//Hs.75063:AL023584
25 F-PLACE1006521//ESTs//0.032:222.63//Hs.23171:AA706542
F-PLACE1006531//EST//2.1e-53:258.100//Hs.117316:AA699358
F-PLACE1006534//EST//1.8e-07:78.89//Hs.157551:AI356219
F-PLACE1006540//Homo sapiens mRNA for cadherin-6, complete cds//0.96:383.58//Hs.32963:D31784
30 F-PLACE1006552//Human (clone N5-4) protein p84 mRNA, complete cds//0.058:464.57//Hs.1540:L36529
F-PLACE1006598//Homo sapiens mRNA for KIAA0737 protein, complete cds//4.1e-17:372.65//Hs.17630:AB018280
F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//2.2e-168:781.99//Hs.155377:U97670
35 F-PLACE1006617//ESTs//6.0e-08:354.60//Hs.42624:H99088
F-PLACE1006626//NUCLEOLIN//0.0044:186.66//Hs.79110:M60858
F-PLACE1006629//Homo sapiens (clone s22171) mRNA fragment//0.097:229.63//Hs.26956:L40396
F-PLACE1006640//ESTs//0.00019:380.59//Hs.13672:AI131473
40 F-PLACE1006673//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//1.6e-12:113.83//Hs.3385:N25917
F-PLACE1006678
F-PLACE1006704//Homo sapiens ALR mRNA, complete cds//0.16:284.60//Hs.153638:AF010403
F-PLACE1006731//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//1.6e-05:382.63//Hs.43627:U35612
45 F-PLACE1006754//Biliary glycoprotein//8.9e-27:305.72//Hs.50964:X16354
F-PLACE1006760//ESTs//0.10:207.62//Hs.152589:AA954152
F-PLACE1006779//Kallmann syndrome 1 sequence//0.00025:251.64//Hs.89591:M97252
F-PLACE1006782//ESTs//1.2e-90:423.100//Hs.132826:AI075783
F-PLACE1006792//ESTs//1.5e-10:439.58//Hs.138501:AI051228
50 F-PLACE1006795//TYROSINE-PROTEIN KINASE RECEPTOR ETK1 PRECURSOR//4.5e-10:84.95//Hs.123642:M83941
F-PLACE1006800//ESTs//0.00068:360.61//Hs.157876:AI422017
F-PLACE1006805//ESTs//4.6e-103:491.98//Hs.140465:AA769892
F-PLACE1006815//Homo sapiens mRNA for KIAA0618 protein, complete cds//0.47:403.56//Hs.15832:AB014518
F-PLACE1006819//Human Line-1 repeat mRNA with 2 open reading frames//3.7e-103:619.87//Hs.23094:M19503
55 F-PLACE1006829//ESTs//1.5e-22:141.94//Hs.142988:AA142876
F-PLACE1006860//EST//0.0062:206.65//Hs.158793:AI376773
F-PLACE1006867//ESTs//0.068:218.62//Hs.91166:AA551273
F-PLACE1006878//Homo sapiens mRNA for KIAA0711 protein, complete cds//1.0:268.58//Hs.5333:AB018254

- F-PLACE1006883//ESTs//1.6e-75:398.94//Hs.119544:T95601
 F-PLACE1006901//ESTs//1.9e-13:87.96//Hs.134737:AI089187
 F-PLACE1006904//EST//1.0-91:70//Hs.148270:AA906443
 F-PLACE1006917
 5 F-PLACE1006932//ESTs//0.98:110:70//Hs.100855:AI423913
 F-PLACE1006935//EST//1.0-92:65//Hs.124554:AA847211
 F-PLACE1006956//PERIPHERIN//0.13:443:57//Hs.37044:L14565
 F-PLACE1006958//Heat shock 70kD protein 4//6.4e-40:456.70//Hs.127.L12723
 10 F-PLACE1006961//ESTs. Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae]//3.2e-07:67.98//Hs.21806:AA630312
 F-PLACE1006962//H.sapiens ir1B mRNA//2.3e-16:202:71//Hs.135202:X63417
 F-PLACE1006966//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds//0.14:191:67//Hs.8813:AF032922
 15 F-PLACE1006989//Cyclin B1//0.99:224:59//Hs.23960:M25753
 F-PLACE1007014//Homo sapiens NBMPR-insensitive nucleoside transporter ei (ENT2) mRNA, complete cds//3.1e-05:594.58//Hs.32951:AF034102
 F-PLACE1007021//ESTs//7.2e-89:446.96//Hs.7111:U55971
 F-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//1.0e-117:775.84//Hs.23094:M19503
 F-PLACE1007053//Homo sapiens mRNA for ARNO3 protein//0.35:63:82//Hs.129811:AJ223957
 20 F-PLACE1007068//Polycystic kidney disease 1 (autosomal dominant)//0.2:361:60//Hs.75813:L33243
 F-PLACE1007097//ESTs//2.9e-25:197.83//Hs.105665:H78987
 F-PLACE1007105//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)//0.18:268:63//Hs.904:U84010
 F-PLACE1007111//EST//0.0066:260.60//Hs.147903:AI223385
 25 F-PLACE1007112
 F-PLACE1007132//ESTs//3.1e-30:195.76//Hs.46158:AI160121
 F-PLACE1007140//TRANSCRIPTION ELONGATION FACTOR S-II//0.13:302:60//Hs.78869:M81601
 F-PLACE1007178//ESTs//9.6e-54:289.95//Hs.12251:H12965
 F-PLACE1007226//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.00090:412:59//Hs.8546:U97669
 30 F-PLACE1007238//Human plectin (PLEC1) mRNA, complete cds//1.4e-07:492.64//Hs.79706:U53204
 F-PLACE1007239//Human mRNA for transcription elongation factor S-II, hS-II-T1, complete cds//0.2e-58:405.87//Hs.80598:D50495
 F-PLACE1007242//EST//0.014:55:89//Hs.88432:AA262141
 F-PLACE1007243//ESTs//2.0e-43:227.97//Hs.124775:AA648467
 35 F-PLACE1007257//Homo sapiens mRNA for dia-156 protein//3.7e-144:677.98//Hs.121556:Y15909
 F-PLACE1007274
 F-PLACE1007276//ATPase, Cu++ transporting, alpha polypeptide (Menkes syndrome)//0.94:167:64//Hs.606:L06133
 F-PLACE1007282
 40 F-PLACE1007286//ESTs//1.0e-25:333.71//Hs.134860:AI091436
 F-PLACE1007301//EST//0.78:171:61//Hs.160990:H52412
 F-PLACE1007317//Homo sapiens oxysterol 7 alpha-hydroxylase (CYP7b1) mRNA, complete cds//0.88:298.58//Hs.144877:AF029403
 F-PLACE1007342
 45 F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds//1.7e-121:567.98//Hs.76596:AF096870
 F-PLACE1007367//H.sapiens mRNA for MACH-alpha-2 protein//2.2e-55:532.77//Hs.19949:X98173
 F-PLACE1007375
 F-PLACE1007386//ESTs//0.00066:61.91//Hs.149318:AI248642
 50 F-PLACE1007402//EST//1.7e-06:193:65//Hs.132124:AI041287
 F-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence//3.8e-18:128.92//Hs.14387:AF093771
 F-PLACE1007416
 F-PLACE1007450//ESTs//2.6e-36:194.97//Hs.22359:AI024436
 55 F-PLACE1007452//EST//1.8e-34:197:94//Hs.134795:AI090359
 F-PLACE1007454//Homo sapiens (clone s153) mRNA fragment//2.6e-53:317.93//Hs.6445:L40391
 F-PLACE1007460//ESTs//0.0012:168.64//Hs.151708:AA554714
 F-PLACE1007478//ESTs//1.0e-42:440.74//Hs.141722:AA769103

- F-PLACE1007484//ESTs//7.1e-18:127.91//Hs.100251:AA535975
F-PLACE1007488
- F-PLACE1007507//ESTs//1.2e-99:274.98//Hs.123462:AA903385
F-PLACE1007511//Keratin 19//4.2e-31:586.64//Hs.23761:Y00503
- 5 F-PLACE1007524//ESTs//6.8e-71:356.97//Hs.163067:AA897296
F-PLACE1007525//ESTs//0.073:242.59//Hs.128711:AA856979
F-PLACE1007537//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.93:468.57//Hs.113283:AF018080
F-PLACE1007544//ESTs//1.7e-74:360.98//Hs.126632:AI076755
F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete cds//1.0e-70:733.71//Hs.65238:
- 10 AB014561
F-PLACE1007557//EST//0.58:80:72//Hs.130267:AI001863
F-PLACE1007583//ESTs//1.8e-46:234.98//Hs.155071:AA584257
F-PLACE1007598//ESTs//1.7e-83:400.99//Hs.120206:AI089163
F-PLACE1007618//Homo sapiens mRNA for KIAA0633 protein, partial cds//7.2e-12:778.56//Hs.33010:AB014533
- 15 F-PLACE1007621
F-PLACE1007632//ESTs//1.7e-32:175.97//Hs.122278:AA781867
F-PLACE1007645
F-PLACE1007649
F-PLACE1007677//ESTs//3.0e-13:125.82//Hs.143382:AA476266
- 20 F-PLACE1007688//ESTs//6.8e-06:311.61//Hs.132926:AI027055
F-PLACE1007690//ESTs//1.9e-13:83.98//Hs.150088:AI348503
F-PLACE1007697//TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR//0.99:216.63//Hs.1103:X02812
F-PLACE1007705//Human mRNA for RTP, complete cds//4.8e-58:637.70//Hs.75789:D87953
F-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//4.1e-149:709.97//Hs.4812:
- 25 AF061243
F-PLACE1007725//ESTs, Weakly similar to No definition line found [C.elegans]//4.5e-36:233.89//Hs.108797:
AA476815
F-PLACE1007729//ESTs, Moderately similar to RETRO VIRUS-RELATED PROTEASE [H.sapiens]//0.00033:270:
64//Hs.104129:AA923278
- 30 F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.6e-156:728.98//Hs.153121:
AB014585
F-PLACE1007737//Coagulation factor II (thrombin) receptor//1.1e-18:364.68//Hs.159347:M62424
F-PLACE1007743//ESTs//0.029:421.58//Hs.106090:AA457030
F-PLACE1007746//ESTs//6.7e-55:330.89//Hs.153392:AI089469
- 35 F-PLACE1007791//EST//0.39:261.62//Hs.145991:AI277656
F-PLACE1007807//ESTs//2.0e-54:385.83//Hs.163930:AA640504
F-PLACE1007810//ESTs//6.1e-53:416.81//Hs.152395:AA533107
F-PLACE1007829//EST//0.28:271.61//Hs.125514:AA883841
F-PLACE1007843//EST//0.020:307.59//Hs.145535:AI261635
- 40 F-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//6.3e-38:396.77//Hs.23094:M19503
F-PLACE1007852
F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//1.3e-190:894.98//Hs.28020:
AB018309
F-PLACE1007868//ESTs//3.0e-50:333.86//Hs.15792:AI038387
- 45 F-PLACE1007877
F-PLACE1007897//EST//1.0:59.72//Hs.138770:N70943
F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//7.3e-156:755.97//Hs.
92381:AB007956
F-PLACE1007946//ESTs//8.9e-16:250.68//Hs.88527:N24002
- 50 F-PLACE1007954//ESTs//1.6e-05:76.90//Hs.63314:AA056538
F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//8.9e-173:813.98//Hs.
5671:AF084530
F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//8.2e-155:
730.98//Hs.78106:AF079529
- 55 F-PLACE1007969//ESTs, Weakly similar to hnRNA-binding protein M4 [H.sapiens]//5.1e-45:264.92//Hs.42222:
W28567
F-PLACE1007990//ESTs//1.2e-104:493.99//Hs.118445:AI097043
F-PLACE1008000//Homo sapiens vcl1 mRNA, complete cds//5.7e-63:578.74//Hs.150380:AF087693

- F-PLACE1008002//ESTs//0.52:236:59//Hs.134292:AA603031
 F-PLACE10080044
 F-PLACE1008045//COL10A1//0.29:221:58//Hs.37075:X60382
 5 F-PLACE1008080//Human homeodomain protein (Prox 1) mRNA, complete cds//0.00037:151:71//Hs.159437:U44060
 F-PLACE1008095//Human hybrid receptor gp250 precursor mRNA, complete cds//1.0:461:58//Hs.155494:U60975
 F-PLACE1008111//Homo sapiens B lymphocyte chemoattractant BLC mRNA, complete cds//0.034:497:58//Hs.100431:AF044197
 10 F-PLACE1008122//ESTs//0.95:198:60//Hs.126776:N28769
 F-PLACE1008129//ESTs//1.1e-99:499:96//Hs.131807:AA778874
 F-PLACE1008132//EST//3.3e-27:218:83//Hs.145258:AI218683
 F-PLACE1008177//ESTs. Moderately similar to meiosis-specific nuclear structural protein 1 [M.musculus]//5.1e-20:124:95//Hs.146238:AI263135
 15 F-PLACE1008181//ESTs//0.018:285:61//Hs.88843:AA281427
 F-PLACE1008198//ESTs//5.9e-07:410:60//Hs.63348:AA643524
 F-PLACE1008201
 F-PLACE1008209
 F-PLACE1008231//ESTs//0.40:188:61//Hs.130266:AI001856
 20 F-PLACE1008244//Miller-Dieker syndrome chromosome region//0.22:247:61//Hs.77318:L13385
 F-PLACE1008273
 F-PLACE1008275//EST//0.77:74:71//Hs.145907:AI275113
 F-PLACE1008280//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.6e-25:389:70//Hs.159897:AB007970
 25 F-PLACE1008309//Homo sapiens serine phosphatase FCP1a (FCP1) mRNA, complete cds//0.16:263:63//Hs.4076:AF081287
 F-PLACE1008329//EST//1.3e-09:94:85//Hs.144135:R82071
 F-PLACE1008330//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.5e-45:291:83//Hs.101414:AB011129
 30 F-PLACE1008331//ESTs. Weakly similar to ORF2-like protein [H. sapiens]//5.4e-74:356:98//Hs.105382:AA496362
 F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//3.4e-139:659:98//Hs.5734:AB014579
 F-PLACE1008368//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.011:355:60//Hs.122967:AF059569
 F-PLACE1008369//ESTs//0.00074:443:61//Hs.102756:AA526911
 35 F-PLACE1008392//EST//7.4e-08:324:60//Hs.149930:AI289171
 F-PLACE1008398
 F-PLACE1008401//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//2.5e-09:461:62//Hs.25674:AF072242
 F-PLACE1008402//Homo sapiens mRNA for p115, complete cds//1.4e-149:711:98//Hs.7763:D86326
 40 F-PLACE1008405//ESTs//2.8e-102:529:95//Hs.116278:AA628943
 F-PLACE1008424//Human DNA sequence from clone 753P9 on chromosome Xq25-26.1. Contains the gene coding for Aminopeptidase P (EC 3.4.11.9, XAA-Pro/X-Pro/Proline/Aminoacylproline Aminopeptidase) and a novel gene. Contains ESTs, STSs, GSSs and a gaaa repeat polymorphism//0.98:113:67//Hs.57922:AL023653
 F-PLACE1008426//ESTs//3.2e-77:393:95//Hs.37585:W28499
 45 F-PLACE1008429//Orf1 5' to PD-ECGF/TP...orf2 5' to PD-ECGF/TP [human, epidermoid carcinoma cell line A431, mRNA, 3 genes, 1718 nt]//0.019:530:58//Hs.72248:S72487
 F-PLACE1008437
 F-PLACE1008455//ESTs//0.51:279:61//Hs.122319:AA782335
 F-PLACE1008457//ESTs//3.0e-30:229:75//Hs.60740:AA053901
 50 F-PLACE1008465//Human mRNA for KIAA0383 gene, partial cds//0.0084:210:63//Hs.27590:AB002381
 F-PLACE1008488//Human density enhanced phosphatase-1 mRNA, complete cds//6.8e-07:469:60//Hs.1177:U10886
 F-PLACE1008524//Homo sapiens TWIK-related acid-sensitive K+ channel (TASK) mRNA, complete cds//1.0:304:60//Hs.24040:AF006823
 55 F-PLACE1008531//ESTs//1.1e-17:190:76//Hs.156041:AI274697
 F-PLACE1008532//Thromboxane A2 receptor//5.6e-17:231:71//Hs.89887:D38081
 F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter//1.1e-45:507:71//Hs.8003:AC004997
 F-PLACE1008568//Homo sapiens mRNA for neuronatin alpha, complete cds//1.0:95:71//Hs.117546:U31767

- F-PLACE1008584//ESTs//1.4e-13:252.68//Hs.153429:Al283069
 F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.9e-175:812.98//Hs.23255:AB018334
 F-PLACE1008621//ESTs, Weakly similar to reverse transcriptase [H.sapiens]//1.2e-15:350.66//Hs.151087:AA649326
 5 F-PLACE1008625//ESTs//0.66:269:57//Hs.94998:N26794
 F-PLACE1008626//ESTs//0.55:69.71//Hs.92096:F10560
 F-PLACE1008627//ESTs//3.0e-62:302.99//Hs.120766:H82458
 F-PLACE1008629//EST//0.0012:174.67//Hs.121195:AA757211
 10 F-PLACE1008630//ESTs//4.5e-77:371.99//Hs.132960:AA252394
 F-PLACE1008643//Human mRNA for PK-120//4.7e-25:299.64//Hs.76415:D38535
 F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//3.5e-135:622.99//Hs.147967:AF044333
 F-PLACE1008693//EST//0.19:36.94//Hs.138817:N93728
 15 F-PLACE1008696//Human mitochondrial NADH dehydrogenase-ubiquinone Fe-S protein 8, 23 kDa subunit precursor (NDUF58) nuclear mRNA encoding mitochondrial protein, complete cds//8.3e-25:137.97//Hs.90443:AF038406
 F-PLACE1008715//Homo sapiens mRNA for matrilin-3//0.99:183.63//Hs.119534:AJ224741
 F-PLACE1008748//ESTs//0.88:204.63//Hs.15139:AA527080
 20 F-PLACE1008757//ESTs, Weakly similar to unknown protein [R.norvegicus]//4.3e-17:285.69//Hs.35460:H65503
 F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds//1.4e-121:503.97//Hs.6458:AF060543
 F-PLACE1008798//ESTs, Weakly similar to putative p150 [H.sapiens]//0.30:127.68//Hs.111380:AA258772
 F-PLACE1008807//ESTs//0.81:346.58//Hs.116901:AA663542
 25 F-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 mRNA, complete cds//6.7e-104:376.98//Hs.7179:AF011905
 F-PLACE1008813//Glutamate decarboxylase 1 (brain, 67kD)//0.17:318.61//Hs.75668:M81883
 F-PLACE1008851//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 2 HOMOLOG [Plasmodium falci-
 ciparum (isolate k1 / thailand)]//0.73:354.59//Hs.26322:AA156858
 30 F-PLACE1008854//ESTs//3.0e-26:391.66//Hs.133260:AI052728
 F-PLACE1008867//ESTs//5.9e-08:64.93//Hs.91115:AI221563
 F-PLACE1008887//Human Line-1 repeat mRNA with 2 open reading frames//5.5e-51:701.68//Hs.23094:M19503
 F-PLACE1008902//EST//0.85:425.60//Hs.140573:AA826323
 F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.1e-159:753.98//Hs.62318:AB018308
 35 F-PLACE1008925//ESTs//0.025:133.67//Hs.103218:W84771
 F-PLACE1008934//ESTs//0.27:307.59//Hs.135168:AI394026
 F-PLACE1008941//ESTs//3.3e-53:266.98//Hs.108677:AA488937
 F-PLACE1008947//Human TBP-associated factor (TAFII130) mRNA, partial cds//2.4e-13:625.58//Hs.24644:U75308
 40 F-PLACE1009020//ESTs//3.3e-11:122.81//Hs.131777:AI024950
 F-PLACE1009027//Homo sapiens mRNA for doublecortin//1.2e-151:763.96//Hs.34780:AJ003112
 F-PLACE1009039//EST//0.76:111.63//Hs.160997:H55762
 F-PLACE1009045//ESTs//2.2e-76:399.95//Hs.114919:AA457689
 45 F-PLACE1009048//GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR//2.6e-16:93.100//Hs.119689:S70585
 F-PLACE1009050//ESTs//1.4e-92:451.98//Hs.66373:Al239698
 F-PLACE1009060//ESTs//1.4e-14:86.100//Hs.131725:AI090525
 F-PLACE1009090//ESTs//2.7e-20:198.78//Hs.110044:AA181800
 50 F-PLACE1009091//ESTs//0.99:342.57//Hs.46903:AI093091
 F-PLACE1009094//ESTs//1.0:225.63//Hs.120374:AI337031
 F-PLACE1009099//H.sapiens ZNF81 gene//2.2e-79:733.74//Hs.104020:X68011
 F-PLACE1009110//ESTs//2.6e-91:453.96//Hs.143756:AI040890
 F-PLACE1009111//ESTs//2.7e-15:159.77//Hs.146811:AA410788
 55 F-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//1.1e-139:671.97//Hs.99742:AF035586
 F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds//1.1e-24:718.59//Hs.35804:D25215
 F-PLACE1009150//Human HsLIM15 mRNA for HsLIM15, complete cds//1.7e-50:440.78//Hs.37181:D64108

- F-PLACE1009155//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.0e-46:440:69//Hs.158095:AB007953
- F-PLACE1009158//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//0.28:245:61//Hs.92614:M62302
- 5 F-PLACE1009166//EST//0.98:114:67//Hs.137706:AA977250
- F-PLACE1009172//EST//6.2e-34:257:84//Hs.161081:N22770
- F-PLACE1009174//ESTs//6.0e-24:234:77//Hs.155196:A1282821
- F-PLACE1009183//EST//0.021:261:62//Hs.144222:N90100
- 10 F-PLACE1009186//ESTs. Weakly similar to No definition line found [C.elegans]//3.6e-117:588:95//Hs.54943:Z78396
- F-PLACE1009190//EST//0.046:95:70//Hs.131646:A1025689
- F-PLACE1009200//EST//2.5e-41:195:78//Hs.162404:AA573131
- F-PLACE1009230//CARCINOEMBRYONIC ANTIGEN PRECURSOR//5.3e-29:157:77//Hs.146403:M29540
- F-PLACE1009246//EST//0.13:178:62//Hs.23298:R22575
- 15 F-PLACE1009298//ESTs. Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae]//1.9e-21:121:98//Hs.124768:AA307735
- F-PLACE1009308//SERUM PROTEIN MSE55//0.44:195:62//Hs.148101:M88338
- F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mRNA, complete cds//9.7e-08:411:59//Hs.23731:U83192
- 20 F-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-91:594:86//Hs.23094:M19503
- F-PLACE1009335//EST//0.037:169:63//Hs.148875:A1240767
- F-PLACE1009338//ESTs//5.7e-22:123:98//Hs.66783:AA059473
- F-PLACE1009368
- F-PLACE1009375
- 25 F-PLACE1009388//Homo sapiens KIAA0395 mRNA, partial cds//1.7e-41:317:81//Hs.43681:AL022394
- F-PLACE1009398//Zinc finger protein 84 (HPF2)//1.4e-79:730:74//Hs.9450:M27878
- F-PLACE1009404//MICROTUBULE-ASSOCIATED PROTEIN TAU//0.099:207:61//Hs.101174:AF047863
- F-PLACE1009410//Homo sapiens BAF57 (BAF57) gene, complete cds//1.4e-27:210:86//Hs.3404:AF035262
- F-PLACE1009434//Human mRNA for KIAA0005 gene, complete cds//2.8e-45:599:68//Hs.155291:D13630
- 30 F-PLACE1009443//H.sapiens 5T4 gene for 5T4 Oncofetal antigen//0.11:350:58//Hs.82128:AJ012159
- F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//1.5e-22:146:93//Hs.76987:AF012872
- F-PLACE1009459//H.sapiens gap gene mRNA, complete CDS//1.0:241:60//Hs.151641:Z24680
- F-PLACE1009468//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//0.00039:347:60//Hs.994:M95678
- 35 F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A//1.4e-91:464:96//Hs.155049:AC004531
- F-PLACE1009477//ESTs//0.30:221:61//Hs.107287:A1308839
- F-PLACE1009493//Homo sapiens mRNA for LAK-4p, complete cds//1.6e-30:608:63//Hs.16165:AB002405
- F-PLACE1009524//Human Sec7p-like protein mRNA, partial cds//2.3e-68:526:78//Hs.8517:U070728
- 40 F-PLACE1009539//ESTs//3.3e-18:186:83//Hs.71922:AA148417
- F-PLACE1009542//EST//7.8e-11:265:65//Hs.159692:A1416956
- F-PLACE1009571//ESTs//6.1e-15:94:97//Hs.151458:AA600866
- F-PLACE1009581//Microtubule-associated protein 1A//1.0:196:59//Hs.147918:U38291
- F-PLACE1009595//EST//1.8e-28:179:92//Hs.60090:AA004806
- 45 F-PLACE1009596//ESTs. Weakly similar to LIS-1 protein [H.sapiens]//4.1e-16:281:66//Hs.13889:A1341394
- F-PLACE1009607//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.9e-52:313:79//Hs.113283:AF018080
- F-PLACE1009613//ESTs//0.50:297:60//Hs.25114:A1074011
- F-PLACE1009621//ESTs//1.4e-98:470:98//Hs.124695:A1094085
- F-PLACE1009622//ESTs//9.8e-14:94:93//Hs.117227:AA682773
- 50 F-PLACE1009637//ESTs//4.9e-92:440:98//Hs.126587:AA917087
- F-PLACE1009639
- F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//4.4e-173:816:98//Hs.21862:AB011159
- F-PLACE1009665//ESTs//9.1e-45:383:79//Hs.61199:AA024494
- 55 F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//8.1e-149:701:98//Hs.109590:AF062534
- F-PLACE1009708//ESTs. Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN HXT14-PHA2 INTERGENIC REGION [S.cerevisiae]//7.5e-51:295:92//Hs.48541:AA827926
- F-PLACE1009721//EST//0.18:467:58//Hs.124358:AA830650

- F-PLACE1009731//ESTs//1.0:207:63//Hs.60440:AA195789
 F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//1.3e-126:602:98//Hs.154320:AF046024
 F-PLACE1009794//ESTs//4.0e-41:252:91//Hs.42927:N20989
 F-PLACE1009798//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubi-
 quinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, Cl-MLRQ), Tubulin Beta and Proto-oncogene
 Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene
 similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs//5.5e-
 130:600:95//Hs.16411:AL030996
 F-PLACE1009845
 F-PLACE1009861
 F-PLACE1009879//ESTs//6.3e-12:293:66//Hs.147071:AI200021
 F-PLACE1009886
 F-PLACE1009888//EST//0.044:255:58//Hs.160695:AI282889
 F-PLACE1009908
 F-PLACE1009921//Apoptosis (APO-1) antigen 1//0.62:407:57//Hs.82359:X63717
 F-PLACE1009924//EST//2.9e-29:155:99//Hs.162937:AA634379
 F-PLACE1009925
 F-PLACE1009935//CATHEPSIN K PRECURSOR//0.43:153:66//Hs.83942:X82153
 F-PLACE1009947//ESTs//1.8e-07:56:100//Hs.149940:AI306446
 F-PLACE1009971//Acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain//0.89:243:61//Hs.127610:Z80345
 F-PLACE1009992//ESTs//0.99:123:68//Hs.91202:AI139114
 F-PLACE1009995//ESTs, Weakly similar to C01A2.4 [C.elegans]//3.3e-24:174:88//Hs.11449:AI201540
 F-PLACE1009997//Homo sapiens mRNA for KIAA0629 protein, partial cds//3.7e-36:196:98//Hs.153545:
 AB014529
 F-PLACE1010023
 F-PLACE1010031//ESTs//1.3e-16:132:87//Hs.46847:W02878
 F-PLACE1010053//ESTs, Moderately similar to M-phase phosphoprotein 4 [H.sapiens]//5.2e-63:312:98//Hs.
 142151:AA984061
 F-PLACE1010069//ESTs//6.6e-33:171:98//Hs.128844:AA977596
 F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//5.9e-168:792:98//Hs.11183:
 AF065482
 F-PLACE1010076//ESTs//0.88:379:55//Hs.5884:N21424
 F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.6e-154:727:98//Hs.5003:AB007925
 F-PLACE1010089//ESTs, Highly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE [Mus
 musculus]//1.8e-38:212:95//Hs.98067:AA236822
 F-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.norvegicus]//1.8e-08:100:89//Hs.11469:
 U69567
 F-PLACE1010102//Homo sapiens stimulator of Fe transport mRNA, complete cds//0.0035:339:60//Hs.129683:
 AF020761
 F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//1.2e-26:728:60//Hs.
 122967:AF059569
 F-PLACE1010106//EST//8.5e-28:394:70//Hs.142044:AA166682
 F-PLACE1010134//H.sapiens hbrn mRNA//1.2e-14:380:64//Hs.77590:X72889
 F-PLACE1010148//Human trans-Golgi p230 mRNA, complete cds//0.26:708:57//Hs.158245:U41740
 F-PLACE1010152
 F-PLACE1010181//EST//1.3e-21:312:71//Hs.141501:N50792
 F-PLACE1010194//ESTs//2.6e-55:284:97//Hs.155940:AA459582
 F-PLACE1010202//ESTs, Weakly similar to No definition line found [C.elegans]//2.3e-72:391:94//Hs.35225:
 H69637
 F-PLACE1010231
 F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.9e-146:693:97//Hs.27349:
 AB007917
 F-PLACE1010270//ESTs//2.0e-104:514:98//Hs.124062:H04590
 F-PLACE1010274//ESTs, Weakly similar to C01A2.4 [C.elegans]//6.8e-25:149:93//Hs.11449:AI201540
 F-PLACE1010293//EST//4.5e-36:358:74//Hs.162398:AA572813
 F-PLACE1010310//HOMEBOX/POU DOMAIN PROTEIN RDC-1//2.1e-10:352:62//Hs.74095:L20433
 F-PLACE1010321//Human hSIAH2 mRNA, complete cds//0.071:604:58//Hs.20191:U76248
 F-PLACE1010324//ESTs//0.22:286:58//Hs.130853:AI367875

- F-PLACE1010329//EST//5.7e-05:351:60//Hs.120644:AA742659
 F-PLACE1010341//EST//4.5e-16:255:72//Hs.141206:H53117
 F-PLACE1010362//ESTs//1.9e-41:246:92//Hs.128771:AA236855
 F-PLACE1010364//EST//0.11:292:58//Hs.135771:AI005648
 5 F-PLACE1010383//EST//6.1e-08:107:76//Hs.136441:AA564986
 F-PLACE1010401
 F-PLACE1010481//Human BLU protein (BLU) mRNA, complete cds//0.94:254:61//Hs.125257:U70824
 F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds//7.2e-152:702:99//Hs.13313:AF039081
 10 F-PLACE1010492//ESTs//1.0:201:60//Hs.146036:AI038500
 F-PLACE1010522//ESTs//3.9e-52:263:97//Hs.125149:AI302100
 F-PLACE1010529//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.0:175:64//Hs.159273:AF054177
 15 F-PLACE1010547//ESTs//0.96:288:57//Hs.87156:AA233472
 F-PLACE1010562//EST//1.0:164:66//Hs.147868:AI222979
 F-PLACE1010579//EST//0.39:279:58//Hs.158960:AI380148
 F-PLACE1010580//ESTs. Moderately similar to PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06 [Schizosaccharomyces pombe]//3.8e-31:193:91//Hs.145229:N44661
 20 F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14p (PEX14) mRNA, complete cds//9.9e-148:707:97//Hs.19851:AF045186
 F-PLACE1010616//EST//3.1e-43:213:100//Hs.128215:AA972394
 F-PLACE1010622//NUCLEOLIN//0.00040:282:60//Hs.79110:M60858
 F-PLACE1010624//Homo sapiens Jagged 2 mRNA, complete cds//1.2e-05:516:61//Hs.106387:AF029778
 F-PLACE1010628//EST, Weakly similar to line-1 protein ORF2 [H.sapiens]//0.012:258:62//Hs.144375:AA484200
 25 F-PLACE1010629//EST//8.3e-23:218:79//Hs.161975:AA501461
 F-PLACE1010630//EST//0.29:319:58//Hs.137277:N62225
 F-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//9.5e-66:363:95//Hs.10801:AB011102
 F-PLACE1010661//ESTs//3.9e-89:504:92//Hs.122666:W27076
 F-PLACE1010662
 30 F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.1e-74:697:74//Hs.37138:U35376
 F-PLACE1010714//EST//0.018:253:59//Hs.148028:A1270027
 F-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//6.1e-77:393:96//Hs.50758:AF092564
 35 F-PLACE1010739//Homo sapiens mRNA for Sec24 protein (Sec24A isoform), partial//0.97:314:59//Hs.14574:AJ131244
 F-PLACE1010743//Human myosin-IXb mRNA, complete cds//2.4e-56:409:86//Hs.159629:U42391
 F-PLACE1010761//ESTs, Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus laevis]//5.1e-80:407:96//Hs.80965:AA493284
 40 F-PLACE1010771//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNPG [Mus musculus]//6.0e-45:251:94//Hs.11379:AA594140
 F-PLACE1010786
 F-PLACE1010800
 F-PLACE1010802//EST//0.94:128:64//Hs.120366:AA719157
 45 F-PLACE1010811//ESTs//0.89:339:59//Hs.127314:N48085
 F-PLACE1010833//ESTs, Weakly similar to allograft inflammatory factor-1 [H.sapiens]//2.9e-28:245:79//Hs.132736:AA583494
 F-PLACE1010856//ESTs//1.5e-06:95:87//Hs.17401:W81048
 50 F-PLACE1010857//ESTs, Weakly similar to KIAA0157 gene product is novel. [H.sapiens]//5.8e-67:336:97//Hs.130135:AA905493
 F-PLACE1010870//Zinc finger protein 43 (HTF6)//9.7e-40:498:69//Hs.74107:X59244
 F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//3.7e-149:694:98//Hs.118087:AB011182
 F-PLACE1010891//ESTs//6.9e-54:377:87//Hs.24453:R31671
 55 F-PLACE1010896//Human homologue of yeast sec7 mRNA, complete cds//0.64:167:65//Hs.1050:M85169
 F-PLACE1010900
 F-PLACE1010916//EST//0.55:151:66//Hs.145800:AI269981
 F-PLACE1010917

- F-PLACE1010925//ESTs//2.6e-81.437.94//Hs.5876:H26537
 F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//3.1e-139:653:98//Hs.74750:AB011126
 F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds//2.9e-91.437.98//Hs.66392:AF064244
- 5 F-PLACE1010944//ESTs//1.3e-17:117.91//Hs.29444:W30985
 F-PLACE1010947//EST//0.97:93.72//Hs.162299:AA555154
 F-PLACE1010954//Apolipoprotein B (including Ag(x) antigen)/0.28:444:59//Hs.585:X04506
 F-PLACE1010960//ESTs//0.98:238:60//Hs.163674:AA506632
- 10 F-PLACE1010965//ESTs//3.1e-74:376:96//Hs.115679:AI379721
 F-PLACE1011026//EST//0.022:222:60//Hs.47154:N50931
 F-PLACE1011032//EST//1.1e-05:88:79//Hs.118024:N34032
 F-PLACE1011041//Human density enhanced phosphatase-1 mRNA, complete cds//0.28:179:67//Hs.1177:U10886
- 15 F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//6.2e-11:207:68//Hs.994:M95678
 F-PLACE1011054//H. sapiens OBF-1 mRNA for octamer binding factor 1//6.1e-35:310:78//Hs.2407:Z49194
 F-PLACE1011056//Human putative serine/threonine protein kinase PRK (prk) mRNA, complete cds//0.74:228:61//Hs.153640:U56998
- 20 F-PLACE1011057//EST//2.5e-80:388:98//Hs.126466:AA913320
 F-PLACE1011090//ESTs//1.4e-94:469:97//Hs.106448:R76663
 F-PLACE1011109//ESTs//0.13:303:62//Hs.49294:AA418037
 F-PLACE1011114//ESTs//5.8e-12:75:100//Hs.147422:AI214317
 F-PLACE1011133//ESTs//0.17:225:62//Hs.132853:AI370857
- 25 F-PLACE1011143//ESTs//0.013:264:63//Hs.115368:AA629949
 F-PLACE1011160
 F-PLACE1011165//Galactokinase 2//2.7e-32:194:92//Hs.129228:M84443
 F-PLACE1011185//EST//1.4e-34:261:83//Hs.140250:AA708114
 F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyltransferase mRNA, complete cds//6.9e-124:576:99//Hs.159140:AF038664
- 30 F-PLACE1011214//ESTs, Weakly similar to B0035.14 [C.elegans]/9.7e-101:469:99//Hs.8241:AA283057
 F-PLACE1011219//ESTs, Weakly similar to coded for by C. elegans cDNA CEESL70F [C.elegans]/2.6e-62:221:88//Hs.101821:W27452
 F-PLACE1011221//ESTs//0.46:238:62//Hs.32853:AA015751
- 35 F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds//1.4e-147:675:99//Hs.23168:AB011101
 F-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21//5.9e-71:350:98//Hs.15144:AC005014
 F-PLACE1011273//ESTs//1.0:222:59//Hs.35274:AA495803
 F-PLACE1011291//Homo sapiens clone 24712 unknown mRNA, partial cds//3.4e-09:191:65//Hs.140950:AF070637
- 40 F-PLACE1011296//ESTs//0.019:137:63//Hs.140654:AA865915
 F-PLACE1011310//EST//0.066:336:58//Hs.162529:AA584160
 F-PLACE1011325//ESTs//7.4e-43:229:96//Hs.21081:H08310
 F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.8e-151:696:99//Hs.5819:AF102265
- 45 F-PLACE1011340//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.5e-20:120:81//Hs.159897:AB007970
 F-PLACE1011371//Human mRNA for PK-120//9.5e-35:684:63//Hs.76415:D38535
 F-PLACE1011375//ESTs, Moderately similar to potassium channel protein Raw3 [R.norvegicus]/6.7e-68:325:99//Hs.107245:AA627053
- 50 F-PLACE1011399//ESTs//8.6e-05:285:61//Hs.130105:AA904868
 F-PLACE1011419//ESTs//0.70:240:62//Hs.159650:N95552
 F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds//1.5e-158:743:98//Hs.10801:AB011102
- 55 F-PLACE1011452//Human Line-1 repeat mRNA with 2 open reading frames//1.9e-53:557:72//Hs.23094:M19503
 F-PLACE1011465//EST//3.1e-58:380:85//Hs.131605:AI025204
 F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.5e-152:703:99//Hs.111138:AB018255

- F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.7e-146:675:99//Hs.11183:AF065482
- F-PLACE1011492//ESTs//2.0e-35:186:98//Hs.125886:AA884264
- F-PLACE1011503//EST//0.67:149:65//Hs.149774:AI285997
- 5 F-PLACE1011520//ESTs//0.00014:213:64//Hs.119889:AA705319
- F-PLACE1011563//ESTs//2.2e-61:394:86//Hs.117718:AA883476
- F-PLACE1011567//Homo sapiens DEC-205 mRNA, complete cds//3.1e-46:325:84//Hs.153563:AF011333
- F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//4.3e-67:268:86//Hs.86371:AF054180
- 10 F-PLACE1011586//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds//0.98:153:65//Hs.143641:AB009462
- F-PLACE1011635//Homo sapiens Jagged 2 mRNA, complete cds//0.00029:585:57//Hs.106387:AF029778
- F-PLACE1011641
- F-PLACE1011643//Homo sapiens mRNA for KIAA0293 gene, partial cds//0.00058:499:58//Hs.12784:AB006631
- 15 F-PLACE1011646//EST//3.2e-26:201:68//Hs.140349:AA757661
- F-PLACE1011649//ESTs//0.25:145:64//Hs.23033:R46086
- F-PLACE1011650//ESTs//0.041:96:77//Hs.119351:AA447745
- F-PLACE1011664//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640
- F-PLACE1011675//Cell division cycle 27//0.098:448:57//Hs.73151:S78234
- 20 F-PLACE1011682//EST//8.6e-06:119:72//Hs.93664:N23366
- F-PLACE1011719//Human mRNA for KIAA0352 gene, complete cds//0.92:365:60//Hs.17262:AB002350
- F-PLACE1011725
- F-PLACE1011729//EST//0.56:304:58//Hs.86378:AA210853
- F-PLACE1011749//ESTs//4.3e-88:443:96//Hs.132850:AA779891
- 25 F-PLACE1011762//ESTs//0.012:149:68//Hs.145075:AI208240
- F-PLACE1011778//ESTs//0.00016:199:64//Hs.160395:AI393693
- F-PLACE1011783//EST//1.0:119:66//Hs.162191:AA534660
- F-PLACE1011858//Human novel homeobox mRNA for a DNA binding protein//8.9e-05:477:59//Hs.37035:U07664
- F-PLACE1011874//EST//0.20:118:66//Hs.127351:AA954775
- 30 F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cds//5.3e-110:526:98//Hs.22572:AB011152
- F-PLACE1011891//ESTs//1.8e-58:397:88//Hs.84698:AA725913
- F-PLACE1011896//ESTs, Weakly similar to Y53C.12A.3 [C.elegans]//9.4e-09:478:56//Hs.107747:AI357868
- F-PLACE1011922//ESTs//0.49:249:62//Hs.152627:AA595817
- F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//3.7e-140:664:98//Hs.3838:AF059617
- 35 F-PLACE1011962//EST//1.7e-07:81:85//Hs.104333:AA250763
- F-PLACE1011964//EST//6.6e-38:412:74//Hs.140562:AA826514
- F-PLACE1011982//ESTs//0.40:405:60//Hs.127743:AI261591
- F-PLACE1011995//ESTs//1.7e-22:486:64//Hs.105157:AA527514
- 40 F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//4.0e-148:690:98//Hs.88756:AB018256
- F-PLACE2000003//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//6.5e-54:290:81//Hs.92381:AB007956
- F-PLACE2000006//ESTs//0.067:224:62//Hs.144100:AI205503
- 45 F-PLACE2000007//ESTs//8.1e-23:147:91//Hs.128530:AA325330
- F-PLACE2000011//Interleukin 10//4.2e-42:362:78//Hs.2180:M57627
- F-PLACE2000014//EST//0.10:214:61//Hs.160247:AI138831
- F-PLACE2000015//Interleukin 10//1.4e-44:393:78//Hs.2180:M57627
- F-PLACE2000017
- 50 F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, partial cds//5.7e-85:844:72//Hs.7928:AF082557
- F-PLACE2000030
- F-PLACE2000033//Human adhesion molecule ninjurin mRNA, complete cds//0.85:234:66//Hs.11342:U91512
- F-PLACE2000034//Homo sapiens mRNA for KIAA0607 protein, partial cds//0.058:348:62//Hs.94653:AB011179
- 55 F-PLACE2000039//Human plectin (PLEC1) mRNA, complete cds//0.0058:473:59//Hs.79706:U53204
- F-PLACE2000047//ESTs//4.9e-32:328:75//Hs.141024:H07128
- F-PLACE2000050//ESTs//3.0e-36:270:83//Hs.155512:AA663966
- F-PLACE2000061

- F-PLACE2000062//Human membrane-associated lectin type-C mRNA//2.9e-114.662.86//Hs.23759:M98457
 F-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//7.1e-135.631.98//Hs.9443:AF027219
 F-PLACE2000097//ESTs//0.021:117.70//Hs.132811:AI034333
 5 F-PLACE2000100
 F-PLACE2000103//ESTs//1.1e-56.284.98//Hs.144786:AI219219
 F-PLACE2000111//H.sapiens mRNA for l-acylglycerol-3-phosphate O-acyltransferase//0.76:215.65//Hs.6587:U56417
 F-PLACE2000115
 10 F-PLACE2000124//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:400.79//Hs.153014:AB002353
 F-PLACE2000132
 F-PLACE2000136//ESTs, Moderately similar to hypothetical protein [H.sapiens]//1.2e-08:245.64//Hs.140343:AA718911
 F-PLACE2000140//Adenylate kinase 2 (adk2)//3.7e-24:162.90//Hs.83833:U54645
 15 F-PLACE2000164
 F-PLACE2000170
 F-PLACE2000172//ESTs//0.64:239.62//Hs.31175:AI219179
 F-PLACE2000176
 F-PLACE2000187
 20 F-PLACE2000216
 F-PLACE2000223//EST//0.0092:171.60//Hs.162830:AA643933
 F-PLACE2000235//Human mRNA for KIAA0298 gene, complete cds//1.6e-38:792.63//Hs.21560:AB0002296
 F-PLACE2000246//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.5e-74:367.98//Hs.22926:AB018338
 F-PLACE2000264//Homo sapiens mRNA for KIAA0792 protein, complete cds//2.0e-29:366.73//Hs.119387:AB007958
 25 F-PLACE2000274//Homo sapiens mRNA for dynein heavy chain//1.0e-23:650.62//Hs.144672:AJ000522
 F-PLACE2000302//ESTs//1.7e-05:66.89//Hs.55572:W37560
 F-PLACE2000305//ESTs//1.6e-78:382.98//Hs.136731:AA745869
 F-PLACE2000317
 30 F-PLACE2000335//Fc fragment of IgE, high affinity I, receptor for; beta polypeptide//6.1e-24:295.76//Hs.30:M89796
 F-PLACE2000341//Human sodium iodide symporter mRNA, complete cds//6.8e-21:593.61//Hs.103983:U66088
 F-PLACE2000342//Centromere protein B (80kD)//1.4e-06:326.61//Hs.85004:X05299
 F-PLACE2000347//ESTs, Moderately similar to F18547_1 [H.sapiens]//3.7e-16:139.82//Hs.28209:AI073817
 35 F-PLACE2000359//ESTs//5.0e-19:251.71//Hs.58272:W76645
 F-PLACE2000366//ESTs//1.7e-37:399.75//Hs.136646:AA748045
 F-PLACE2000371//EST//0.65:107.65//Hs.157677:AI358861
 F-PLACE2000373//ESTs//0.30:207.59//Hs.143902:AI131032
 F-PLACE2000379//ESTs//1.3e-64:402.87//Hs.146307:AA584638
 40 F-PLACE2000394//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.0e-87:694.80//Hs.158095:AB007953
 F-PLACE2000398
 F-PLACE2000399
 F-PLACE2000404
 45 F-PLACE2000411
 F-PLACE2000419//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.0e-52:463.74//Hs.113283:AF018080
 F-PLACE2000425//EST//0.44:168.62//Hs.44677:N34966
 F-PLACE2000427
 F-PLACE2000433//ESTs//4.7e-18:213.74//Hs.110187:AA699719
 50 F-PLACE2000435//EST//4.7e-05:159.64//Hs.123604:AA815257
 F-PLACE2000438//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T2)//1.9e-20:418.64//Hs.130181:X85019
 F-PLACE2000450//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.0e-83:324.81//Hs.113283:AF018080
 F-PLACE2000455//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//4.0e-05:100.73//Hs.104239:AA488082
 55 F-PLACE2000458//H.sapiens mRNA for hFat protein//0.0010:545.57//Hs.91107:X87241
 F-PLACE2000465//ESTs//4.4e-38:377.75//Hs.55855:AA621381
 F-PLACE2000477//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.8e-68:520.81//Hs.113283:AF018080

- F-PLACE3000004//Human EYA3 homolog (EYA3) mRNA, complete cds//3.9e-14:204:73//Hs.46925:Y10262 ,
 F-PLACE3000009//Human mRNA for KIAA0386 gene, complete cds//4.8e-59:696:69//Hs.101359:AB002384
 F-PLACE3000020//Prostaglandin 12 (prostacyclin) receptor (IP)/0.00081:500:61//Hs.393:D38128
 F-PLACE3000029
 5 F-PLACE3000059//ESTs//0.0026:49:100//Hs.42913:AI082248
 F-PLACE3000070//ESTs//5.6e-15:202:74//Hs.154993:AA142842
 F-PLACE3000103//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds//1.0:186:62//Hs.122752:AF026445
 10 F-PLACE3000119//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.8e-48:283:83//Hs.23711:AB018295
 F-PLACE3000121
 F-PLACE3000124//Thromboxane A2 receptor//1.1e-55:195:83//Hs.89887:D38081
 F-PLACE3000136//Homo sapiens mRNA for KIAA0703 protein, complete cds//1.0:194:59//Hs.6168:AB014603
 F-PLACE3000142//EST//0.41:179:59//Hs.137438:AA282243
 F-PLACE3000145//ESTs//3.5e-25:145:96//Hs.163950:AA683016
 15 F-PLACE3000147//EST//5.0e-43:285:86//Hs.160895:AI365871
 F-PLACE3000148
 F-PLACE3000155//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-80:382:99//Hs.6336:AB014572
 F-PLACE3000156//ESTs//0.0015:277:62//Hs.156834:AI336023
 20 F-PLACE3000157//Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit//0.54:320:60//Hs.96253:U79666
 F-PLACE3000158//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-66:319:88//Hs.153468:AB011147
 F-PLACE3000160
 25 F-PLACE3000169//Small inducible cytokine A5 (RANTES)//1.3e-64:501:80//Hs.155464:AF088219
 F-PLACE3000194
 F-PLACE3000197
 F-PLACE3000199//EST//1.0:108:68//Hs.98488:AA426546
 F-PLACE3000207//EST//1.0e-32:184:75//Hs.160146:AI049975
 30 F-PLACE3000208//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR//1.0:271:61//Hs.77522:X62744
 F-PLACE3000218//EST//1.3e-46:317:84//Hs.162197:AA535216
 F-PLACE3000220//EST//9.3e-95:443:99//Hs.112702:AA609377
 F-PLACE3000221//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//9.2e-56:200:85//Hs.133089:AF064019
 35 F-PLACE3000226
 F-PLACE3000230//EST//6.1e-16:173:72//Hs.148578:AI201568
 F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//1.2e-54:434:80//Hs.4943:Z98046
 40 F-PLACE3000244
 F-PLACE3000254//NUCLEOLIN//2.6e-05:445:60//Hs.79110:M60858
 F-PLACE3000271//ESTs//1.6e-25:195:72//Hs.108452:H78650
 45 F-PLACE3000276//ESTs//1.0e-13:274:66//Hs.28589:AI004944
 F-PLACE3000304//EST//0.043:210:61//Hs.132378:AI026770
 F-PLACE3000310
 F-PLACE3000320//EST//1.2e-12:188:70//Hs.145771:AI269586
 50 F-PLACE3000322//Small inducible cytokine A5 (RANTES)//4.7e-29:252:80//Hs.155464:AF088219
 F-PLACE3000331
 F-PLACE3000339//Homo sapiens mRNA for KIAA0645 protein, complete cds//0.91:222:61//Hs.155987:AB014545
 F-PLACE3000341//EST//1.8e-05:394:58//Hs.112894:AA620741
 F-PLACE3000350//ESTs. Highly similar to SERINE/THREONINE-PROTEIN KINASE SULU [Caenorhabditis elegans]//2.9e-59:474:77//Hs.125850:AA885355
 55 F-PLACE3000352//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.5e-48:442:78//Hs.2407:Z49194
 F-PLACE3000353//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T1)//0.78:234:63//Hs.7498:U41514

- F-PLACE3000362//EST//6.5e-25:302:73//Hs.140504:AA810441
F-PLACE3000363
F-PLACE3000365//ESTs//0.81:200:60//Hs.141556:N49928
F-PLACE3000373//ESTs//0.0071:82:73//Hs.136310:AA442641
5 F-PLACE3000388//ESTs//7.9e-16:235:71//Hs.44701:AA830432
F-PLACE3000399//Clathrin, light polypeptide (Lcb)/5.2e-70:391:81//Hs.73919:X81637
F-PLACE3000400//ESTs//0.53:162:66//Hs.49303:AA810785
F-PLACE3000401//EST//2.3e-35:178:100//Hs.162851:AA632270
F-PLACE3000402//ESTs//2.4e-84:425:96//Hs.148962:AI219715
10 F-PLACE3000405//EST//2.1e-39:452:73//Hs.140414:AA778541
F-PLACE3000406//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-07:
116:78//Hs.77579:AF013263
F-PLACE3000413//ESTs, Weakly similar to methyl sterol oxidase [H.sapiens]//1.6e-51:260:98//Hs.122512:
H61502
15 F-PLACE3000416//Homo sapiens mRNA for KIAA0801 protein, complete cds//0.00020:630:57//Hs.17585:
AB018344
F-PLACE3000425//EST//3.8e-34:286:79//Hs.135301:AI039161
F-PLACE3000455//Homo sapiens mRNA for cytochrome b small subunit of complex II, complete cds//3.6e-32:
183:93//Hs.108326:AB006202
20 F-PLACE3000475//ESTs//1.9e-09:422:61//Hs.145783:AA081874
F-PLACE3000477//H.sapiens mRNA for chemokine receptor D6//1.0:426:54//Hs.117572:U94888
F-PLACE4000009//TRICHOHYALIN//3.1e-09:692:60//Hs.82276:L09190
F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//3.6e-118:331:100//Hs.105399:
AB018352
25 F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//1.1e-06:244:63//Hs.154050:
AC004131
F-PLACE4000049//Homo sapiens clone 24619 mRNA sequence//4.3e-45:371:79//Hs.139088:AF070533
F-PLACE4000052//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//1.4e-53:669:67//Hs.
40993:AF000148
30 F-PLACE4000063
F-PLACE4000089//ESTs//2.2e-10:121:85//Hs.49391:W00713
F-PLACE4000093//ESTs//0.0053:273:60//Hs.136952:AA825819
F-PLACE4000100//ESTs//8.0e-21:246:73//Hs.140207:N32058
F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//3.8e-147:684:99//Hs.129937:
35 AB007931
F-PLACE4000128//Homo sapiens ES/130 mRNA, complete cds//0.23:398:60//Hs.98614:AF006751
F-PLACE4000129
F-PLACE4000131//ESTs//2.4e-13:194:72//Hs.41418:H90627
F-PLACE4000147//ESTs//0.0060:324:60//Hs.85640:AA535856
40 F-PLACE4000156//Zinc finger protein 136 (clone pHZ-20)//2.3e-89:764:76//Hs.69740:U09367
F-PLACE4000192
F-PLACE4000211
F-PLACE4000222//EST//1.9e-15:317:66//Hs.149206:AI246594
F-PLACE4000230//Human mRNA for KIAA0331 gene, complete cds//0.0048:258:60//Hs.146395:AB002329
45 F-PLACE4000233//ESTs//4.4e-38:240:80//Hs.114605:AI304317
F-PLACE4000247//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding
mitochondrial protein, complete cds//0.0095:156:69//Hs.30928:AF043250
F-PLACE4000250//ESTs//3.8e-72:377:94//Hs.124234:T89609
F-PLACE4000252//ESTs//1.0:196:64//Hs.144869:AA493886
50 F-PLACE4000259//Homo sapiens mRNA for KIAA0788 protein, partial cds//6.2e-27:191:87//Hs.2397:Z70200
F-PLACE4000261
F-PLACE4000269//ESTs, Weakly similar to coded for by C. elegans cDNA yk52b10.3 [C.elegans]//9.5e-41:202:
100//Hs.118849:AA215645
F-PLACE4000270
55 F-PLACE4000300
F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN//4.5e-23:135:96//Hs.155952:U88966
F-PLACE4000323//EST//6.7e-09:180:68//Hs.116769:AA630365
F-PLACE4000326//ESTs//2.1e-94:453:98//Hs.103177:W72798

- F-PLACE4000344//EST//6.4e-05:135.67//Hs.146729:AI147292
 F-PLACE4000367
 F-PLACE4000369
- 5 F-PLACE4000379//EST//3.9e-42:381.79//Hs.162335:AA564256
 F-PLACE4000387//ESTs//0.19:93:69//Hs.154173:AI379823
 F-PLACE4000392//ESTs//0.0015:381.59//Hs.120172:AA709046
 F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1e-47:605.71//Hs.153026:AB014540
- 10 F-PLACE4000411//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//4.7e-33:159.81//Hs.154257:AI275982
 F-PLACE4000431//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.3e-45:263.92//Hs.2397:Z70200
 F-PLACE4000445
 F-PLACE4000450
 F-PLACE4000465//ESTs//1.5e-11:273.65//Hs.145783:AA081874
 F-PLACE4000487//Sialoporphin (gpl115, leukosialin, CD43)//3.0e-14:189.71//Hs.80738:X52075
- 15 F-PLACE4000489//ESTs//0.94:104.68//Hs.125119:R38951
 F-PLACE4000494//ESTs//1.0:185.60//Hs.143053:AI126289
 F-PLACE4000521//ESTs//0.0027:161.70//Hs.135740:AA651731
 F-PLACE4000522//ESTs, Highly similar to NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG 1 PRECURSOR [Homo sapiens]//0.047:119.65//Hs.129053:AA767022
- 20 F-PLACE4000548
 F-PLACE4000558//Homo sapiens mRNA for DFFRY protein, abundant transcript//0.0035:510.59//Hs.39163:AF000986
 F-PLACE4000581
 F-PLACE4000590//ESTs, Highly similar to POL POLYPROTEIN [Friend murine leukemia virus (isolate 57)]//3.4e-13:275.68//Hs.113980:AI034080
- 25 F-PLACE4000593//ESTs, Weakly similar to F25D7.1 [C.elegans]//5.2e-28:239.79//Hs.109084:AI004675
 F-PLACE4000612//Keratin 9//0.27:207.64//Hs.2783:Z29074
 F-PLACE4000638//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//3.5e-47:562.69//Hs.129685:AB002446
- 30 F-PLACE4000650
 F-PLACE4000654
 F-PLACE4000670//ESTs//6.1e-88:411.100//Hs.130688:AI028132
 F-SKNMC1000011//Centromere protein B (80kD)//0.0013:243.62//Hs.85004:X05299
 F-SKNMC1000013//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HOMOLOG 50 [Drosophila melanogaster]//2.5e-36:197.96//Hs.118634:U66688
- 35 F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5e-148:706.98//Hs.109299:AB014554
 F-SKNMC1000050//Calpain, large polypeptide L2//4.1e-53:330.90//Hs.76288:M23254
 F-SKNMC1000091//ESTs//3.3e-64:420.88//Hs.90997:AA946877
- 40 F-THYRO1000017//Human mRNA for KIAA0315 gene, partial cds//1.0:310.60//Hs.3989:AB002313
 F-THYRO1000026//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.9e-35:299.81//Hs.2407:Z49194
 F-THYRO1000034
 F-THYRO1000035//ESTs//4.1e-37:317.79//Hs.141254:AI334099
 F-THYRO1000040//ESTs//0.30:331.59//Hs.87176:AI148326
- 45 F-THYRO1000070//Human mRNA for KIAA0347 gene, complete cds//0.069:278.63//Hs.101996:AB002345
 F-THYRO1000072//Homo sapiens clone 23584 mRNA sequence//8.7e-86:722.77//Hs.6654:AB014557
 F-THYRO1000085
 F-THYRO1000092//ESTs//3.1e-100:469.99//Hs.132207:AI148065
 F-THYRO1000107
- 50 F-THYRO1000111//Human Line-1 repeat mRNA with 2 open reading frames//6.8e-106:690.86//Hs.23094:M19503
 F-THYRO1000121
 F-THYRO1000124//Human mRNA for alanine aminotransferase//0.0026:420.58//Hs.103502:U07032
 F-THYRO1000129//Homo sapiens TED protein (TED).mRNA, complete cds//2.8e-155:732.98//Hs.87619:AF087142
- 55 F-THYRO1000132//ESTs//1.9e-35:164.79//Hs.139179:AA650203
 F-THYRO1000156//EST//0.32:102.68//Hs.139634:AA478416
 F-THYRO1000163//Small inducible cytokine A5 (RANTES)//5.2e-50:331.85//Hs.155464:AF088219
 F-THYRO1000173//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//1.1e-05:261.61//Hs.

152936:D63475

F-THYRO1000186//H.sapiens mRNA for phosphoinositide 3-kinase//3.7e-41:270:87//Hs.101238:Y11312

F-THYRO1000187//EST//0.11:227:62//Hs.101773:H23270

F-THYRO1000190//ESTs//0.82:194:63//Hs.128818:AA976883

5 F-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//2.4e-175:805:99//Hs.43445:AJ005698

F-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.0e-88:616:84//Hs.79672:AB014552

F-THYRO1000206//EST//0.96:291:61//Hs.104962:AA443848

10 F-THYRO1000221//Human clone 23589 mRNA sequence//0.035:242:62//Hs.11506:U79297

F-THYRO1000241//EST//0.48:102:69//Hs.160764:AI313322

F-THYRO1000242//Zinc finger protein 84 (HPF2)//1.2e-42:534:64//Hs.9450:M27878

F-THYRO1000253//Homo sapiens mRNA for KIAA0690 protein, partial cds//0.61:211:64//Hs.60103:AB014590

F-THYRO1000270

15 F-THYRO1000279//ESTs//0.0020:104:72//Hs.121476:AI215500

F-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds//1.3e-180:848:98//Hs.25846:AB016068

F-THYRO1000320//ESTs, Weakly similar to Similar to glutamate decarboxylase [C.elegans]//7.6e-92:431:99//Hs.122719:AA777803

F-THYRO1000327//Autocrine motility factor receptor//2.8e-52:290:93//Hs.80731:M63175

20 F-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//7.2e-164:763:98//Hs.12002:AB018333

F-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds//6.9e-34:177:84//Hs.7833:U29091

F-THYRO1000368//ESTs//0.0011:55:96//Hs.34994:AA252919

25 F-THYRO1000381//Homo sapiens mRNA for KIAA0562 protein, complete cds//0.081:240:62//Hs.118401:AB011134

F-THYRO1000387//EST//3.6e-14:197:71//Hs.139399:AA416855

F-THYRO1000394//ESTs, Weakly similar to No definition line found [C.elegans]//5.8e-39:245:91//Hs.119095:T79413

30 F-THYRO1000395//EST//5.8e-69:333:99//Hs.156524:AA724572

F-THYRO1000401//ESTs//1.8e-24:132:98//Hs.54852:W26238

F-THYRO1000438//EST//1.9e-05:217:63//Hs.115930:AA579773

F-THYRO1000452//B cell lymphoma protein 6 (zinc finger protein 51)//0.096:306:60//Hs.155024:U00115

F-THYRO1000471//Tyrosine aminotransferase//5.6e-44:403:77//Hs.2999:X52520

35 F-THYRO1000484//EST, Weakly similar to putative p150 [H.sapiens]//8.9e-22:248:76//Hs.162011:AA513663

F-THYRO1000488

F-THYRO1000501//H.sapiens Staf50 mRNA//3.2e-75:615:77//Hs.68054:X82200

F-THYRO1000502//ESTs//1.0:350:57//Hs.119749:AA689298

F-THYRO1000505//Interleukin 13//0.095:245:60//Hs.845:U31120

40 F-THYRO1000558//EST//1.3e-24:351:64//Hs.142326:AA351877

F-THYRO1000569//Homo sapiens mRNA for dihydropyrimidinase related protein 4, complete cds//0.28:229:61//Hs.100058:AB006713

F-THYRO1000570//EST//0.80:171:61//Hs.112790:AA609949

45 F-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds//2.4e-168:808:97//Hs.151411:AF075587

F-THYRO1000596//EST//9.5e-94:461:96//Hs.135397:AI056322

F-THYRO1000602//EST//4.9e-06:80:80//Hs.162135:AA526331

F-THYRO1000605//Guanylate cyclase 1, soluble, alpha 2//0.44:182:62//Hs.2685:Z50053

F-THYRO1000625//Thromboxane A2 receptor//4.5e-45:323:82//Hs.89887:D38081

50 F-THYRO1000637//ESTs//4.4e-24:255:75//Hs.101014:AA194941

F-THYRO1000641//ESTs//0.00017:375:58//Hs.32703:AA054125

F-THYRO1000658//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.8e-09:127:77//Hs.116007:S79267

F-THYRO1000662

55 F-THYRO1000666//ESTs//1.9e-28:149:99//Hs.105187:AI394157

F-THYRO1000676//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//5.7e-49:281:77//Hs.116007:S79267

F-THYRO1000684//ESTs, Weakly similar to band-6-protein [H.sapiens]//0.46:368:57//Hs.26557:AA480380

F-THYRO1000699//ESTs//1.6e-10:314:65//Hs.139212:AA243452
 F-THYRO1000712//ESTs//3.3e-42:211:99//Hs.69330:AI056324
 F-THYRO1000715//Human plectin (PLEC1) mRNA, complete cds//2.9e-06:631:59//Hs.79706:U53204
 F-THYRO1000734//ESTs//8.4e-08:226:64//Hs.125754:AA806085
 5 F-THYRO1000748//Homo sapiens KIAA0411 mRNA, complete cds//3.1e-35:339:74//Hs.7977:AB007871
 F-THYRO1000758//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//1.0:209:62//Hs.19492:AF061573
 F-THYRO1000777//Human mRNA for KIAA0147 gene, partial cds//0.00069:636:57//Hs.158132:D63481
 F-THYRO1000783//Homo sapiens Arp2/3 protein complex subunit p41-Arc (ARC41) mRNA, complete cds//0.70:452:58//Hs.11538:AF006084
 10 F-THYRO1000787
 F-THYRO1000793
 F-THYRO1000796
 F-THYRO1000805//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//9.4e-36:561:68//Hs.129685:AB002446
 F-THYRO1000815//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:465:75//Hs.154326:D42087
 F-THYRO1000829//ESTs//1.7e-66:361:95//Hs.7906:H16339
 F-THYRO1000843
 F-THYRO1000852//ESTs//6.2e-23:204:81//Hs.144452:AA838788
 20 F-THYRO1000855//ESTs//0.049:159:64//Hs.163532:AI424170
 F-THYRO1000865//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-33:190:75//Hs.133526:N21103
 F-THYRO1000895//ESTs//3.8e-24:191:84//Hs.132722:AA618531
 F-THYRO1000916//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.8e-43:318:79//Hs.92381:AB007956
 25 F-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//3.0e-179:839:98//Hs.78106:AF079529
 F-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE//1.1e-33:759:63//Hs.79217:M77836
 F-THYRO1000951//MUELLERIAN INHIBITING FACTOR PRECURSOR//0.055:662:56//Hs.112432:AC005263
 30 F-THYRO1000952//Human mRNA for KIAA0208 gene, complete cds//0.98:177:65//Hs.83558:D86963
 F-THYRO1000974//Homo sapiens putative ATP-dependent mitochondrial RNA helicase (SUV3) mRNA, nuclear gene encoding mitochondrial protein, complete cds//2.7e-15:123:90//Hs.106469:AF042169
 F-THYRO1000975//EST//0.45:172:62//Hs.105449:AA513907
 F-THYRO1000983
 35 F-THYRO1000984//EST//0.0075:119:65//Hs.150347:AA984646
 F-THYRO1000988//ESTs//0.056:99:71//Hs.153409:AI224307
 F-THYRO1001003
 F-THYRO1001031//Thiopurine S-methyltransferase//3.8e-44:568:71//Hs.51124:AF019369
 F-THYRO1001033//H.sapiens mRNA for cylicin II//0.0061:287:60//Hs.3232:Z46788
 40 F-THYRO1001062//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.2e-45:394:79//Hs.51048:X68830
 F-THYRO1001093//Human mRNA for KIAA0355 gene, complete cds//3.4e-33:421:72//Hs.153014:AB002353
 F-THYRO1001100//Human DNA-binding protein mRNA, 3'end//2.1e-74:741:74//Hs.159249:Z99130
 F-THYRO1001120//Homo sapiens deltex (Dx) mRNA, complete cds//4.5e-18:447:62//Hs.124024:AF053700
 F-THYRO1001121//ESTs//0.92:257:61//Hs.118246:N95416
 45 F-THYRO1001133//EST//1.1e-38:367:75//Hs.144175:H70425
 F-THYRO1001134//ESTs//1.4e-28:186:91//Hs.109468:W52074
 F-THYRO1001142//ESTs//1.8e-44:332:82//Hs.146811:AA410788
 F-THYRO1001173
 F-THYRO1001177//ESTs//7.7e-40:240:84//Hs.155384:Z78385
 50 F-THYRO1001189//ESTs//2.1e-36:323:76//Hs.120206:AI089163
 F-THYRO1001204
 F-THYRO1001213//Small inducible cytokine A5 (RANTES)//3.1e-43:256:81//Hs.155464:AF088219
 F-THYRO1001262//ESTs//7.9e-44:279:87//Hs.138856:H47461
 F-THYRO1001271//Homo sapiens mRNA for synaptogyrin 3//0.0045:273:60//Hs.6467:AJ002309
 55 F-THYRO1001287//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//0.014:178:66//Hs.125315:AF027156
 F-THYRO1001290//ESTs//3.9e-43:145:99//Hs.147797:AA069836
 F-THYRO1001313//ESTs//1.0:244:61//Hs.127488:AA528182

- F-THYRO1001320//ESTs//0.062:126:67//Hs.133296:AI311872
 F-THYRO1001321//Homo sapiens DEC-205 mRNA, complete cds//2.5e-35:560:68//Hs.153563:AF011333
 F-THYRO1001322//ESTs//0.12:238:61//Hs.29169:N66545
 F-THYRO1001347//ESTs//7.5e-61:293:99//Hs.129962:AA927207
 5 F-THYRO1001363//ESTs//1.0e-16:178:78//Hs.163954:N57939
 F-THYRO1001365//Homo sapiens KIAA0417 mRNA, complete cds//3.6e-18:187:79//Hs.12385:AB007877
 F-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds//7.4e-157:740:97//Hs.138488:AB014607
 F-THYRO1001401//EST//4.6e-14:171:76//Hs.157587:AI356993
 10 F-THYRO1001403//ESTs//2.2e-50:464:79//Hs.118046:N49946
 F-THYRO1001405//ESTs//1.7e-44:226:99//Hs.156667:AI347694
 F-THYRO1001406//Hydroxysteroid (17-beta) dehydrogenase 3//2.8e-20:459:62//Hs.477:U05659
 F-THYRO1001411//ESTs//1.9e-41:342:78//Hs.146811:AA410788
 F-THYRO1001426//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//4.6e-33:153:81//
 15 Hs.102877:U41315
 F-THYRO1001434//ESTs//1.1e-07:274:60//Hs.151093:AI224099
 F-THYRO1001458//Myosin, heavy polypeptide 9, non-muscle//6.2e-60:653:71//Hs.44782:Z82215
 F-THYRO1001480//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.3e-42:370:78//Hs.51048:X68830
 F-THYRO1001487//EST//1.0:88:71//Hs.160760:AI311943
 20 F-THYRO1001534//ESTs//1.2e-94:457:98//Hs.125523:AA883904
 F-THYRO1001537//ESTs//3.5e-94:469:97//Hs.106448:R76663
 F-THYRO1001541//EST//1.4e-10:158:65//Hs.145159:AI150211
 F-THYRO1001559//ESTs//1.4e-07:91:81//Hs.43507:N24046
 F-THYRO1001570//ESTs//2.3e-41:280:80//Hs.119752:AA703335
 25 F-THYRO1001573//Homo sapiens clone 24778 unknown mRNA//2.7e-105:546:95//Hs.25306:AF070572
 F-THYRO1001584//Human RGP3 mRNA, complete cds//0.14:335:58//Hs.82294:U27655
 F-THYRO1001595//Human RSU-1/RSP-1 mRNA, complete cds//3.6e-35:165:84//Hs.75551:L12535
 F-THYRO1001602//ESTs//3.1e-42:350:80//Hs.138384:R72849
 F-THYRO1001605//EST//0.11:426:57//Hs.151206:AI126071
 30 F-THYRO1001617//ESTs//5.2e-43:345:81//Hs.8710:W07046
 F-THYRO1001637//ESTs, Weakly similar to anion exchanger [H. sapiens]//5.2e-13:108:86//Hs.141045:AA191659
 F-THYRO1001656//Solute carrier family 2 (facilitated glucose transporter), member 4//0.099:540:55//Hs.95958:M91463
 F-THYRO1001661//ESTs//0.12:53:92//Hs.151586:W45568
 35 F-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform//8.0e-166:780:98//
 Hs.118633:AJ225089
 F-THYRO1001673//Von Hippel-Lindau syndrome//4.6e-25:212:73//Hs.78160:AF010238
 F-THYRO1001703//Homo sapiens clone 24767 mRNA sequence//0.27:421:57//Hs.122908:AF070552
 F-THYRO1001706//ESTs//1.8e-24:142:95//Hs.112536:AI147691
 40 F-THYRO1001721//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//2.5e-51:296:92//
 Hs.3826:U69560
 F-THYRO100173 8//EST//6.9e-30:180:94//Hs.58641:W81229
 F-THYRO1001745//ESTs//6.1e-49:244:98//Hs.97534:AA398813
 F-THYRO1001746//EST//0.96:119:63//Hs.144107:AI053590
 45 F-THYRO1001772//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-21:
 182:81//Hs.118053:N75725
 F-THYRO1001793//ESTs//1.9e-93:439:99//Hs.150116:AI299324
 F-THYRO1001809//Human mRNA for KIAA0297 gene, partial cds//0.47:168:67//Hs.11711:AB002295
 F-THYRO1001828
 50 F-THYRO1001854//EST//0.038:128:67//Hs.160649:AI241823
 F-THYRO1001895//Interleukin adhesion molecule 1 (CD54), human rhinovirus receptor//9.6e-13:288:65//Hs.
 51061:M24283
 F-THYRO1001907//EST//1.9e-12:126:80//Hs.139296:AA350198
 F-VESEN1000122
 55 F-Y79AA1000013//ESTs//1.7e-72:369:96//Hs.97176:AA447885
 F-Y79AA1000033
 F-Y79AA1000037//Murine leukemia viral (bmi-1) oncogene homolog//7.8e-21:230:66//Hs.431:L13689
 F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, complete cds//7.3e-40:629:64//Hs.75305:

U78521

F-Y79AA1000065//CD81 ANTIGEN//0.0050:241:60//Hs.54457:M33680

F-Y79AA1000131//Guanylate cyclase 1, soluble, alpha 2//0.078:477:58//Hs.2685:Z50053

F-Y79AA1000181//Fatty acid synthase [3' region] [human, breast and HepG2 cells, mRNA Partial, 2237 nt]//0.0022:684:58//Hs.83190:U29344

F-Y79AA1000202//ESTs//2.5e-17:143:86//Hs.76925:AA211860

F-Y79AA1000214//Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds//3.9e-73:345:100//Hs.9242:AF081192

F-Y79AA1000230//Polymeric immunoglobulin receptor//0.98:335:59//Hs.842:X73079

F-Y79AA1000231//ESTs//0.11:209:66//Hs.132184:AI278623

F-Y79AA1000258//Homo sapiens metase (MET-1) mRNA, complete cds//0.30:444:61//Hs.99941:L23134

F-Y79AA1000268//Human mRNA for KIAA0367 gene, partial cds//9.1e-11:300:64//Hs.23311:AB002365

F-Y79AA1000313//Human mRNA for KIAA0129 gene, complete cds//0.89:744:56//Hs.44361:D50919

F-Y79AA1000328

F-Y79AA1000342//Homo sapiens OPA-containing protein mRNA, complete cds//8.4e-15:223:75//Hs.85313:AF071309

F-Y79AA1000346

F-Y79AA1000349//ALPHA-2C-1 ADRENERGIC RECEPTOR//8.3e-06:180:73//Hs.123022:J03853

F-Y79AA1000355

F-Y79AA1000368//ESTs//0.0062:235:64//Hs.114777:AA782908

F-Y79AA1000405//ESTs//0.76:244:62//Hs.153027:AA648897

F-Y79AA1000410//Small inducible cytokine A5 (RANTES)//8.1e-31:229:83//Hs.155464:AF088219

F-Y79AA1000420//ESTs//1.1e-53:271:87//Hs.13056:AA181018

F-Y79AA1000469//Homo sapiens l-1 receptor candidate protein mRNA, complete cds//0.0047:315:66//Hs.26285:AF082516

F-Y79AA1000480

F-Y79AA1000538//ESTs//5.7e-09:110:77//Hs.98790:AA284871

F-Y79AA1000539//ESTs//2.6e-52:412:77//Hs.81648:W26521

F-Y79AA1000540//Homo sapiens chromosome 7q22 sequence//0.70:133:69//Hs.151555:AF053356

F-Y79AA1000560//Homo sapiens gamma2-adaptin (G2AD) mRNA, complete cds//1.2e-07:371:63//Hs.8991:AF068706

F-Y79AA1000574//Human mRNA for GC box bindig protein, complete cds//0.95:258:62//Hs.150557:D31716

F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence//2.8e-154:755:97//Hs.21811:AF091080

F-Y79AA10006277//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//1.7e-136:644:98//Hs.60580:AF060503

F-Y79AA1000705//Homo sapiens CHD1 mRNA, complete cds//0.0023:523:59//Hs.22670:AF006513

F-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds//1.6e-181:850:98//Hs.83023:AF093670

F-Y79AA1000748//ESTs//4.2e-12:95:90//Hs.33687:R85969

F-Y79AA1000752//ESTs//8.1e-114:551:97//Hs.153471:AI198377

F-Y79AA1000774//ESTs//2.9e-59:296:98//Hs.150536:W20067

F-Y79AA1000782//EST//0.97:78:69//Hs.147351:AI208468

F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds//1.1e-178:847:97//Hs.5151:AF098799

F-Y79AA1000794//G-rich RNA sequence binding factor 1//0.83:228:61//Hs.79295:U07231

F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds//0.12:244:60//Hs.12307:AF056085

F-Y79AA1000802//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.87:466:59//Hs.122967:AF059569

F-Y79AA1000805

F-Y79AA1000824//Titin//1.0:437:58//Hs.83049:X90568

F-Y79AA1000827//Fatty acid synthase [3' region] [human, breast and HepG2 cells, mRNA Partial, 2237 nt]//0.0048:630:57//Hs.83190:U29344

F-Y79AA1000833//TUBULIN ALPHA-4 CHAIN//6.9e-107:603:90//Hs.75318:X06956

F-Y79AA1000850//ESTs, Weakly similar to T22C1.7 [C.elegans]//6.0e-77:368:99//Hs.86660:AA398644

F-Y79AA1000962//Homo sapiens orphan nuclear hormone receptor BD73 mRNA, 3' end//0.14:499:58//Hs.37288:D16815

F-Y79AA1000966//ESTs//0.80:52:86//Hs.6671:AI341699

- F-Y79AA1000968//ESTs, Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]/6.9e-69:310.94//Hs.76822:AI359536
- F-Y79AA1000969//LYMPHOTOXIN-BETA RECEPTOR PRECURSOR//1.0:150.64//Hs.1116:L04270
- F-Y79AA1000976//Arachidonate 15-lipoxygenase//0.87:174.66//Hs.73809:M23892
- 5 F-Y79AA1000985//Human plectin (PLEC1) mRNA, complete cds//0.091:385.58//Hs.79706:U53204
- F-Y79AA1001023
- F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds//0.99:37:100//Hs.78489:U63329
- F-Y79AA1001048//Acyl-Coenzyme A dehydrogenase, very long chain//7.8e-30:772.60//Hs.82208:L46590
- 10 F-Y79AA1001061//ESTs//6.3e-41:303.84//Hs.55855:AA621381
- F-Y79AA1001068//EST//3.0e-23:165.90//Hs.157607:AI357511
- F-Y79AA1001077//ESTs//4.9e-40:237.94//Hs.11197:AA309047
- F-Y79AA1001078
- F-Y79AA1001105//Homo sapiens homeodomain protein (OG12) mRNA, complete cds//6.5e-11:247.66//Hs.55967:AF022654
- 15 F-Y79AA1001145//ESTs//1.3e-20:234.75//Hs.55855:AA621381
- F-Y79AA1001167//Homo sapiens mRNA for KIAA0750 protein, complete cds//1.0:155.63//Hs.5444:AB018293
- F-Y79AA1001177//Human hSIAH2 mRNA, complete cds//6.5e-09:299.65//Hs.20191:U76248
- F-Y79AA1001185//ESTs//1.7e-56:318.93//Hs.102991:AA639646
- F-Y79AA1001211//ESTs//9.1e-108:503.99//Hs.100605:AA305965
- 20 F-Y79AA1001216//Peroxisome receptor 1//0.00028:458.57//Hs.158084:Z48054
- F-Y79AA1001228//Fragile X mental retardation 2//0.040:207.64//Hs.54472:U48436
- F-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1//6.5e-25:731.60//Hs.85279:U34879
- F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc1101133Q7 (RZPD Berlin))//4.0e-135:441.97//Hs.23170:AJ005892
- 25 F-Y79AA1001281//ESTs//2.7e-21:157.88//Hs.163825:AI393240
- F-Y79AA1001299//Human In1 mRNA, complete cds//2.2e-116:323.93//Hs.155626:U04847
- F-Y79AA1001312//ESTs//3.7e-95:448.99//Hs.104469:W38395
- F-Y79AA1001323//ESTs//8.9e-50:340.86//Hs.144198:AI017555
- F-Y79AA1001384
- 30 F-Y79AA1001391//Human Hoxb-13 mRNA, complete cds//8.6e-42:505.70//Hs.66731:U81599
- F-Y79AA1001394//ESTs, Weakly similar to F54B3.3 [C.elegans]//1.5e-90:424.96//Hs.154221:H23167
- F-Y79AA1001402//ESTs//1.0:245.62//Hs.134695:AI088489
- F-Y79AA1001493//SRY (sex determining region Y)-box 4//0.38:311.61//Hs.83484:X07683
- F-Y79AA1001511//ESTs//9.9e-105:487.99//Hs.153581:AA630465
- 35 F-Y79AA1001533//ESTs, Highly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Homo sapiens]//0.95:256.63//Hs.29974:AI360447
- F-Y79AA1001541//EST//0.96:202.61//Hs.99141:AA447744
- F-Y79AA1001548//ESTs//2.6e-25:166.90//Hs.164036:AA845659
- F-Y79AA1001555//ESTs//1.6e-35:191.97//Hs.52885:H29851
- 40 F-Y79AA1001581//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//2.5e-05:272.64//Hs.106070:U22398
- F-Y79AA1001585//ESTs//1.1e-84:473.93//Hs.42547:AA210783
- F-Y79AA1001594//ESTs//1.7e-08:169.71//Hs.97366:AA393109
- F-Y79AA1001603//ESTs//4.6e-07:429.59//Hs.160422:AI363426
- F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds//0.00078:520.57//Hs.12334:AB014583
- 45 F-Y79AA1001647//ESTs, Weakly similar to ZK1058.5 [C.elegans]//9.4e-79:421.94//Hs.107039:W27244
- F-Y79AA1001665//VON WILLEBRAND FACTOR PRECURSOR//1.0:386.60//Hs.110802:X04385
- F-Y79AA1001679//Guanine nucleotide binding protein (G protein), beta polypeptide 1//0.88:243.61//Hs.3620:X04526
- 50 F-Y79AA1001692//Insulin-like growth factor binding protein 2//1.9e-06:426.59//Hs.162:X16302
- F-Y79AA1001696//ESTs//2.3e-44:249.94//Hs.163665:AA250877
- F-Y79AA1001705//Homo sapiens interleukin-1 receptor-associated kinase (IRAK) mRNA, complete cds//0.19:609.58//Hs.77297:L76191
- F-Y79AA1001711//ESTs//5.2e-29:224.83//Hs.100461:AI018620
- 55 F-Y79AA1001781//Homo sapiens KIAA0443 mRNA, complete cds//0.49:183.66//Hs.113082:AB007903
- F-Y79AA1001805//ESTs//1.1e-62:315.98//Hs.16141:W56079
- F-Y79AA1001827//ESTs, Weakly similar to Similar to S.cerevisiae YD9335.03c protein [H.sapiens]//2.9e-62:313.98//Hs.15709:W81213

F-Y79AA1001846//ESTs//9.4e-16:146.82//Hs.140588:H60533
 F-Y79AA1001848//ESTs, Weakly similar to KIAA0390 [H.sapiens]//1.6e-19:142.90//Hs.103349:AI141124
 F-Y79AA1001866//Homo sapiens mRNA for zinc finger protein 10//5.1e-09:215.67//Hs.104115:X52332
 F-Y79AA1001874//Homo sapiens Jagged 2 mRNA, complete cds//5.4e-06:412.62//Hs.106387:AF029778
 5 F-Y79AA1001875//ESTs//6.8e-09:198.67//Hs.138036:AI343173
 F-Y79AA1001923//Homo sapiens growth-arrest-specific protein (gas) mRNA, complete cds//0.98:430.58//Hs.78501:L13720
 F-Y79AA1001963//ESTs//8.1e-131:642.97//Hs.54971:AI424382
 F-Y79AA1002027//ESTs//0.00042:58.91//Hs.5375:AA620611
 10 F-Y79AA1002083//ESTs//2.5e-51:285.95//Hs.117205:W88943
 F-Y79AA1002089//ESTs, Weakly similar to putative p150 [H.sapiens]//8.3e-53:348.88//Hs.18122:AI338045
 F-Y79AA1002093
 F-Y79AA1002103//ESTs//1.5e-15:223.71//Hs.97427:AA411865
 F-Y79AA1002115
 15 F-Y79AA1002125//ESTs//6.5e-41:206.99//Hs.159257:N40395
 F-Y79AA1002139//ESTs, Weakly similar to B0035.14 [C.elegans]//1.2e-24:165.90//Hs.6473:AA853955
 F-Y79AA1002204//Homo sapiens mRNA for KIAA0638 protein, partial cds//9.5e-05:393.62//Hs.77864:AB014538
 F-Y79AA1002208//ESTs//2.7e-13:211.69//Hs.112469:AA598515
 F-Y79AA1002209//ESTs, Weakly similar to TYROSYL-TRNA SYNTHETASE [Bacillus caldoteax]//2.3e-113:568:96//Hs.111637:AA305890
 20 F-Y79AA1002210//ESTs, Weakly similar to D2045.8 [C.elegans]//8.6e-33:338.73//Hs.26662:U55984
 F-Y79AA1002211//ESTs//2.6e-15:121.75//Hs.159584:AA524477
 F-Y79AA1002220//EST//0.010:360.60//Hs.136341:AA482508
 F-Y79AA1002229//Homo sapiens mRNA for KIAA0086 gene, complete cds//0.0041:203.63//Hs.1560:D42045
 25 F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//4.1e-176:821.98//Hs.100729:AB014592
 F-Y79AA1002246//Human involucrin mRNA//5.6e-05:525.59//Hs.157091:M13903
 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.2e-160:748.98//Hs.96731:AB014555
 30 F-Y79AA1002298//ESTs//2.5e-05:115.77//Hs.87164:T84489
 F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//2.1e-130:622.97//Hs.30898:AB014534
 F-Y79AA1002311//ESTs//4.9e-19:126.94//Hs.58595:AA830999
 F-Y79AA1002351//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete cds//0.028:587.58//Hs.2363:L36069
 35 F-Y79AA1002361//ESTs//8.7e-29:149.100//Hs.156074:AA824377
 F-Y79AA1002399
 F-Y79AA1002407//ESTs//1.5e-25:183.89//Hs.110031:T52569
 F-Y79AA1002416//CTP synthetase//9.1e-51:489.72//Hs.84112:X52142
 40 F-Y79AA1002431
 F-Y79AA1002433//EST//0.0037:94.71//Hs.136780:AA772318
 F-Y79AA1002472//Homo sapiens DNA from chromosome 19, BAC 33152//1.1e-37:263.69//Hs.55452:AC003973
 F-Y79AA1002482//ESTs//1.4e-49:313.80//Hs.132590:AI160765
 F-Y79AA1002487//Insulin-like growth factor binding protein 2//0.43:249.61//Hs.162:X16302

Homology Search Result Data 5.

[0310] The result of the homology search of the Human Unigene using the clone sequence of 3'-end.

[0311] Data include

the name of clone,
 title of the top hit data,
 the P-value: the length of the compared sequence: identity (%), and
 the Accession No. of the top hit data, as in the order separated by //.

[0312] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

[0313] Data are not shown for the clones in which the P-value was higher than 1.

R-HEMBA1000005/ESTs. Highly similar to HYPOTHETICAL 31.6 KD PROTEIN F54F2.9 IN CHROMOSOME II [Caenorhabditis elegans]]/5.6e-93:501.93//Hs. 13015:AA628434
R-HEMBA1000030//Human POU domain protein (Bm-3b) mRNA, complete cds//0.83:314.61//Hs. 266:U06233
5 R-HEMBA1000042//Archain//1.4e-45:282.89//Hs. 33642:X81198
R-HEMBA1000046//Human mRNA for KIAA0118 gene, partial cds//8.3e-52:528.72//Hs. 154326:D42087
R-HEMBA1000050//EST//0.043:155.63//Hs. 149031:A1243340
R-HEMBA1000076//ESTs//3.1e-77:394.97//Hs. 111742:R39329
R-HEMBA1000111//ESTs//1.7e-33:228.85//Hs. 146811:AA410788
R-HEMBA1000129//ESTs. Weakly similar to contains similarity to helicases [C.elegans]]/4.4e-90:502.90//Hs. 55918:AA151667
10 R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.1e-100:514.94//Hs. 27197:AB018340
R-HEMBA1000150//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1e-45:435.77//Hs. 153026:AB014540
15 R-nnnnnnnnnnnn/ESTs. Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]]/7.7e-92:428:100//Hs. 126925:AA931237
R-HEMBA1000158
R-nnnnnnnnnnnn/ESTs. Weakly similar to F13B12 [C. elegans]]/1.3e-05:58.91//Hs. 5570:A377863
R-HEMBA1000180//ESTs//7.7e-90:461.95//Hs. 159200:N50545
20 R-HEMBA1000185//ESTs//1.3e-72:37.196//Hs. 134506:AA308366
R-HEMBA1000193//ESTs//4.2e-103:481.99//Hs. 143251:AA769927
R-HEMBA1000201//Human Inl1 mRNA, complete cds//3.0e-25:137.99//Hs. 155626:U04847
R-HEMBA1000213//ESTs//5.4e-85:465.94//Hs. 23412:AA133311
R-HEMBA1000216//ESTs//3.0e-37:311.79//Hs. 137875:AA993532
25 R-nnnnnnnnnnnn/EST//2.2e-100:498.98//Hs. 161570:W80404
R-HEMBA1000231//Homo sapiens KIAA0414 mRNA, partial cds//2.7e-34:287.70//Hs. 127649:AB007874
R-HEMBA1000243//Homo sapiens mRNA for KIAA0475 protein, complete cds//11.3e-23:276.75//Hs. 5737:AB007944
30 R-HEMBA1000244//ESTs//2.3e-88:455.96//Hs. 8929:AA719019
R-HEMBA1000251//ESTs//0.96:411.56//Hs. 120277:A1243808
R-HEMBA1000264//ESTs//3.7e-97:487.96//Hs. 29258:W37424
R-nnnnnnnnnnnn/ESTs. Moderately similar to ovarian-specific protein [R.norvegicus]]/4.9e-14:208.73//Hs. 93332:AA811920
35 R-HEMBA1000282//ESTs//2.5e-38:216.94//Hs. 120757:R92485
R-HEMBA1000288//ESTs//2.6e-43:289.96//Hs. 151365:AA643962
R-HEMBA1000290//ESTs//5.1e-110:543.96//Hs. 139068:AA516409
R-HEMBA1000302//Homo sapiens mRNA for KIAA0527 protein, partial cds//1.0:122.67//Hs. 129748:AB011099
R-nnnnnnnnnnnn/ESTs//7.4e-76:386.97//Hs. 22276:AA191323
40 R-nnnnnnnnnnnn//Human Ca2+-dependent activator protein for secretion mRNA, complete cds//8.8e-30:160.98//Hs. 151301:U36448
R-HEMBA1000307//ESTs. Highly similar to 8A-2V protein [M.musculus]]/1.1e-103:489.99//Hs. 108881:AI018024
R-nnnnnnnnnnnn/ESTs//9.3e-99:472.98//Hs. 163512:AA903238
R-HEMBA1000338//EST//5.1e-49:278.92//Hs. 150815:AI302560
45 R-HEMBA1000351//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.1e-42:270.88//Hs. 73614:U83460
R-HEMBA1000355//ESTs//1.0e-105:531.96//Hs. 61762:AA422243
R-HEMBA1000357//Human knip1 repeat mma (cdna clone pc-d-knip-4), 3' end//9.4e-89:432.87//Hs. 139107:K00629
50 R-HEMBA1000366//ESTs//1.1e-99:524.95//Hs. 11785:T65857
R-HEMBA1000369//ESTs//6.5e-70:355.96//Hs. 124847:AA843938
R-HEMBA1000376//Human mRNA for KIAA0205 gene, complete cds//3.6e-44:388.77//Hs. 3610:D86960
R-HEMBA1000387//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.5e-47:337.83//Hs. 73614:U83460
55 R-HEMBA1000390//Oxytocin receptor//2.4e-16:428.62//Hs. 2820:X64878
R-HEMBA1000392//ESTs//3.9e-105:531.96//Hs. 130661:A1340248
R-HEMBA1000396//ESTs. Weakly similar to line-1 protein ORF2 [H.sapiens]]/1.1e-44:447.75//Hs. 42849:N31920
R-HEMBA1000411//ESTs. Weakly similar to ankyrin 3, long form [H.sapiens]]/6.1e-92:373.99//Hs. 48675:AI005282

- R-HEMBA1000418//ESTs//3.1e-66:315:100//Hs.94133:AI270700
 R-HEMBA1000422//ESTs//1.6e-99:464:99//Hs.33024:AA002140
 R-HEMBA1000428//Homo sapiens mRNA for oligophrenin 1/4.9e-85:535:87//Hs.158122:AJ001189
 R-HEMBA1000434//ESTs//3.7e-53:266:99//Hs.22782:Z38143
 5 R-HEMBA1000442//ESTs//0.93:322:57//Hs.144763:AI218014
 R-HEMBA1000456//ESTs//4.1e-48:277:93//Hs.6937:AA524349
 R-HEMBA1000459//ESTs//0.010:184:63//Hs.128797:AI246316
 R-HEMBA1000460
 R-HEMBA1000464//EST//0.082:87:70//Hs.147977:AI262370
 10 R-HEMBA1000469//Small inducible cytokine A5 (RANTES)//1.4e-65:494:81//Hs.155464:AF088219
 R-HEMBA1000488//ESTs, Weakly similar to The KIAA0132 gene product is related to Drosophila melanogaster ring canal protein. [H.sapiens]//1.1e-31:181:94//Hs.61454:AA312449
 R-HEMBA1000490//ESTs//6.4e-17:132:86//Hs.32855:N25528
 R-HEMBA1000491//ESTs//2.2e-22:171:85//Hs.8035:AA195087
 15 R-HEMBA1000504//ESTs//0.016:282:58//Hs.130778:AI077571
 R-HEMBA1000505//EST//6.1e-15:116:87//Hs.162783:AA627318
 R-HEMBA1000508//ESTs//1.1e-28:244:81//Hs.132722:AA618531
 R-HEMBA1000518//EST//0.60:141:60//Hs.97831:AA400885
 R-HEMBA1000519//ESTs//2.8e-64:334:96//Hs.97885:AA402414
 20 R-HEMBA1000520//ESTs//6.9e-104:503:97//Hs.18370:AA947280
 R-HEMBA1000523//Cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD//4.0e-55:203:92//Hs.155510:U15782
 R-HEMBA1000531//ESTs, Weakly similar to HEAT SHOCK 70 KD PROTEIN 1 [H.sapiens]//1.3e-117:550:99//Hs.99722:AI422277
 25 R-HEMBA1000540//ESTs//4.7e-72:350:98//Hs.109755:AA180809
 R-HEMBA1000545//Homo sapiens clone 23892 mRNA sequence//3.7e-68:549:80//Hs.91916:AF035317
 R-nnnnnnnnnnn//ESTs//2.3e-66:342:97//Hs.71916:AA219699
 R-HEMBA1000557//EST//1.5e-49:297:90//Hs.149580:AI281881
 R-HEMBA1000561//ESTs, Moderately similar to zinc finger protein [R.norvegicus]//1.8e-108:550:96//Hs.26799:W74481
 30 R-HEMBA1000563//Adenosine kinase//0.16:367:58//Hs.94382:U50196
 R-HEMBA1000568//ESTs//5.1e-42:321:82//Hs.141024:H07128
 R-nnnnnnnnnnn
 R-HEMBA1000575//ESTs//3.8e-45:352:80//Hs.146811:AA410788
 35 R-HEMBA1000588//ESTs//0.18:122:67//Hs.140507:AA761944
 R-HEMBA1000591//Homo sapiens mRNA for EIB-55kDa-associated protein//3.9e-113:591:94//Hs.155218:AJ007509
 R-HEMBA1000592//TYROSINE-PROTEIN KINASE
 ITK/TSK//0.024:309:61//Hs.89519:L10717
 40 R-HEMBA1000594//ESTs//8.6e-07:172:68//Hs.160289:AI168041
 R-HEMBA1000604//Human telomerase-associated protein TP-1 mRNA, complete cds//1.5e-19:129:93//Hs.158334:U86136
 R-HEMBA1000608//ESTs//2.2e-95:506:94//Hs.6103:AA496424
 R-HEMBA1000622//ESTs//3.8e-10:440:61//Hs.137538:AA769438
 45 R-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//1.4e-86:442:97//Hs.26252:AA643235
 R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.7e-99:443:97//Hs.60103:AB014590
 R-HEMBA1000655//Human mRNA for KIAA0392 gene, partial cds//1.3e-50:426:79//Hs.40100:AB002390
 50 R-HEMBA1000657//ESTs//3.0e-74:419:93//Hs.109477:AA477929
 R-HEMBA1000662//EST//1.1e-90:425:99//Hs.122144:AA780136
 R-HEMBA1000673//ESTs//1.2e-101:473:99//Hs.138215:AI123922
 R-HEMBA1000682//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403
 R-HEMBA1000686//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//6.8e-18:137:86//Hs.7049:AI141736
 55 R-HEMBA1000702//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//7.4e-52:345:84//Hs.144563:AF057280
 R-HEMBA1000705//EST//0.21:139:63//Hs.132687:AI033672

- R-HEMBA1000719//ESTs//8.4e-90:484.94//Hs.29005:AA477213
 R-HEMBA1000722//ESTs, Weakly similar to similar to enoyl-CoA hydratases/isomerases [C.elegans]//7.2e-113:572.95//Hs.28644:AI018612
 R-HEMBA1000726//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//2.8e-40:449.75//Hs.74478:U33931
 R-HEMBA1000727//ESTs//0.0047:267.60//Hs.133095:AA927777
 R-HEMBA1000747//EST//3.9e-20:160.85//Hs.99048:AA446110
 R-HEMBA1000749//Small inducible cytokine A5 (RANTES)//4.7e-37:286.82//Hs.155464:AF088219
 R-HEMBA1000752//EST//0.041:39.94//Hs.127772:AA961131
 R-HEMBA1000769//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.6e-32:309.75//Hs.10458:AF088219
 R-HEMBA1000773//EST//7.5e-05:201.63//Hs.122887:AA767612
 R-HEMBA1000774//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//1.3e-48:284.90//Hs.103458:X53795
 R-HEMBA1000791//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:291.87//Hs.154326:D42087
 R-HEMBA1000817//ESTs//8.3e-95:445.99//Hs.107357:AA983939
 R-HEMBA1000822//ESTs//1.1e-107:522.97//Hs.92832:AA631027
 R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRM160) mRNA, complete cds//2.2e-44:228.98//Hs.18192:AF048977
 R-HEMBA1000843//Homo sapiens LIM protein mRNA, complete cds//6.6e-46:410.77//Hs.154103:AF061258
 R-HEMBA1000851
 R-HEMBA1000852//Aldehyde dehydrogenase 10 (fatty aldehyde dehydrogenase)//3.7e-33:284.80//Hs.159608:U46689
 R-HEMBA1000867//EST//2.0e-17:211.74//Hs.145670:AI265794
 R-HEMBA1000869//ESTs//3.1e-16:237.71//Hs.116518:AA653202
 R-HEMBA1000870//ESTs//1.6e-43:222.98//Hs.69564:AA203608
 R-HEMBA1000872//ESTs//1.9e-93:453.98//Hs.152622:AA594951
 R-HEMBA1000876//Small inducible cytokine A5 (RANTES)//3.0e-41:329.79//Hs.155464:AF088219
 R-HEMBA1000908//ESTs//1.6e-51:291.92//Hs.12247:AI203154
 R-HEMBA1000910//EST//0.98:139.64//Hs.132687:AI033672
 R-HEMBA1000918//EST//9.6e-30:152.84//Hs.162136:AA526508
 R-HEMBA1000919
 R-HEMBA1000934//ESTs//4.1e-38:254.89//Hs.87784:AA460597
 R-HEMBA1000942//ESTs//3.5e-20:172.69//Hs.160065:AI018619
 R-HEMBA1000943//Homo sapiens mRNA for KIAA0748 protein, complete cds//1.3e-44:281.78//Hs.33187:AB018291
 R-HEMBA1000946//ESTs//1.6e-68:352.96//Hs.21331:H93074
 R-HEMBA1000960//Homo sapiens tapasin (NGS-17) mRNA, complete cds//4.0e-61:347.81//Hs.5247:AF029750
 R-HEMBA1000968//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//6.8e-51:362.84//Hs.159187:AB007977
 R-HEMBA1000971//ESTs//2.8e-41:246.91//Hs.104287:AI363498
 R-HEMBA1000972//Homo sapiens mRNA for XPR2 protein//7.3e-44:341.81//Hs.44766:AJ007590
 R-HEMBA1000974//ESTs//1.4e-32:166.100//Hs.149274:AI018170
 R-HEMBA1000975//Oxytocin receptor//2.7e-46:563.73//Hs.2820:X64878
 R-HEMBA1000985//ESTs//4.4e-05:125.69//Hs.147434:AI214464
 R-HEMBA1000986//ESTs//7.8e-44:266.84//Hs.163784:N54902
 R-HEMBA1000991//EST//1.4e-42:162.86//Hs.149580:AI281881
 R-HEMBA1001007
 R-HEMBA1001008//ESTs//2.3e-82:463.92//Hs.10339:AA058764
 R-HEMBA1001009//ESTs, Weakly similar to non-lens beta gamma-crystallin like protein [H.sapiens]//2.6e-58:280:100//Hs.128738:AA970836
 R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//3.3e-115:587.95//Hs.158287:AB007937
 R-HEMBA1001019//Cell division cycle 2, G1 to S and G2 to M//1.1e-24:140.95//Hs.58393:X05360
 R-HEMBA1001020//ESTs//0.52:86.72//Hs.69683:AA115292
 R-HEMBA1001022//ESTs//3.4e-18:102.100//Hs.63243:AI123912
 R-HEMBA1001024//ESTs//1.9e-07:262.61//Hs.124399:AA832336
 R-HEMBA1001026//ESTs//0.0017:142.67//Hs.144109:AI345543

- R-nnnnnnnnnnnnn//Ankyrin G//0.23:244:60//Hs.75893:U13616
 R-HEMBA1001051//Homo sapiens mRNA for KIAA0621 protein, partial cds//6.4e-21:186:79//Hs.132942:AB014521
 R-HEMBA1001052//ESTs//5.4e-107:497:99//Hs.121773:AI357886
 5 R-HEMBA1001060//ESTs//1.1e-31:298:80//Hs.24821:AA044813
 R-HEMBA1001071//Alpha-1 type 3 collagen//9.1e-34:179:98//Hs.119571:X14420
 R-HEMBA1001077//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//2.7e-21:417:64//Hs.127338:AB007961
 R-HEMBA1001080
 10 R-HEMBA1001085//ESTs//1.9e-47:385:79//Hs.146811:AA107088
 R-HEMBA1001088//ESTs//2.8e-102:548:93//Hs.127273:AA522674
 R-HEMBA1001094
 R-HEMBA1001099//ESTs//0.24:41:97//Hs.18612:T99245
 R-HEMBA1001109//Small inducible cytokine A5 (RANTES)//2.4e-46:396:80//Hs.155464:AF088219
 15 R-HEMBA1001121//ESTs//1.7e-15:216:71//Hs.141605:H92974
 R-HEMBA1001122//ESTs//2.0e-90:474:94//Hs.107884:AA131320
 R-HEMBA1001123//B-CELL GROWTH FACTOR PRECURSOR//2.7e-45:319:84//Hs.99879:M15530
 R-HEMBA1001133//ESTs//1.2e-92:443:99//Hs.99626:AA632341
 R-HEMBA1001137//ESTs//2.0e-86:426:97//Hs.157103:W60265
 20 R-HEMBA1001140//Small inducible cytokine A5 (RANTES)//2.9e-45:323:83//Hs.155464:AF088219
 R-HEMBA1001172//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.1e-39:309:82//Hs.96337:AA225358
 R-HEMBA1001174//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.21:238:60//Hs.127338:AB007961
 25 R-HEMBA1001197//ESTs//0.010:388:61//Hs.14881:R91896
 R-HEMBA1001208//ESTs, Highly similar to Similar to S.cerevisiae hypothetical protein 5 [H.sapiens]//0.27:305:62//Hs.100238:U69194
 R-HEMBA1001226//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.0e-54:333:81//Hs.113283:AF018080
 R-HEMBA1001235//EST//2.3e-07:42:92//Hs.141620:N63316
 30 R-HEMBA1001247//ESTs, Weakly similar to WWP2 [H.sapiens]//2.9e-20:160:87//Hs.103102:W55932
 R-HEMBA1001257//ESTs//3.3e-112:544:97//Hs.128749:AA779728
 R-HEMBA1001265//ESTs//8.7e-116:564:98//Hs.155150:AI061435
 R-nnnnnnnnnnnnn//ESTs, Weakly similar to Lpa8p [S. cerevisiae]//2.4e-35:239:87//Hs.103919:AA159181
 R-HEMBA1001286//ESTs//1.4e-97:507:95//Hs.26244:AI352674
 35 R-HEMBA1001289//ESTs//8.2e-44:122:96//Hs.76267:AA877534
 R-HEMBA1001294//ESTs//1.0:140:65//Hs.149638:AI298324
 R-HEMBA1001299//Small inducible cytokine A5 (RANTES)//1.1e-45:307:84//Hs.155464:AF088219
 R-HEMBA1001302//Homo sapiens mRNA for APC 2 protein, complete cds//0.53:89:68//Hs.20912:AB012162
 R-HEMBA1001303//EST//0.00053:271:60//Hs.156148:AI333214
 40 R-HEMBA1001310//ESTs//1.4e-91:486:93//Hs.86228:AA206019
 R-HEMBA1001319//ESTs//0.051:228:61//Hs.99404:AA953977
 R-HEMBA1001323//ESTs//6.2e-83:401:98//Hs.47343:AI282950
 R-HEMBA1001326//ESTs, Weakly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION [S. cerevisiae]//1.3e-77:458:92//Hs.9398:N41838
 45 R-HEMBA1001327//ESTs//0.60:251:58//Hs.117162:AA701259
 R-HEMBA1001330//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-46:249:78//Hs.113283:AF018080
 R-HEMBA1001351//ESTs//0.13:230:57//Hs.138510:R94816
 R-HEMBA1001361//ESTs//3.5e-107:570:94//Hs.7727:AA142837
 R-HEMBA1001375//ESTs//1.1e-96:454:99//Hs.59584:AA587334
 50 R-HEMBA1001377//ESTs//8.5e-91:459:95//Hs.61859:AA628550
 R-HEMBA1001383//ESTs//0.077:381:56//Hs.163093:AA745458
 R-HEMBA1001387//ESTs//2.0e-85:405:99//Hs.152127:AI246482
 R-HEMBA1001388//ESTs//1.5e-83:395:99//Hs.105191:AA133439
 R-HEMBA1001391//ESTs//7.7e-90:455:96//Hs.120905:R22204
 55 R-HEMBA1001398//Thromboxane A2 receptor//4.0e-46:279:89//Hs.89887:D38081
 R-HEMBA1001405//ESTs//1.2e-98:485:97//Hs.73267:W16714
 R-HEMBA1001407//ESTs//2.2e-76:365:99//Hs.110128:AA584364
 R-HEMBA1001411//ESTs//1.2e-102:476:100//Hs.143162:AI380343

- R-HEMBA1001413//ESTs//3.7e-66:321:98//Hs.152472:AA041199
 R-HEMBA1001415
 R-HEMBA1001432//Putative mismatch repair/binding protein hMSH3//7.9e-42:183:82//Hs.42674:U61981
 R-HEMBA1001433//ESTs//1.4e-34:240:77//Hs.95611:U51704
 5 R-HEMBA1001435//ESTs//5.6e-33:292:70//Hs.116315:AA629263
 R-HEMBA1001442//ESTs//0.76:414:58//Hs.156189:AI419982
 R-HEMBA1001446//ESTs//2.2e-95:447:99//Hs.154091:AA767546
 R-HEMBA1001450//ESTs//1.0e-93:491:94//Hs.16130:AA195077
 R-HEMBA1001454//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-47:304:88//Hs.23094:M19503
 10 R-HEMBA1001455//ESTs//7.1e-103:482:99//Hs.97407:AI417220
 R-HEMBA1001463
 R-HEMBA1001476//Human mRNA for KIAA0186 gene, complete cds//2.0e-25:409:66//Hs.36232:D80008
 R-HEMBA1001478
 R-HEMBA1001497
 15 R-HEMBA1001510//ESTs//3.3e-44:381:78//Hs.139882:AA864426
 R-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//5.9e-79:528:84//Hs.23094:M19503
 R-HEMBA1001517//ESTs//5.8e-32:272:81//Hs.119512:AA487269
 R-HEMBA1001522//ESTs//1.7e-84:364:95//Hs.117858:AA-702493
 R-HEMBA1001526//ESTs//1.8e-93:527:93//Hs.10624:N64723
 20 R-HEMBA1001533//ESTs//1.9e-42:211:100//Hs.55830:AA580270
 R-HEMBA1001557//ESTs//4.2e-83:413:97//Hs.47546:AA181348
 R-HEMBA1001566//Small inducible cytokine A5 (RANTES)//3.4e-50:304:88//Hs.155464:AF088219
 R-HEMBA1001569//POU domain, class 3, transcription factor 4//2.3e-06:259:62//Hs.2229:X82324
 R-HEMBA1001570//Homo sapiens pendrin (PDS) mRNA, complete cds//3.5e-47:456:77//Hs.159275:AF030880
 25 R-HEMBA1001579//ESTs//0.11:299:60//Hs.106090:AA457030
 R-HEMBA1001581//ESTs//0.016:350:61//Hs.124664:AI015652
 R-HEMBA1001585//Human mRNA for KIAA0331 gene, complete cds//0.30:251:63//Hs.146395:AB002329
 R-HEMBA1001589
 R-HEMBA1001595//ESTs, Weakly similar to SEPTIN 2 [D.melanogaster]//6.9e-71:431:88//Hs.26625:W25874
 30 R-HEMBA1001608//Human kpnI repeat mrna (cdna clone pcd-kpnI-8), 3' end//1.3e-73:533:82//Hs.103948:K00627
 R-HEMBA1001620//ESTs, Highly similar to MYO-INOSITOL-1-PHOSPHATE SYNTHASE [Arabidopsis thaliana] //4.5e-93:537:90//Hs.20218:AA628530
 R-HEMBA1001636//ESTs//4.9e-53:267:97//Hs.47459:AA700158
 35 R-HEMBA1001640//ESTs//2.9e-27:299:72//Hs.65236:AA927623
 R-HEMBA1001655//ESTs, Weakly similar to Mi-2 protein [H.sapiens]//1.2e-86:442:95//Hs.63888:AA203398
 R-HEMBA1001655//ESTs//1.5e-101:516:95//Hs.86541:AA214554
 R-HEMBA1001658
 40 R-HEMBA1001661//Homo sapiens protocadherin 68 (PCH68) mRNA, complete cds//1.3e-16:427:61//Hs.106511:AF029343
 R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-93:493:92//Hs.107254:AC005943
 R-HEMBA1001675
 45 R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA, complete cds//4.2e-103:534:94//Hs.7381:AF038962
 R-HEMBA1001681//ESTs//6.0e-49:292:92//Hs.65588:AA523424
 R-HEMBA1001702//ESTs//9.0e-98:478:97//Hs.28661:AA805916
 R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete cds//6.3e-98:483:96//Hs.31720:AB014598
 50 R-HEMBA1001711//ESTs//5.8e-83:398:98//Hs.34804:AA514960
 R-HEMBA1001712//ESTs//0.028:202:63//Hs.105790:AA528095
 R-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]//1.8e-46:236:98//Hs.132948:AA194452
 55 R-HEMBA1001718//Small inducible cytokine A5 (RANTES)//8.6e-43:166:88//Hs.155464:AF088219
 R-HEMBA1001723//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisiae]//7.1e-88:431:96//Hs.29203:AI344105
 R-HEMBA1001731//EST//0.25:100:68//Hs.149171:AI245712

- R-HEMBA1001734//Human mRNA for KIAA0355 gene, complete cds//2.6e-39:366:77//Hs.153014:AB002353
R-HEMBA1001744
- R-HEMBA1001745//ESTs//6.6e-05:244:62//Hs.157663:AI358623
R-HEMBA1001746//EST//4.9e-65:409:88//Hs.124673:AA858162
- 5 R-HEMBA1001761//ESTs//1.9e-44:315:84//Hs.159510:AA297145
R-HEMBA1001781//ESTs//3.0e-98:462:99//Hs.60059:AI057306
R-HEMBA1001784//EST//1.0e-12:250:68//Hs.152366:AA486721
R-HEMBA1001791//EST//1.4e-47:292:89//Hs.163333:AA879053
R-HEMBA1001800//ESTs//8.4e-37:314:79//Hs.105151:AA970243
- 10 R-HEMBA1001803//ESTs//4.5e-99:465:99//Hs.135159:AI095823
R-nnnnnnnnnnn/Zinc finger protein 148 (pHZ-52)//0.78:232:57//Hs.112180:AF039019
R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//9.0e-114:548:98//Hs.118164:AB007969
R-HEMBA1001809//EST//3.8e-63:292:89//Hs.158591:AI369334
R-HEMBA1001815//Calcium modulating ligand//1.1e-47:299:87//Hs.13572:AF068179
R-HEMBA1001819//ZINC FINGER PROTEIN HF.12//1.2e-16:259:69//Hs.155470:X07290
R-HEMBA1001820//ESTs//2.6e-86:404:100//Hs.112881:AA620707
R-nnnnnnnnnnn/ESTs//2.2e-101:480:99//Hs.159940:AA971578
R-HEMBA1001824//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//6.2e-27:147:97//Hs.23476:AA401210
- 20 R-HEMBA1001835//EST//0.79:216:64//Hs.47437:N52250
R-HEMBA1001844//ESTs//4.7e-62:319:95//Hs.55200:N98513
R-HEMBA1001847//ESTs//2.3e-102:522:95//Hs.20879:AA845446
R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//1.1e-109:553:96//Hs.78946:AB014517
- 25 R-HEMBA1001864//ESTs//7.4e-94:449:99//Hs.132776:AI142853
R-HEMBA1001866//Myelin oligodendrocyte glycoprotein (alternative products)//1.9e-37:357:76//Hs.53217:Z48051
R-nnnnnnnnnnn/ESTs, Weakly similar to trithorax homolog HTX, version 2 [H.sapiens]//2.3e-32:193:94//Hs.9489:R64329
- 30 R-HEMBA1001888//H.sapiens mRNA for urea transporter//2.0e-47:425:78//Hs.66710:X96969
R-HEMBA1001896//ESTs//3.5e-56:274:99//Hs.129018:H03128
R-HEMBA1001910
R-HEMBA1001912//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.5e-73:347:100//Hs.30991:AA994438
- 35 R-HEMBA1001913//ESTs, Highly similar to GCN20 PROTEIN [Saccharomyces cerevisiae]//5.1e-57:320:91//Hs.91251:U66685
R-HEMBA1001915//ESTs//4.9e-88:459:95//Hs.122810:AI273706
R-HEMBA1001918//ESTs//1.2e-106:505:99//Hs.98518:AI027125
R-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//5.5e-107:534:96//Hs.154934:AF000145
- 40 R-HEMBA1001939//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.9e-99:482:98//Hs.96849:AA879470
R-HEMBA1001940//Human mRNA for KIAA0392 gene, partial cds//5.6e-45:336:82//Hs.40100:AB002390
R-HEMBA1001942//EST//2.6e-84:397:99//Hs.145444:AI203668
R-HEMBA1001945//ESTs//1.4e-92:437:99//Hs.144565:AI192452
R-HEMBA1001950//ESTs//3.9e-43:280:88//Hs.84429:N28866
R-HEMBA1001960//ESTs//0.040:243:62//Hs.29567:AA640421
R-HEMBA1001962//ESTs//0.0071:113:69//Hs.49792:N70048
R-HEMBA1001964//ESTs//3.0e-38:239:87//Hs.158126:W26825
- 50 R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolat of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs//1.8e-106:517:97//Hs.11050:AL031178
R-HEMBA1001979//EST//0.039:167:63//Hs.129451:AA993932
R-HEMBA1001987//ESTs//3.1e-44:320:83//Hs.136839:H93717
R-HEMBA1001991//Human mRNA for KIAA0355 gene, complete cds//9.5e-47:303:88//Hs.153014:AB002353
- 55 R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase 2C (beta)//1.6e-91:448:97//Hs.5687:AJ005801
R-HEMBA1002008//ESTs//9.2e-47:297:87//Hs.142314:AA347930
R-HEMBA1002018//ESTs//9.4e-21:118:97//Hs.7871:AI041837

- R-HEMBA1002022//Human mRNA for KIAA0075 gene, partial cds//0.25:196:63//Hs.1189:D38550
 R-HEMBA1002035//ESTs//7.7e-101:475:99//Hs.8858:AI131538
 R-HEMBA1002039//H. sapiens mRNA for phosphoinositide 3-kinase//0.68:256:64//Hs.101238:Y11312
 R-HEMBA1002049//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.4e-51:254:85//Hs.15731:AB011135
 R-HEMBA1002084//EST//0.31:219:60//Hs.162396:AA572764
 R-HEMBA1002092//EST//6.4e-72:342:99//Hs.148533:AI200996
 R-HEMBA1002100//EST//5.6e-38:258:85//Hs.103094:W52354
 R-HEMBA1002102//Thiopurine S-methyltransferase//1.4e-46:403:79//Hs.51124:AF019369
 R-HEMBA1002113//Prostaglandin 12 (prostacyclin) synthase //1.4e-76:280:90//Hs.61333:D83402
 R-HEMBA1002119//Homo sapiens ORF12P pseudogene, complete sequence//1.4e-87:362:94//Hs.103443:AF065854
 R-HEMBA1002125//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.7e-16:94:100//Hs.107747:AI357868
 R-HEMBA1002139//H. sapiens mRNA for nebulin//0.0019:68:88//Hs.83870:X33957
 R-HEMBA1002144//ESTs//3.1e-30:259:72//Hs.141575:AA211734
 R-HEMBA1002150//ESTs//7.1e-105:543:95//Hs.32275:AA595199
 R-HEMBA1002151//ESTs//2.2e-35:178:100//Hs.77703:W19642
 R-HEMBA1002153//EST//4.5e-49:458:77//Hs.141708:W44337
 R-HEMBA1002160//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds//1.4e-36:400:75//Hs.75474:AF023674
 R-HEMBA1002161//Homo sapiens EVI5 homolog mRNA, complete cds//1.9e-33:294:77//Hs.26929:AF008915
 R-HEMBA1002162//ESTs//1.0e-47:317:85//Hs.48919:N64043
 R-HEMBA1002166//Thromboxane A2 receptor//6.8e-46:296:81//Hs.89887:D38081
 R-HEMBA1002177//EST//2.6e-42:215:99//Hs.116880:AA662457
 R-HEMBA1002185//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//6.0e-42:419:73//Hs.159523:AF001622
 R-HEMBA1002189//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.4e-29:244:72//Hs.119387:AB007959
 R-HEMBA1002191//ESTs//2.6e-31:275:66//Hs.133852:AI076357
 R-HEMBA1002199//Human Line-1 repeat mRNA with 2 open reading frames//4.3e-84:557:84//Hs.23094:M19503
 R-HEMBA1002204//EST//0.00057:113:71//Hs.144868:AI202342
 R-HEMBA1002212//ESTs//1.5e-48:277:93//Hs.104741:AI393315
 R-HEMBA1002215//ESTs//1.1e-23:158:90//Hs.152529:AA897151
 R-HEMBA1002226//Homo sapiens mRNA for KIAA0706 protein, complete cds//5.1e-21:230:75//Hs.139648:AB014606
 R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//1.5e-47:238:98//Hs.25664:AF089814
 R-HEMBA1002237//ESTs//6.9e-35:357:76//Hs.116518:AA653202
 R-HEMBA1002253//EST//6.0e-19:125:81//Hs.140596:AA829426
 R-HEMBA1002257
 R-HEMBA1002267//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGENIC REGION [S. cerevisiae]//1.3e-31:201:91//Hs.114673:W72675
 R-HEMBA1002270//ESTs//4.6e-100:483:97//Hs.34940:AI264314
 R-HEMBA1002321//ESTs//2.3e-85:403:99//Hs.120388:AA723595
 R-HEMBA1002328//ESTs//1.3e-90:423:100//Hs.117936:AI280818
 R-HEMBA1002337//ESTs//8.7e-24:147:93//Hs.9893:AA007679
 R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8e-130:642:96//Hs.6162:AB018314
 R-HEMBA1002348//ESTs//5.0e-71:387:93//Hs.30494:H04822
 R-HEMBA1002349//ESTs//9.7e-88:420:98//Hs.132972:AA543094
 R-nnnnnnnnnnn//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//3.9e-123:661:93//Hs.119023:AF092563
 R-HEMBA1002381//ESTs//1.3e-73:352:99//Hs.56121:AA781435
 R-HEMBA1002389//EST//2.3e-05:132:69//Hs.37558:H58237
 R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//3.9e-63:358:91//Hs.25527:AC005954
 R-HEMBA1002419//ESTs, Weakly similar to APK1 antigen [H. sapiens]//5.6e-87:429:96//Hs.13209:AI417849
 R-HEMBA1002430//ESTs//0.10:388:57//Hs.119238AA476267
 R-HEMBA1002439//Human mRNA for KIAA0080 gene, partial cds//2.0e-22:181:80//Hs.74554:D38522

- R-HEMBA1002458//ESTs//1.8e-88.448.95//Hs.97914:AA769069
 R-HEMBA1002460//Catalase//0.67.314.60//Hs.76359:X04085
 R-HEMBA1002462//EST//0.032:44.88//Hs.161536:N80395
- 5 R-nnnnnnnnnnn//ESTs, Weakly similar to F08G12.1 [C. elegans]//5.4e-95.488.95//Hs.108115:AA582193
 R-HEMBA1002477//Homo sapiens KIAA0395 mRNA, partial cds//2.5e-37:281:80//Hs.43681:AL022394
 R-HEMBA-1002486//Small inducible cytokine A5 (RANTES)//1.1e-49:311.88//Hs.155464:AF088219
- R-HEMBA1002495//ESTs//1.2e-94.457.98//Hs.42140:A1188995
 R-HEMBA1002498//ESTs//1.7e-35:240.78//Hs.119871:AA705133
 R-HEMBA1002503//ESTs//2.3e-14.64.85//Hs.140190:AA701449
- 10 R-HEMBA1002508//ESTs//0.00057:160.62//Hs.149661:AA872990
 R-nnnnnnnnnnn//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//2.3e-113:456.92//Hs.6764:AJ011972
 R-HEMBA1002515//EST//1.0:153.63//Hs.118045:N51715
- R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds//5.1e-106:564.93//Hs.129928:AB007923
- 15 R-HEMBA1002542//ESTs//1.0e-101:539.93//Hs.93872:AA524700
 R-HEMBA1002547//EST//8.7e-27:151.96//Hs.132145:A1041804
 R-HEMBA1002552//EST//5.9e-49:335.85//Hs.149580:A1281881
 R-HEMBA1002555//ESTs//1.1e-77:461.91//Hs.38750:N30012
- 20 R-HEMBA1002558//Homo sapiens 4F5S mRNA, complete cds//1.3e-42:264.89//Hs.32567:AF073519
 R-HEMBA1002561//Small inducible cytokine A5 (RANTES)//6.4e-40:196.78//Hs.155464:AF088219
 R-nnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds//1.4e-120:587.97//Hs.151411:AF075587
- R-HEMBA1002583//ESTs//7.1e-79:410.95//Hs.21599:AA478904
- 25 R-HEMBA1002590//EST//3.3e-54:278.97//Hs.138637:N20838
 R-HEMBA1002592//ESTs//2.6e-44:500.74//Hs.110934:N26055
 R-HEMBA1002621
- R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//2.2e-77:380.97//Hs.91338:AB018351
- 30 R-HEMBA1002628//ESTs//0.0020:167.66//Hs.140605:AA830881
 R-HEMBA1002629//ESTs//0.00014:50.100//Hs.119132:AA398715
 R-HEMBA1002645//EST//2.1e-37:285.82//Hs.141728:W73041
 R-HEMBA1002651//EST//2.2e-23:374.69//Hs.139357:AA420970
- R-HEMBA1002659//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.5e-53:406.81//Hs.108966:U48696
- 35 R-HEMBA1002661//Homo sapiens mRNA for KIAA0764 protein, complete cds//1.1e-41:296.84//Hs.6232:AB018307
 R-HEMBA1002666//EST//4.4e-09:79.88//Hs.72015:AA151945
- R-HEMBA1002678//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//7.6e-104:560.92//Hs.161748:T64896
- 40 R-nnnnnnnnnnn//EST//0.15:136.69//Hs.129570:AA995396
 R-HEMBA1002688//T-CELL SURFACE PROTEIN TACTILE PRECURSOR//0.16:247.62//Hs.142023:M88282
 R-HEMBA1002696//ESTs//3.5e-94:529.92//Hs.16725:AA196477
- R-HEMBA1002712//Homo sapiens mRNA for KIAA0772 protein, complete cds//6.0e-46:302.86//Hs.15519:AB018315
- 45 R-HEMBA1002716//ESTs//1.3e-109:555.96//Hs.9812:AA147884
 R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.8e-37:287.81//Hs.132942:AB014521
- R-HEMBA1002730//ESTs//1.2e-95:488.95//Hs.22030:AA521168
- 50 R-HEMBA1002742//ESTs//1.0e-91:437.99//Hs.139987:AA652163
 R-HEMBA1002746//ESTs//4.4e-97:468.98//Hs.129903:AA576526
 R-HEMBA1002748//ESTs//5.0e-98:475.98//Hs.125461:A1375792
 R-HEMBA1002750//ESTs//1.6e-42:223.97//Hs.40460:N36090
- R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//4.0e-106:545.95//Hs.74750:AB011126
- 55 R-HEMBA1002770//EST//0.34:294.59//Hs.43091:N22127
 R-HEMBA1002777//ESTs//3.0e-85:316.98//Hs.17537:C06491
 R-HEMBA1002779//Human mRNA for KIAA0013 gene, complete cds//0.25:342.58//Hs.48824:D87717

R-HEMBA1002780/Homo sapiens DEC-205 mRNA, complete cds//4.2e-46;449:75/Hs.153563.AF011333

R-HEMBA1002794/ESTs//1.2e-115;559:97/Hs.79741.AI279709

R-HEMBA1002801/EST//0.00049;287:60/Hs.126466.AA913320

R-HEMBA1002810/Homo sapiens formin binding protein 21 mRNA, complete cds//1.4e-116;559:97/Hs.28307.AF071185

R-HEMBA1002816/Human plectin (PLEC1) mRNA, complete cds//0.28;281:62/Hs.79706.U53204

R-HEMBA1002826/EST//6.7e-25;134:99/Hs.134683.AI092013

R-HEMBA1002833/ESTs, Highly similar to ribosome-binding protein p34 [R.norvegicus]//4.3e-25;137:98/Hs.5337.AA243757

R-HEMBA1002850/ESTs//0.010;323:57/Hs.18282.W67514

R-HEMBA1002863/ESTs//1.1e-67;359:94/Hs.124699.W27830

R-HEMBA1002876/ESTs//0.72;202:62/Hs.144816.AI220827

R-HEMBA1002886/EST//3.2e-85;401:99/Hs.96580.AA405670

R-HEMBA1002966/Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds//1.2e-107;541:95/Hs.33787.AF037261

R-HEMBA1002921/Human mRNA for KIAA0189 gene, complete cds//0.84;103:71/Hs.95140.D80011

R-HEMBA1002924/ESTs//3.5e-86;423:98/Hs.27513.N34820

R-HEMBA1002934/Human mRNA for KIAA0118 gene, partial cds//2.1e-50;308:88/Hs.154326.D42087

R-HEMBA1002935/ESTs//1.0e;73;384:95/Hs.118193.W74481

R-HEMBA1002937/ESTs//0.052;167:65/Hs.145504.AI254165

R-HEMBA1002939/ESTs//1.6e-94;467:97/Hs.9893.AA007679

R-HEMBA1002944/ESTs//2.7e-17;176:80/Hs.143768.AA229732

R-HEMBA1002951/ESTs//3.7e-119;565:98/Hs.16218.AI190892

R-HEMBA1002954/EST//0.076;285:58/Hs.98706.AA431085

R-HEMBA1002968/Thiopurine S-methyltransferase//1.9e-46;314:85/Hs.51124.AF019369

R-HEMBA1002970/EST//0.00050;164:64/Hs.129630.AI000405

R-HEMBA1002971/Homo sapiens mRNA for KIAA0679 protein, partial cds//2.3e-30;162:99/Hs.5734.AB014579

R-HEMBA1002973/Small inducible cytokine A5 (RANTES)//5.7e-42;318:81/Hs.155464.AF088219

R-nnnnnnnnnnnn/ESTs//3.2e-18;102:100/Hs.146255.AA197064

R-HEMBA1002999/ESTs, Moderately similar to lamina associated polypeptide 1C [R.norvegicus]//7.9e-113;560:96/Hs.125749.AI377682

R-HEMBA1003021/Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.3e-42;290:85/Hs.113283.AF018080

R-HEMBA1003033/ESTs//2.8e-77;417:94/Hs.138860.W47480

R-HEMBA1003034/ESTs//3.7e-42;429:74/Hs.132818.AI038577

R-HEMBA1003035/ESTs//0.025;156:64/Hs.8473.T40827

R-HEMBA1003037/ESTs//0.69;381:57/Hs.47312.AI240366

R-HEMBA1003041/ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4 IN CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//5.6e-34;280:79/Hs.114905.AA088442

R-HEMBA1003046/Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds//1.3e-119;578:97/Hs.44097.AF054182

R-HEMBA1003064/ESTs//7.8e-35;419:96/Hs.87020.AU706627

R-HEMBA1003067/Von Hippel-Lindau syndrome//2.0e-30;299:75/Hs.78160.AF010238

R-HEMBA1003071/ESTs//2.3e-74;360:98/Hs.12720.AA010193

R-HEMBA1003077/ESTs, Weakly similar to KIAA0405 [H.sapiens]//1.1e-90;434:99/Hs.14146.W92235

R-HEMBA1003078/ESTs//5.9e-16;156:77/Hs.142684.AA902402

R-HEMBA1003079/ESTs//0.16;341:58/Hs.95923.AI075249

R-HEMBA1003083/Small inducible cytokine A5 (RANTES)//1.9e-39;284:83/Hs.155464.AF088219

R-HEMBA1003086/EST//1.0e-48;372:82/Hs.161917.AA483223

R-HEMBA1003096/ESTs, Weakly similar to Mouse 19.5 mRNA, complete cds [M.musculus]//4.2e-100;531:94/Hs.104800.AA709155

R-HEMBA1003098/ESTs//4.2e-107;537:96/Hs.107213.AA121624

R-HEMBA1003117/ESTs//2.4e-67;331:97/Hs.157158.AI150058

R-HEMBA1003129/Human nuclear fibrillar center protein (ASE-1) mRNA, complete cds//2.1e-13;109:88/Hs.118717.U86751

R-HEMBA1003133/ESTs//1.1e-34;180:98/Hs.159387.AI370845

R-HEMBA1003136/ESTs, Weakly similar to MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE [Saccharomyces cerevisiae]//9.2e-114;577:95/Hs.27059.AA088615

R-HEMBA1003142/Small inducible cytokine A5 (RANTES)//1.1e-45;285:88/Hs.155464.AF088219

- R-HEMBA1003148//Homo sapiens mRNA for dachshund protein//3.6e-118:586:96//Hs.63931:AJ005670
 R-HEMBA1003166//ESTs//1.6e-96:479:96//Hs.119940:AA705933
 R-HEMBA1003175//ESTs//2.7e-74:407:92//Hs.139167:AA715389
 R-HEMBA1003197//ESTs//1.6e-68:384:94//Hs.120969:W92000
- 5 R-HEMBA1003199//Sjogren syndrome antigen B (autoantigen La)//0.19:328:57//Hs.83715:X69804
 R-HEMBA1003202//Homo sapiens mRNA for KIAA0640 protein, partial cds//1.3e-40:290:83//Hs.153026:AB014540
 R-HEMBA1003204//ESTs//1.1e-34:215:91//Hs.108090:AA424943
 R-HEMBA1003212//ESTs//1.9e-81:44:1:93//Hs.28471:W20265
- 10 R-HEMBA1003250//ESTs, Weakly similar to MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S28 PRECURSOR [S.cerevisiae]//1.6e-40:232:93//Hs.107707:N32817
 R-HEMBA1003222//ESTs, Weakly similar to weak similarity to HSP90 [C.elegans]//1.1e-42:310:85//Hs.23294:W27666
 R-HEMBA1003229//ESTs//4.8e-18:133:90//Hs.61763:AA035305
 R-HEMBA1003235//ESTs//7.7e-35:201:78//Hs.163979:AA828834
- 15 R-HEMBA1003250//Homo sapiens p21-activated kinase 3 (PAK3) mRNA, complete cds//7.4e-05:534:58//Hs.152663:AF068864
 R-HEMBA1003257//EST//1.4e-95:473:97//Hs.32443:H28929
 R-HEMBA1003273//Small inducible cytokine A5 (RANTES)//2.6e-38:253:86//Hs.155464:AF088219
- 20 R-HEMBA1003276//ESTs//7.6e-55:269:99//Hs.23817:AA526392
 R-HEMBA1003278//ESTs//2.6e-45:301:71//Hs.51652:AI084785
 R-HEMBA1003281
 R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//9.7e-117:551:99//Hs.12836:AB011109
- 25 R-HEMBA1003296//ESTs//4.8e-17:210:72//Hs.44451:AA203266
 R-HEMBA1003304//ESTs//2.8e-98:468:98//Hs.120849:AI148353
 R-HEMBA1003309//ESTs//1.8e-97:455:99//Hs.11571:AA713504
 R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//8.9e-113:545:97//Hs.124224:AB001872
- 30 R-HEMBA1003322//ESTs//4.9e-79:419:95//Hs.138760:N66869
 R-HEMBA1003327//Homo sapiens clone 23622 mRNA sequence//1.4e-16:177:78//Hs.151608:AF052119
 R-HEMBA1003328//H. sapiens mRNA for MACH-alpha-2 protein//2.1e-43:269:88//Hs.19949:X98173
 R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds//0.66:64:76//Hs.117176:AF026029
- 35 R-HEMBA1003348//ESTs//1.4e-35:185:78//Hs.117879:H77357
 R-HEMBA1003369//ESTs, Weakly similar to F59C6.9 [C.elegans]//3.2e-113:553:97//Hs.65539:AI148540
 R-HEMBA1003370//ESTs//2.0e-46:319:86//Hs.37573:H59651
 R-HEMBA1003373//ESTs//1.6e-31:136:81//Hs.114849:AI139588
 R-HEMBA1003376//ESTs//3.0e-47:383:80//Hs.138852:AA284247
- 40 R-HEMBA1003380//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.1e-11:261:65//Hs.87578:AI125363
 R-HEMBA1003384//EST//0.00013:82:75//Hs.141237:H57847
 R-HEMBA1003395//ESTs//5.2e-78:379:98//Hs.162208:AA536127
 R-HEMBA1003402//ESTs//8.6e-14:108:89//Hs.55424:AA774204
- 45 R-HEMBA1003402//ESTs//1.7e-24:188:85//Hs.70266:Z78309
 R-HEMBA1003417//ESTs//4.2e-74:396:94//Hs.55220:D11563
 R-HEMBA1003418//ESTs//3.1e-107:545:95//Hs.3494:AI421013
 R-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//3.2e-115:544:98//Hs.25812:AF058696
 R-HEMBA1003461//ESTs//2.8e-62:304:99//Hs.148747:AI25121
- 50 R-HEMBA1003463//ESTs//2.3e-112:549:97//Hs.104627:AA885516
 R-HEMBA1003480//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.7e-76:529:84//Hs.113283:AF018080
 R-HEMBA1003528//ESTs//2.1e-59:312:96//Hs.22505:R41688
 R-HEMBA1003531//ESTs//2.2e-17:116:93//Hs.140217:AA702760
 R-HEMBA1003538//Complement component C1r//4.7e-25:333:68//Hs.1279:M14058
- 55 R-HEMBA1003545//ESTs//8.7e-89:432:98//Hs.99497:AA776817
 R-HEMBA1003548//EST//0.0091:274:60//Hs.148336:AA911673
 R-HEMBA1003555//ESTs, Weakly similar to NUCLEOTIDE-BINDING PROTEIN [H.sapiens]//2.8e-93:495:93//Hs.91619:AA552351

- R-HEMBA1003556//ESTs//7.1e-44:406:77//Hs.141575:AA211734
 R-HEMBA1003560//ESTs//4.0e-34:182:97//Hs.14811:AA434522
 R-HEMBA1003568//ESTs//2.0e-10:118:486:98//Hs.118570:AI342058
 R-HEMBA1003569//ESTs, Moderately similar to metastasis-associated gene [H.sapiens]//4.0e-63:343:93//Hs.58598:AA625440
 R-HEMBA1003571//Homo sapiens clone 23632 mRNA sequence//3.7e-47:338:84//Hs.46918:AF052099
 R-HEMBA1003579//EST//0.00057:239:60//Hs.162828:AA643892
 R-HEMBA1003581//ESTs//2.6e-10:118:79//Hs.44856:N37065
 R-HEMBA1003591//ESTs//2.4e-96:460:98//Hs.128741:AI244212
 R-HEMBA1003595//Human mRNA for KIAA0118 gene, partial cds//1.7e-48:421:78//Hs.154326:D42087
 R-HEMBA1003597//EST//1.6e-38:313:80//Hs.160911:AI371042
 R-HEMBA1003598//ESTs//0.0085:273:61//Hs.145333:AI251374
 R-HEMBA1003615
 R-HEMBA1003617//ESTs//1.0e-111:574:95//Hs.4552:W68167
 R-HEMBA1003621//EST//1.7e-31:288:78//Hs.140909:R49387
 R-HEMBA1003622//EST//1.1e-46:468:75//Hs.139093:AA166888
 R-HEMBA1003630//ESTs//1.4e-21:411:69//Hs.128729:AA973021
 R-HEMBA1003637//ESTs, Weakly similar to !!! ALU SUBFAMILY SB WARNING ENTRY !!! [H.sapiens]//9.3e-24:189:84//Hs.142208:AA209438
 R-HEMBA1003640//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.5e-42:332:81//Hs.51048:X68830
 R-HEMBA1003645//ESTs//2.4e-77:423:94//Hs.99539:R59010
 R-HEMBA1003646//ESTs//2.6e-98:549:91//Hs.96427:AA151783
 R-HEMBA1003650//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//5.6e-44:245:77//Hs.67619:AB007957
 R-HEMBA1003662//Human TBX2 (TBX2) mRNA, complete cds//2.6e-17:144:84//Hs.32931:U28049
 R-HEMBA1003667//Farnesyltransferase, CAA box, beta//1.3e-22:170:88//Hs.117596:L00635
 R-HEMBA1003679//ESTs, Weakly similar to trithorax homolog HTX, version 2 [H.sapiens]//4.1e-87:434:97//Hs.9489:R84329
 R-HEMBA1003680//Human DNA-binding protein (HRC1) mRNA, complete cds//0.86:315:61//Hs.72925:M91083
 R-HEMBA1003684//ESTs, Highly similar to ZINC FINGER PROTEIN 7 [Homo sapiens]//1.1e-101:528:95//Hs.22934:AA581379
 R-HEMBA1003690//ESTs//0.0021:119:69//Hs.98641:AA429916
 R-HEMBA1003692//Human cytochrome P450-IIB (H1B3) mRNA, complete cds//2.0e-43:360:80//Hs.110194:M29873
 R-HEMBA1003711//ESTs//1.0e-70:375:94//Hs.150407:AI279064
 R-HEMBA1003714//NASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR//0.94:367:62//Hs.1139:X77777
 R-HEMBA1003715//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.1e-77:299:85//Hs.113283:AF018080
 R-HEMBA1003720//Homo sapiens TWIK-related acid-sensitive K⁺ channel (TASK) mRNA, complete cds//1.2e-33:377:74//Hs.24040:AF006823
 R-HEMBA1003725//ESTs//3.8e-103:481:99//Hs.122518:AA778847
 R-HEMBA1003729//ESTs//2.5e-51:277:95//Hs.26270:AA258839
 R-HEMBA1003733//ESTs//1.9e-69:350:96//Hs.139278:AA702592
 R-HEMBA1003742//ESTs, Moderately similar to T13H5.2 [C.elegans]//4.6e-70:348:96//Hs.11282:AI147040
 R-HEMBA1003758//ESTs//1.7e-52:306:85//Hs.138852:AA284247
 R-HEMBA1003760//ESTs//7.4e-76:420:93//Hs.26501:H05089
 R-HEMBA1003773//ESTs, Highly similar to SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT [Mus musculus]//1.9e-77:364:100//Hs.12152:AA156214
 R-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]//2.1e-101:558:93//Hs.18171:AA524327
 R-HEMBA1003784//EST//0.83:127:62//Hs.144002:F01600
 R-HEMBA1003799//EST//9.7e-30:362:71//Hs.156577:AA860236
 R-HEMBA1003803//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//2.8e-16:93:100//Hs.107747:AI357868
 R-HEMBA1003804//Interleukin 15//0.13:227:62//Hs.111867:AB007295
 R-HEMBA1003805//ESTs//0.029:199:65//Hs.91582:T25344
 R-HEMBA1003807//EST//2.4e-13:137:81//Hs.145645:AI264163
 R-HEMBA1003836//Small inducible cytokine A5 (RANTES)//3.2e-39:284:83//Hs.155644:AF088219
 R-HEMBA1003838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 [Paramecium tetraurelia]//6.5e-71:357:96//Hs.107573:AA524333

- R-HEMBA1003856//ESTs//8.2e-20:266:71//Hs.48312:N68161
 R-HEMBA1003864//ESTs//1.6e-99:528:93//Hs.26890:AA449033
 R-HEMBA1003866//POLYPOSIS LOCUS PROTEIN 1//0.30:146:64//Hs.74648:M73547
 5 R-HEMBA1003879//EST, Weakly similar to DNA-REPAIR PROTEIN COMPLEMENTING XP-A CELLS [Homo sapiens]//2.1e-59:295:98//Hs.161661:AA166911
 R-HEMBA1003880//Homo sapiens clone 24760 mRNA sequence//3.8e-34:286:79//Hs.61408:AF070621
 R-HEMBA1003885//ESTs//4.6e-50:293:90//Hs.142314:AA347930
 R-HEMBA1003893//Calcium modulating ligand//2.1e-43:294:86//Hs.13572:AF068179
 10 R-HEMBA1003902//ESTs//1.8e-43:300:85//Hs.146811:AA410788
 R-HEMBA1003908//ESTs//3.5e-91:477:94//Hs.6638:AA536187
 R-HEMBA1003926//ESTs//7.9e-44:294:87//Hs.164036:AA845659
 R-HEMBA1003937//Homo sapiens mRNA for KIAA0585 protein, partial cds//3.5e-48:276:81//Hs.72660:AB011157
 R-HEMBA1003939
 15 R-HEMBA1003942//ESTs//1.6e-81:428:94//Hs.50418:AA524669
 R-HEMBA1003950//ESTs//8.1e-54:283:95//Hs.145528:AI261545
 R-HEMBA1003953//ESTs//3.8e-30:194:89//Hs.99681:AA504591
 R-HEMBA1003958//ESTs//4.0e-45:394:77//Hs.141602:N63562
 R-HEMBA1003959//ESTs//5.2e-28:197:86//Hs.9951:W56253
 R-HEMBA1003976//ESTs//2.0e-29:232:84//Hs.133947:AI074525
 20 R-HEMBA1003978//ESTs//3.2e-115:549:98//Hs.76798:AI050882
 R-HEMBA1003985//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-91:448:97//Hs.117834:AA766771
 R-HEMBA1003987//ESTs//8.1e-36:193:88//Hs.151844:N92756
 R-HEMBA1003989//Human mRNA for KIAA0241 gene, partial cds//3.6e-43:360:81//Hs.150275:D87682
 25 R-HEMBA1004000//EST//5.5e-62:308:97//Hs.50438:N74105
 R-HEMBA1004011//ESTs//8.6e-85:431:96//Hs.36185:R99899
 R-HEMBA1004012//ESTs//1.3e-40:309:83//Hs.140329:AA714011
 R-HEMBA1004015//ESTs//5.1e-97:453:99//Hs.111446:AI333774
 R-HEMBA1004024//ESTs//5.2e-19:159:79//Hs.138856:H47461
 30 R-HEMBA1004038//ESTs//1.3e-41:346:79//Hs.146173:AA906191
 R-HEMBA1004042//ESTs//0.0012:201:69//Hs.24248:AA528253
 R-HEMBA1004045//ESTs, Weakly similar to putative p150 [H. sapiens]//1.5e-22:365:70//Hs.99692:AA811804
 R-HEMBA1004048//ESTs//9.5e-104:497:98//Hs.77735:AI125469
 R-HEMBA1004049//HEAT SHOCK 70 KD PROTEIN 1//6.3e-31:176:96//Hs.8997:M11717
 35 R-HEMBA1004055//ESTs//1.7e-115:577:96//Hs.59503:W63754
 R-HEMBA1004056//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.2e-78:577:82//Hs.113283:AF018080
 R-HEMBA1004074//EST//1.0:152:61//Hs.149093:AI243988
 R-HEMBA1004086//ESTs//4.0e-53:266:98//Hs.34658:N98652
 R-HEMBA1004097//ESTs//4.4e-46:279:91//Hs.110533:H16251
 40 R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds//3.0e-43:534:69//Hs.90998:D50918
 R-HEMBA1004132//ESTs//4.6e-47:316:86//Hs.141602:N63562
 R-HEMBA1004133
 R-HEMBA1004138//EST//1.7e-08:211:64//Hs.129189:AA988736
 R-HEMBA1004143//ESTs//4.0e-25:137:97//Hs.21307:AA203320
 45 R-HEMBA1004146//Small inducible cytokine A5 (RANTES)//4.1e-27:191:86//Hs.155464:AF088219
 R-HEMBA1004150//GRANALCALCIN//0.99:357:59//Hs.79381:M81637
 R-HEMBA1004164//Human mRNA for KIAA0118 gene, partial cds//9.5e-47:313:84//Hs.154326:D42087
 R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//7.7e-112:563:96//Hs.59988:AF067855
 R-HEMBA1004199
 50 R-HEMBA1004200//EST//3.1e-89:441:97//Hs.141173:R97701
 R-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays]//1.7e-107:552:94//Hs.10092:AI189282
 R-HEMBA1004203//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.5e-96:275:98//Hs.15832:AB014518
 55 R-HEMBA1004207//Leptin receptor//1.1e-117:573:97//Hs.54515:U50748
 R-HEMBA1004225//EST//9.7e-34:186:95//Hs.137567:R20617
 R-HEMBA1004227//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//4.0e-16:117:91//Hs.92033:AA255832

- R-HEMBA1004238//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:338:83//Hs.153014:AB002353
 R-HEMBA1004241//ESTs//1.3e-10:93:87//Hs.137511:AA456389
 R-HEMBA1004246//Homo sapiens LIM protein mRNA, complete cds//2.7e-43:511:72//Hs.154103:AF061258
 R-HEMBA1004248//ESTs, Highly similar to INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 [Rattus norvegicus]//2.1e-61:221:86//Hs.7089:W37284
 R-HEMBA1004264//ESTs//1.5e-80:425:95//Hs.107206:AA234962
 R-HEMBA1004267//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//1.4e-89:465:95//Hs.113660:D20018
 R-HEMBA1004272//ESTs//4.5e-111:577:94//Hs.115696:N57931
 R-nnnnnnnnnnn/Homo sapiens clone 617 unknown mRNA, complete sequence//1.4e-111:553:96//Hs.93677:AF091081
 R-HEMBA1004276//ESTs, Highly similar to BETA-ADAPTIN [Homo sapiens; Rattus norvegicus; Bos taurus]//4.4e-92:559:89//Hs.28298:AA203228
 R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds//6.2e-108:538:97//Hs.101766:AF022795
 R-HEMBA1004289//Sulfoltransferase, dehydroepiandrosterone (DHEA) -preferring//1.7e-34:223:75//Hs.81884:U13061
 R-HEMBA1004295//ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-orf7 protein [C. elegans]//3.6e-93:496:94//Hs.14337:AA534961
 R-HEMBA1004306//ESTs//3.4e-26:363:68//Hs.70279:AA757426
 R-HEMBA1004312//ESTs//4.8e-64:351:94//Hs.138611:H82679
 R-HEMBA1004321//Zinc finger protein 44 (KOX 7)//2.6e-37:415:64//Hs.51199:X16281
 R-HEMBA1004323//ESTs//2.1e-40:280:70//Hs.153300:AA928904
 R-HEMBA1004327//ESTs//3.8e-72:343:99//Hs.151708:AA554714
 R-HEMBA1004330//ESTs//4.0e-52:270:97//Hs.24654:AA456561
 R-HEMBA1004334//ESTs//1.6e-46:234:98//Hs.47159:AI310231
 R-HEMBA1004335//ESTs//1.9e-25:250:76//Hs.155880:AA703336
 R-HEMBA1004341//ESTs//3.7e-101:480:98//Hs.69321:AA633240
 R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds//1.3e-75:444:90//Hs.80686:D89667
 R-HEMBA1004354//Human mRNA for KIAA0355 gene, complete cds//5.9e-39:286:83//Hs.153014:AB002353
 R-HEMBA1004356//SINGLE-STRANDED DNA-BINDING PROTEIN MSSP-1//1.3e-107:576:93//Hs.55458:X77494
 R-HEMBA1004366//ESTs//2.3e-94:524:91//Hs.111496:AA652869
 R-HEMBA1004372//EST//0.27:198:60//Hs.162665:AA605057
 R-HEMBA1004389//ESTs//1.4e-102:490:98//Hs.153708:AA687264
 R-HEMBA1004394//ESTs//1.5e-94:471:96//Hs.151647:AA002084
 R-HEMBA1004396//Small inducible cytokine A5 (RANTES)//6.2e-41:285:83//Hs.155464:AF088219
 R-HEMBA1004405//ESTs//2.0e-44:329:83//Hs.136839:H93717
 R-HEMBA1004408//ESTs, Weakly similar to homologous to mouse Rsu-1 [H.sapiens]//6.1e-89:420:99//Hs.88365:AA648933
 R-HEMBA1004429//ESTs, Weakly similar to homeotic protein protein zhx-1 [M.musculus]//3.0e-112:552:96//Hs.12940:AI123518
 R-HEMBA1004433//Human Line-1 repeat mRNA with 2 open reading frames//2.9e-32:463:68//Hs.23094:M19503
 R-HEMBA1004460//ESTs//2.0e-104:574:93//Hs.46848:AA195829
 R-HEMBA1004461//ESTs//2.9e-102:503:98//Hs.16370:AA017033
 R-HEMBA1004479//ELK1, member of ETS oncogene family//1.1e-45:310:75//Hs.116549:AL009172
 R-HEMBA1004482//ESTs//9.1e-05:322:62//Hs.34489:AA759306
 R-HEMBA1004502//ESTs//6.9e-112:566:96//Hs.93985:N50034
 R-HEMBA1004506//EST//5.3e-59:456:80//Hs.72412:AA160941
 R-HEMBA1004507
 R-HEMBA1004509//ESTs, Moderately similar to HYPOTHETICAL 52.2 KD PROTEIN IN MPR1-GCN20 INTERGENIC REGION [Saccharomyces cerevisiae]//2.9e-82:262:99//Hs.12820:AA004271
 R-HEMBA1004534//ESTs, Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]//1.1e-43:281:89//Hs.58414:AA196947
 R-HEMBA1004538//EST//3.3e-15:270:71//Hs.136667:AA707972
 R-HEMBA1004554
 R-HEMBA1004560//ESTs//8.2e-25:179:88//Hs.96580:W22924

- R-HEMBA1004573//ESTs, Moderately similar to ALR [H.sapiens]/1.0.305.60//Hs.30272:AA134913
 R-HEMBA1004577//ESTs/17.9e-50.319.89//Hs.22660:AA582243
 R-HEMBA1004586//ESTs/2.6e-73.384.96//Hs.9582:R39769
 R-nnnnnnnnnnnnn//ESTs/6.0e-22.190.82//Hs.42530:N41661
 5 R-HEMBA1004610//ESTs/1.2e-91.438.98//Hs.47823:AA780767
 R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501/4.6e-52.327.85//Hs.159897:AB007970
 R-HEMBA1004629//ESTs/2.3e-19.215.76//Hs.111995:AI375915
 R-HEMBA1004631//ESTs/3.6e-99.470.98//Hs.49303:AA810785
 10 R-HEMBA1004632//ESTs/1.0.128.66//Hs.159182:AA831152
 R-HEMBA1004637//ESTs, Highly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III [Caenorhabditis elegans]/4.8e-111.532.98//Hs.12263:AA282393
 R-HEMBA1004638//ESTs/1.2e-66.341.95//Hs.122687:AI278454
 R-HEMBA1004666//ESTs/2.1e-65.333.96//Hs.98873:AA625442
 15 R-HEMBA1004669//ESTs/0.00039.116.74//Hs.138725:N76348
 R-HEMBA1004670//ESTs/1.7e-16.116.89//Hs.56825:AI057560
 R-HEMBA1004672//EST/6.7e-76.315.97//Hs.20821:R19368
 R-HEMBA1004693//ESTs/6.4e-68.327.99//Hs.159066:AI093252
 R-HEMBA1004697//ESTs/9.3e-98.467.98//Hs.62637:AA043562
 20 R-HEMBA1004705//EST/0.0034.271.58//Hs.112503:AA599042
 R-HEMBA1004709//EST/1.3e-55.392.85//Hs.149580:AI281881
 R-HEMBA1004711//Small inducible cytokine A5 (RANTES)/1.9e-47.449.76//Hs.155464:AF088219
 R-HEMBA1004725//EST/1.8e-71.424.88//Hs.155712:AI309235
 R-HEMBA1004730//Homo sapiens clone 23892 mRNA sequencer/2.1e-44.467.73//Hs.91916:AF035317
 25 R-HEMBA1004733//EST/0.99.84.65//Hs.161372:AI423151
 R-HEMBA1004734//EST/1.8e-82.421.96//Hs.21275:N73275
 R-HEMBA1004736//Ataxia telangiectasia mutated (includes complementation groups A, C and D)/9.5e-39.296.82//Hs.51187:U82828
 R-HEMBA1004748//ESTs/1.7e-43.166.86//Hs.37573:H59651
 30 R-HEMBA1004751//ESTs/8.0e-23.155.98//Hs.149464:AI279428
 R-HEMBA1004752//Thromboxane A2 receptor/2.7e-45.281.89//Hs.89887:D38081
 R-HEMBA1004753//40S RIBOSOMAL PROTEIN S20/8.3e-67.475.84//Hs.8102:L06498
 R-HEMBA1004756//ESTs/2.0e-81.384.99//Hs.129545:N68679
 R-HEMBA1004758//EST/2.0e-43.367.80//Hs.133006:AI049504
 35 R-HEMBA1004763//ESTs/2.0e-108.567.94//Hs.3757:W87380
 R-HEMBA1004768//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]/1.4e-47.379.81//Hs.141273:H66705
 R-HEMBA1004770//ESTs/0.0014.246.61//Hs.124857:AA687092
 R-HEMBA1004771//ESTs/1.1e-12.323.63//Hs.124146:AA699633
 40 R-HEMBA1004776//ESTs/2.5e-112.567.95//Hs.12680:W74476
 R-HEMBA1004778//ESTs/1.4e-33.272.75//Hs.141123:AA848167
 R-nnnnnnnnnnnnn
 R-HEMBA1004803//ESTs/1.0e-48.319.86//Hs.139231:W87732
 R-HEMBA1004806
 45 R-HEMBA1004807//ESTs/6.2e-77.362.100//Hs.140945:N47676
 R-HEMBA1004816//EST/4.3e-18.246.72//Hs.150552:AI053784
 R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds/5.0e-14.141.85//Hs.80510:M74002
 R-HEMBA1004847
 50 R-HEMBA1004850//ESTs/1.2e-83.395.99//Hs.30925:AA577120
 R-HEMBA1004863//ESTs/7.5e-21.204.79//Hs.35036:H95267
 R-HEMBA1004864
 R-HEMBA1004865//EST/6.7e-18.191.75//Hs.129944:AA429362
 R-HEMBA1004880//EST/4.4e-70.346.98//Hs.145094:AA452409
 55 R-HEMBA1004889//ESTs/4.8e-117.496.97//Hs.15641:W63676
 R-HEMBA1004900//ESTs/1.2e-15.283.68//Hs.157606:AI357470
 R-HEMBA1004909//ESTs/7.3e-44.366.79//Hs.140329:AA714011
 R-HEMBA1004918//Human mRNA for KIAA0392 gene, partial cds/4.6e-50.313.89//Hs.40100:AB002390

- R-HEMBA1004923/ESTs//0.013:162:64//Hs.143655:AI128388
 R-HEMBA1004929/EST//2.3e-48:250:97//Hs.131589:AI025053
 R-HEMBA1004930/Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.2e-70:547:80//Hs.1361:M55053
- 5 R-HEMBA1004933/ESTs, Weakly similar to R06C7.6 [C elegans]//5.3e-110:530:98//Hs.18029:AI422883
 R-HEMBA1004934/ESTs//1.3e-103:522:96//Hs.40415:AA037215
 R-HEMBA1004944/ESTs//6.0e-21:97:84//Hs.141973:N21434
 R-HEMBA1004954/ESTs//7.9e-112:596:93//Hs.6226:W61007
 R-HEMBA1004956/ESTs//3.1e-58:280:100//Hs.120750:AA741074
- 10 R-HEMBA1004960/ESTs//6.9e-89:476:93//Hs.163738:AA601040
 R-HEMBA1004972/ESTs//3.0e-72:381:95//Hs.55014:AA934035
 R-HEMBA1004973/ESTs//2.7e-91:441:98//Hs.28144:AI292065
 R-HEMBA1004977/ESTs//2.0e-95:446:99//Hs.29690:AI168404
 R-HEMBA1004978/Homo sapiens natural killer cell group 2-F (NKG2-F) mRNA, complete cds//0.43:187:67//Hs.129734:AJ001683
- 15 R-HEMBA1004980/Human mRNA for KIAA0331 gene, complete cds//6.4e-53:305:91//Hs.146395:AB002329
 R-HEMBA1004983/ESTs//0.16:482:57//Hs.131929:AI021894
 R-HEMBA1004995
 R-HEMBA1005008/EST, Weakly similar to mariner transposase [H.sapiens]//6.9e-51:482:78//Hs.141601:N63520
- 20 R-HEMBA1005009/ESTs, Highly similar to ACTIN I [Naegleria fowleri]//3.8e-109:551:96//Hs.103180:AI365212
 R-HEMBA1005019/Homo sapiens mRNA for KIAA0648 protein, partial cds//2.0e-105:542:94//Hs.31921:AB014548
 R-HEMBA1005029/ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.4e-95:491:94//Hs.16085:AI261382
- 25 R-HEMBA1005035/Human mRNA for KIAA0033 gene, partial cds//2.3e-64:312:85//Hs.22271:D26067
 R-HEMBA1005039/ESTs, Weakly similar to zinc finger protein [H.sapiens]//2.6e-48:443:78//Hs.139019:N99348
 R-HEMBA1005047/ESTs, Highly similar to RAS-RELATED PROTEIN RAB-5A [Canis familiaris]//1.2e-87:542:87//Hs.16258:AI376436
 R-HEMBA1005050/ESTs//6.3e-46:311:86//Hs.159510:AA297145
- 30 R-HEMBA1005062/ESTs//1.1e-14:216:68//Hs.129935:AA994451
 R-HEMBA1005066/Human clone Z3574 mRNA sequence//2.2e-24:303:73//Hs.79385:U90905
 R-HEMBA1005075/EST//0.65:214:62//Hs.133991:AI075789
 R-HEMBA1005079/Human BENE mRNA, partial cds//1.9e-44:304:83//Hs.85889:U10777
 R-HEMBA1005083/ESTs//2.8e-74:356:98//Hs.132272:AI393958
- 35 R-HEMBA1005101/Homo sapiens SYT interacting protein SIP mRNA, complete cds//1.7e-111:545:96//Hs.11170:AF080561
 R-HEMBA1005113/ESTs//1.1e-101:512:95//Hs.7972:AI052739
 R-HEMBA1005123/Ley L-L//3.6e-58:519:77//Hs.37062:AC005952
 R-HEMBA1005133/H.sapiens mRNA for MACH-alpha-2 protein//8.3e-46:309:85//Hs.19949:X98173
- 40 R-HEMBA1005149/Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//4.7e-36:394:75//Hs.67619:AB007957
 R-HEMBA1005152/Homo sapiens antigen NY-CO-16 mRNA, complete cds//3.6e-32:362:77//Hs.132206:AF039694
 R-HEMBA1005159/EST//7.4e-47:252:94//Hs.134930:AI093397
- 45 R-HEMBA1005185/ESTs//5.2e-48:305:89//Hs.14920:AA910914
 R-HEMBA1005201/ESTs//4.7e-58:293:97//Hs.23752:C05766
 R-HEMBA1005202/ESTs//1.0:169:59//Hs.153423:AI198239
 R-HEMBA1005219/Homo sapiens putative tumor suppressor protein (123F2) mRNA, complete cds//0.84:191:61//Hs.26931:AF061836
- 50 R-HEMBA1005223/ESTs//0.75:90:70//Hs.127446:AA167284
 R-HEMBA1005232/EST//0.056:162:67//Hs.65649:F13687
 R-HEMBA1005241/ESTs//3.6e-113:564:96//Hs.12770:W84331
 R-HEMBA1005244/ESTs//6.4e-22:118:100//Hs.21396:AA114834
 R-HEMBA1005251/ESTs//8.5e-36:213:92//Hs.161554:AA393896
- 55 R-HEMBA1005252/Homo sapiens mRNA for KIAA0585 protein, partial cds//6.1e-49:277:93//Hs.72660:AB011157
 R-HEMBA1005274/ESTs//3.7e-65:322:98//Hs.105166:AA668862
 R-HEMBA1005275/ESTs//2.1e-29:298:73//Hs.33393:R83391
 R-HEMBA1005293/ESTs//3.5e-93:448:98//Hs.12066:AI208611

- R-HEMBA1005296//ESTs/4.3e-33:168:100//Hs.13916:AI025750
 R-HEMBA1005304//Small inducible cytokine A5 (RANTES)//2.8e-50:315:82//Hs.155464:AF088219
 R-HEMBA1005311//Homo sapiens 4F5S mRNA, complete cds//1.3e-44:318:83//Hs.32567:AF073519
 R-HEMBA1005314//ESTs/3.0e-103:491:98//Hs.41606:AI095046
 5 R-HEMBA1005315//EST//1.9e-29:370:72//Hs.161483:N59169
 R-HEMBA1005318//ESTs/3.9e-110:535:97//Hs.26771:AA126472
 R-HEMBA1005331//Intercellular adhesion molecule 2//7.6e-39:256:87//Hs.83733:X15606
 R-HEMBA1005353//ESTs/1.7e-81:406:96//Hs.155374:AI341467
 R-HEMBA1005359//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//4.7e-46:294:81//Hs.129735:AF010144
 10 R-HEMBA1005367//Alcohol dehydrogenase 2 (class I), beta polypeptide//1.0:210:62//Hs.4:X03350
 R-HEMBA1005372//ESTs/6.2e-95:451:99//Hs.135219:AI091653
 R-HEMBA1005374//ESTs/1.5e-107:502:99//Hs.118208:AA947305
 R-HEMBA1005389//Fc fragment of IgA, receptor for//1.0e-39:311:80//Hs.54486:X54150
 15 R-HEMBA1005394//ESTs, Weakly similar to coded for by C. elegans cDNA yk30b3.5 [C.elegans]//4.0e-88:489:92//Hs.43864:AA131568
 R-HEMBA1005403//EST//0.0011:78:75//Hs.127061:AA863278
 R-HEMBA1005408//ESTs/3.2e-29:395:71//Hs.117532:AA676725
 R-HEMBA1005410//ESTs/1.5e-18:271:70//Hs.144604:AI052059
 20 R-HEMBA1005411//ESTs/1.1e-35:335:77//Hs.141181:R98757
 R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//1.8e-118:453:99//Hs.4854:AF041248
 R-HEMBA1005426//Chromosome 1 specific transcript KIAA0491//0.25:264:61//Hs.136309:AB007960
 R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment//1.7e-47:305:87//Hs.6445:LA40391
 25 R-HEMBA1005447//ESTs/5.7e-83:529:86//Hs.114253:AA745961
 R-HEMBA1005468//ESTs/7.3e-23:249:73//Hs.61199:AA024494
 R-HEMBA1005469//Human mRNA for KIAA0355 gene, complete cds//4.5e-45:320:85//Hs.153014:AB002353
 R-HEMBA1005472//Human kpnI repeat mma (cdna clone pcd-kpnI-8), 3' end//8.4e-73:464:87//Hs.103948:K00627
 30 R-HEMBA1005475//ESTs/0.32:192:59//Hs.62694:AA100445
 R-HEMBA1005497
 R-HEMBA1005500//ESTs/2.2e-43:307:85//Hs.146811:AA410788
 R-HEMBA1005506//75 kda infertility-related sperm protein [human, testis, mRNA Partial, 2427 nt]//0.11:295:60//Hs.62608:S58544
 35 R-HEMBA1005508//ESTs/2.8e-55:319:93//Hs.50150:N90870
 R-HEMBA1005511//ESTs, Weakly similar to similar to mouse MMR1 [C.elegans]//2.6e-82:387:99//Hs.67466:AI219740
 R-HEMBA1005517//ESTs/4.6e-77:469:90//Hs.126787:AA203322
 R-HEMBA1005518//ESTs/1.5e-108:561:94//Hs.123167:AA601045
 40 R-HEMBA1005520//Putative mismatch repair/binding protein hMSH3//7.5e-44:179:84//Hs.42674:U61981
 R-HEMBA1005526//ESTs/8.7e-46:308:86//Hs.146811:AA410788
 R-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//8.6e-115:578:95//Hs.17035:AI080471
 R-HEMBA1005530//ESTs/1.5e-110:551:96//Hs.107294:W72350
 45 R-HEMBA1005548//ESTs/1.7e-100:510:96//Hs.9115:N90926
 R-HEMBA1005552//Interleukin 10//2.4e-38:306:80//Hs.2180:M57627
 R-HEMBA1005558//ESTs, Weakly similar to unknown [S.cerevisiae]//5.3e-77:439:91//Hs.22897:R43193
 R-HEMBA1005568//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.4e-31:182:76//Hs.133526:N21103
 50 R-HEMBA1005570//ESTs/3.3e-67:411:88//Hs.142245:AA489709
 R-HEMBA1005576//EST//0.91:52:73//Hs.149518:AI280497
 R-HEMBA1005577
 R-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//3.1e-28:561:64//Hs.57929:AB011538
 R-HEMBA1005582//ESTs/6.0e-73:371:97//Hs.103758:C06392
 55 R-HEMBA1005583//ESTs/8.3e-79:413:95//Hs.62348:AA419539
 R-HEMBA1005588//Human c-yes-1 mRNA//2.6e-52:403:83//Hs.75680:M15990
 R-HEMBA1005593//ESTs/3.3e-30:139:80//Hs.142273:W37905
 R-HEMBA1005595//ESTs/1.1e-97:454:100//Hs.27497:AI274820

R-HEMBA1005606//ESTs/1.0e-12:313.64//Hs.162402:AA53125
R-HEMBA1005609//ESTs/1.0e-278.58//Hs.76235:W6390
R-HEMBA1005616//ESTs/1.3e-98:470:99//Hs.122230:AA781422
R-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]//2.8e-95:539:92//Hs.
19400:AA662845
R-HEMBA1005627//Human mRNA for adipogenesis inhibitory factor//5.5e-38:317.78//Hs.1721:X58377
R-HEMBA1005631//Human mRNA for KIAA0393 gene, complete cds//2.3e-11:279:65//Hs.15245:AF041081
R-HEMBA1005632//EST/1.5e-10:181:70//Hs.120259:AA731522
R-HEMBA1005634//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.4e-25:234:80//Hs.
10458:AF088219
R-HEMBA1005666//ESTs//2.3e-103:534:95//Hs.14512:AA205973
R-HEMBA1005670//ESTs/2.6e-39:166:81//Hs.139414:A1279477
R-HEMBA1005679//Esterase D/formylglylithione hydrolase//1.3e-50:322:88//Hs.82193:M13450
R-HEMBA1005680//Homo sapiens LIM protein mRNA, complete cds//3.3e-43:343:81//Hs.154103:AF061258
R-HEMBA1005685//Human homeodomain protein (Prox 1) mRNA, complete cds//0.0050:235:64//Hs.159437:
U44060
R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//
1.7e-47:376:84//Hs.26988:U66406
R-HEMBA1005705//ESTs/3.0e-53:259:99//Hs.55314:AA772055
R-HEMBA1005717//EST//2.5e-59:287:99//Hs.146870:AI159943
R-HEMBA1005732//Homo sapiens mRNA for cartilage-associated protein (CASP)/1.2e-45:398:79//Hs.155481:
AJ006470
R-HEMBA1005737//ESTs/2.5e-57:416:83//Hs.23245:AA053815
R-nnnnnnnnnnnn//EST/0.098:125:68//Hs.136945:AA785672
R-HEMBA1005755//EST/1.2e-22:180:84//Hs.141488:NA47096
R-HEMBA1005765//Human peptide transporter (HPEPT1) mRNA, complete cds//3.9e-47:404:80//Hs.2217:
U21936
R-HEMBA1005780//ESTs/1.3e-106:512:97//Hs.11901:AA173974
R-HEMBA1005813//Homo sapiens mRNA for chemokine LEC precursor, complete cds//2.0e-33:195:84//Hs.
10458:AF088219
R-HEMBA1005815//ESTs/7.6e-19:290:71//Hs.112218:AIO38601
R-HEMBA1005822//ESTs/5.4e-49:246:98//Hs.34804:AA514960
R-HEMBA1005829//ESTs/2.7e-72:344:99//Hs.54548:AO139201
R-HEMBA1005834//ESTs/1.6e-44:317:82//Hs.157029:AI080618
R-HEMBA1005852//ESTs/1.6e-102:544:93//Hs.9911:AA089811
R-HEMBA1005853//ESTs/1.8e-78:398:95//Hs.140248:AA757917
R-HEMBA1005884//EST//2.6e-18:275:67//Hs.139357:AA420970
R-HEMBA1005891//ESTs/2.1e-89:427:98//Hs.67317:AIO22252
R-HEMBA1005894
R-HEMBA1005909//ESTs/2.6e-91:436:99//Hs.147492:AI215686
R-HEMBA1005911//ESTs/1.1e-85:446:95//Hs.134494:AI078633
R-HEMBA1005921//ESTs/1.8e-44:428:95//Hs.127993:AA970632
R-HEMBA1005931//Homo sapiens mRNA for KIAA0526 protein, complete cds//9.5e-45:446:75//Hs.59403:
AB011098
R-HEMBA1005934//ESTs/0.20:142:65//Hs.97079:AA370867
R-HEMBA1005962//ESTs/1.8e-87:409:100//Hs.161292:AI199418
R-HEMBA1005963
R-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//2.2e-113:580:95//Hs.
26285:AF082516
R-HEMBA1005991//Human antiserotype factor-1 mRNA, complete cds//2.0e-45:551:70//Hs.148495:AF050199
R-HEMBA1005999//ESTs/7.5e-24:201:69//Hs.157029:AI080618
R-HEMBA1006002//ESTs/3.1e-112:573:95//Hs.61233:AI379875
R-HEMBA1006005//EST//1.0:105:63//Hs.145273:AI249436
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0725 protein, partial cds//2.4e-28:444:67//Hs.26450:AB018268
R-HEMBA1006035//ESTs/4.5e-94:465:97//Hs.44625:NA49951
R-HEMBA1006036//ESTs/6.1e-90:420:100//Hs.126771:AA916508
R-HEMBA1006042//EST//1.5e-88:424:98//Hs.132551:AA948490
R-nnnnnnnnnnnn

- R-HEMBA1006081/ESTs//7.8e-68:356:95//Hs.27410:N25612
 R-HEMBA1006090/EST//5.1e-66:320:99//Hs.99551:AA461517
 R-HEMBA1006091/ESTs//2.0e-66:44:1.94//Hs.9658:AA506313
 R-HEMBA1006100/Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//3.4e-43:328:82//
 5 Hs.73614:U83460
 R-HEMBA1006108/ESTs//1.5e-44:228:98//Hs.26368:AA789297
 R-HEMBA1006121/ESTs//1.6e-116:547:99//Hs.34151:A1279293
 R-HEMBA1006124/EST//1.6e-20:286:64//Hs.148457:A1198931
 R-HEMBA1006130/ESTs//8.8e-47:231:99//Hs.16470:AA121635
 10 R-nnnnnnnnnnn/Homo sapiens mRNA for KIAA0792 protein, complete cds//8.7e-27:296:73//Hs.119387:
 AB007958
 R-HEMBA1006142/ESTs//1.5e-27:255:70//Hs.139507:T77542
 R-HEMBA1006155/ESTs//4.9e-64:353:94//Hs.84560:R41212
 R-HEMBA1006158/Deoxyuridine triphosphatase//0.99:162:62//Hs.82113:U31930
 15 R-HEMBA1006173/ESTs//7.5e-85:462:92//Hs.79092:H29627
 R-HEMBA1006182/ESTs//5.5e-29:218:72//Hs.141466:H96906
 R-HEMBA1006198/ESTs//2.1e-34:282:82//Hs.142068:AA176125
 R-HEMBA1006235/Homo sapiens clone 24422 mRNA sequence//6.9e-112:545:97//Hs.109268:AF070557
 R-HEMBA1006248/ESTs, Highly similar to ZINC FINGER PROTEIN MFG1 [Mus musculus]//3.3e-114:581:95//
 20 Hs.23617:AA928683
 R-HEMBA1006252/Human mRNA for KIAA0080 gene, partial cds//7.0e-48:284:76//Hs.74554:D38522
 R-HEMBA1006253/Homo sapiens 45kDa splicing factor mRNA, complete cds//5.7e-30:179:91//Hs.15836:
 AF083384
 R-HEMBA1006259/Homo sapiens KIAA0421 mRNA, partial cds//1.5e-45:326:84//Hs.41742:AB007881
 25 R-HEMBA1006268/ESTs, Highly similar to c-Jun leucine zipper interactive [M.musculus]//1.2e-97:529:93//Hs.
 10552:AA524401
 R-HEMBA1006272/ESTs, Moderately similar to RETROVIRUS-RELATED PROTEASE [H.sapiens]//2.7e-88:484:
 92//Hs.104129:AA923278
 R-nnnnnnnnnnn/H.sapiens PAP mRNA//5.2e-56:585:71//Hs.49007:X76770
 30 R-HEMBA1006283/ESTs, Weakly similar to NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2 [S.
 cerevisiae]//1.6e-66:377:91//Hs.108674:W25821
 R-HEMBA1006284/ESTs//3.7e-110:544:96//Hs.55296:A1084735
 R-HEMBA1006291/ESTs//2.2e-91:457:96//Hs.114611:N37019
 R-HEMBA1006293/ESTs//5.4e-78:370:99//Hs.155111:A1202037
 35 R-HEMBA1006309/ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//3.7e-40:167:86//Hs.74478:
 U33931
 R-HEMBA1006310/ESTs, Weakly similar to reverse transcriptase [M.musculus]//5.6e-76:417:94//Hs.111754:
 AI204587
 R-HEMBA1006328/Small inducible cytokine A5 (RANTES)//2.8e-60:397:78//Hs.155464:AF088219
 40 R-HEMBA1006334/Human occludin mRNA, complete cds//0.72:369:59//Hs.93518:U49184
 R-HEMBA1006344/Human plectin (PLEC1) mRNA, complete cds//0.016:217:64//Hs.79706:U53204
 R-HEMBA1006347/ESTs, Highly similar to HYPOTHETICAL 97.6 KD PROTEIN IN SHP1-SEC17 INTERGENIC
 REGION [Saccharomyces cerevisiae]//3.6e-119:582:97//Hs.42343:AI417075
 R-HEMBA1006349/ESTs//5.2e-57:305:94//Hs.6338:AA411382
 45 R-HEMBA1006359/ESTs//8.2e-90:426:99//Hs.100873:AA678008
 R-HEMBA1006364/ESTs//2.2e-98:582:91//Hs.23837:AA541787
 R-HEMBA1006377/EST//0.0097:145:621//Hs.133027:AI049830
 R-HEMBA1006380/Homo sapiens mRNA for KIAA0594 protein, partial cds//1.0e-41:349:79//Hs.154872:
 AB011166
 50 R-HEMBA1006381/ESTs//5.1e-46:320:85//Hs.37573:H59651
 R-HEMBA1006398/Human Line-1 repeat mRNA with 2 open reading frames//9.0e-87:5:82:84//Hs.23094:M19503
 R-HEMBA1006416/ESTs//1.5e-17:251:73//Hs.33950:AI218923
 R-HEMBA1006419/EST//8.5e-65:353:94//Hs.141309:H72778
 R-HEMBA1006421/Oxytocin receptor//1.2e-12:249:68//Hs.2820:X64878
 55 R-HEMBA1006424/ESTs, Weakly similar to pot. ORF II [H.sapiens]//6.3e-13:263:66//Hs.43127:AA258004
 R-HEMBA1006426/ESTs//6.5e-84:401:99//Hs.37303:C16964
 R-HEMBA1006438/EST//0.87:266:57//Hs.99456:AA457380
 R-HEMBA1006445/ESTs//2.0e-81:414:96//Hs.58153:W72033

- R-HEMBA1006446//Homo sapiens mRNA for cadherin-6, complete cds//1.6e-05:487:58//Hs.32963:D31784
 R-HEMBA1006461//ESTs//5.1e-78:393:97//Hs.142677:R95895
 R-HEMBA1006467//ESTs, Weakly similar to putative p150 [H.sapiens]//3.0e-17:342:63//Hs.111730:AA604403
 R-HEMBA1006471//ESTs//3.8e-66:370:92//Hs.14063:T77441
 5 R-HEMBA1006474
 R-HEMBA1006483//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.2e-40:365:78//Hs.46468:U45984
 R-HEMBA1006485//H.sapiens mRNA for aminopeptidase//2.5e-92:517:91//Hs.132243:Y07701
 R-HEMBA1006486//EST//7.0e-47:240:76//Hs.161917:AA483223
 10 R-HEMBA1006489//ESTs//2.1e-93:440:99//Hs.125264:AA873350
 R-HEMBA1006492//ESTs//0.00034:52:90//Hs.163219:AA810720
 R-HEMBA1006494//EST//1.8e-06:192:67//Hs.141401:H93387
 R-HEMBA1006497//ESTs//6.2e-45:232:97//Hs.118015:N33117
 R-HEMBA1006502//Complement component 5 receptor 1 (C5a ligand)//8.7e-16:135:72//Hs.2161:M62505
 15 R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//3.9e-117:570:96//Hs.153858:AB014566
 R-HEMBA1006521//ESTs//9.9e-99:496:96//Hs.64906:AA677300
 R-HEMBA1006530//ESTs//0.18:260:60//Hs.24970:AI057628
 R-HEMBA1006535//GS1 PROTEIN//0.52:267:62//Hs.78991:M86934
 20 R-HEMBA1006540//EST//0.016:143:66//Hs.148189:AA897331
 R-HEMBA1006546//Homo sapiens mRNA for KIAA0582 protein, partial cds//2.2e-48:287:91//Hs.79507:AB011154
 R-HEMBA1006597//ESTs, Moderately similar to neurodegeneration-associated protein 1 [R.norvegicus]//1.8e-109:547:96//Hs.21122:AA191594
 R-HEMBA1006562//EST//1.1e-13:327:63//Hs.149641:AI283064
 25 R-HEMBA1006566//ESTs//2.6e-59:311:97//Hs.146014:R51876
 R-HEMBA1006569//ESTs//4.7e-89:458:96//Hs.42861:W74725
 R-HEMBA1006579//ESTs//2.9e-19:110:99//Hs.126191:AA873876
 R-HEMBA1006583//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.5e-29:276:76//Hs.144563:AF057280
 30 R-HEMBA1006595//ESTs//1.3e-96:487:96//Hs.43228:N67390
 R-HEMBA1006597//Small inducible cytokine A5 (RANTES)//9.8e-44:291:85//Hs.155644:AF088219
 R-HEMBA1006612
 R-HEMBA1006624//ESTs//1.2e-25:225:80//Hs.138852:AA284247
 R-HEMBA1006624//ESTs//1.9e-93:454:98//Hs.72531:AA773630
 35 R-HEMBA1006631//Human mRNA for KIAA0033 gene, partial cds//7.5e-60:286:90//Hs.22271:D26067
 R-HEMBA1006635//ESTs, Moderately similar to ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//2.7e-91:426:100//Hs.139469:AI299889
 R-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]//3.4e-37:186:100//Hs.109818:AA411185
 40 R-HEMBA1006643//ESTs//1.8e-35:189:97//Hs.139640:AA846777
 R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//8.1e-108:567:94//Hs.6196:U40282
 R-HEMBA1006652//ESTs//7.6e-100:536:93//Hs.142613:AA129427
 R-HEMBA1006653//ESTs//2.0e-33:181:87//Hs.153599:AI282511
 45 R-HEMBA1006665//EST//1.2e-13:141:72//Hs.145596:AI263102
 R-HEMBA1006674//ESTs//3.1e-32:212:83//Hs.95115:AA206594
 R-HEMBA1006676//ESTs//2.6e-95:510:93//Hs.39140:AI041842
 R-HEMBA1006682//EST//1.4e-05:277:62//Hs.145762:AI269435
 R-HEMBA1006695//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-32:261:79//Hs.77579:AF013263
 50 R-HEMBA1006696//ESTs//4.5e-95:448:99//Hs.155694:AI032695
 R-HEMBA1006708//ESTs, Weakly similar to Miller-Dieker lissencephaly gene [H.sapiens]//1.1e-92:483:94//Hs.6525:AI205313
 R-HEMBA1006709//ESTs//3.4e-25:207:80//Hs.88617:AA872062
 55 R-HEMBA1006717
 R-HEMBA1006737//EST//5.9e-30:317:75//Hs.140568:AA826002
 R-HEMBA1006744//Interleukin 10//3.7e-41:419:74//Hs.2180:M57627
 R-HEMBA1006754//ESTs//1.2e-46:276:83//Hs.141254:AI334099

- R-HEMBA1006758//ESTs//0.00043:48:100//Hs.157265:AA489646
 R-HEMBA1006767//EST//0.094:120:65//Hs.159873:R92763
 R-HEMBA1006779//EST//9.3e-45:298:85//Hs.149580:AI281881
 R-HEMBA1006780//ESTs//1.6e-46:423:77//Hs.141602:N63562
 5 R-HEMBA1006789//ESTs//7.6e-55:245:95//Hs.6459:AI092936
 R-HEMBA1006795//ESTs//8.6e-47:315:78//Hs.140491:W52705
 R-HEMBA1006796//ESTs//0.26:175:65//Hs.103280:AI334978
 R-HEMBA1006807//Homo sapiens DEC-205 mRNA, complete cds//5.7e-47:461:75//Hs.153563:AF011333
 R-HEMBA1006821//ESTs//3.5e-12:222:68//Hs.150439:AO16305
 10 R-HEMBA1006824//Homo sapiens mRNA, clone:RES4-16//6.7e-51:298:90//Hs.121493:D25272
 R-HEMBA1006832//ESTs//0.0050:108:70//Hs.12853:T65556
 R-HEMBA1006849//Human mRNA for KIAA0118 gene, partial cds//2.1e-49:367:83//Hs.154326:D42087
 R-HEMBA1006865//ESTs//0.85:112:63//Hs.116430:AA644665
 R-nnnnnnnnnnn//Homo sapiens mRNA for KIAA0772 protein, complete cds//1.8e-67:611:74//Hs.15519:
 15 AB018315
 R-HEMBA1006885//ESTs//2.4e-66:347:96//Hs.100624:N95453
 R-HEMBA1006900//ESTs//2.7e-91:466:96//Hs.32984:R89739
 R-HEMBA1006921//ESTs//2.2e-33:170:100//Hs.152277:AA593117
 R-HEMBA1006926//ESTs, Weakly similar to ZK1053.6 [C.elegans]//2.9e-28:213:84//Hs.9096:AA029400
 20 R-HEMBA1006929//ESTs//4.0e-13:210:66//Hs.100895:AA479308
 R-HEMBA1006936//ESTs//3.9e-05:60:93//Hs.8737:W22712
 R-HEMBA1006938//EST//0.0021:244:62//Hs.144237:W52382
 R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//6.5e-77:371:98//Hs.42644:
 AJ010841
 25 R-HEMBA1006949//ESTs//1.2e-67:335:98//Hs.25780:R51321
 R-HEMBA1006973//ESTs//0.029:242:61//Hs.146074:N34457
 R-HEMBA1006976//EST//0.70:206:61//Hs.147092:AI189827
 R-HEMBA1006993//Human mRNA for KIAA0327 protein, complete cds//2.6e-47:368:80//Hs.149323:AB002325
 R-HEMBA1006996//ESTs//0.027:326:58//Hs.105008:AA451679
 30 R-HEMBA1007002//ESTs//0.13:116:66//Hs.26928:Z41440
 R-HEMBA1007017//ESTs//4.3e-47:208:87//Hs.155243:N70293
 R-HEMBA1007018//ESTs, Moderately similar to LIC-2 [R.norvegicus]//2.8e-112:558:96//Hs.107905:AI248363
 R-HEMBA1007045
 R-HEMBA1007051//ESTs//2.5e-39:321:80//Hs.146811:AA410788
 35 R-HEMBA1007052//EST//3.4e-41:377:74//Hs.44634:N34839
 R-HEMBA1007062//ESTs//1.2e-92:439:99//Hs.162882:AA807140
 R-HEMBA1007066//ESTs//0.85:204:61//Hs.22795:AI208272
 R-HEMBA1007073//ESTs//6.6e-52:362:85//Hs.30821:AI096866
 R-HEMBA1007078//EST, Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//7.2e-
 40 40:163:83//Hs.152369:AA504818
 R-HEMBA1007085//ESTs//8.1e-103:519:96//Hs.90638:AI348087
 R-HEMBA1007087//ESTs//3.1e-51:354:86//Hs.6449:W95025
 R-HEMBA1007112//EST//0.090:328:59//Hs.136623:AA633597
 R-HEMBA1007113//Homo sapiens mRNA, clone:RES4-16//1.1e-47:427:76//Hs.121493:D25272
 45 R-HEMBA1007129//ESTs//6.1e-13:314:65//Hs.137538:AA769438
 R-HEMBA1007147
 R-HEMBA1007149//ESTs//9.7e-103:540:94//Hs.127240:AA149818
 R-HEMBA1007151//ESTs//8.2e-102:505:96//Hs.24948:AA977674
 R-nnnnnnnnnnn//Homo sapiens epsin 2b mRNA, complete cds//1.6e-104:529:94//Hs.22396:AF062085
 50 R-HEMBA1007178//ESTs//2.2e-57:366:90//Hs.21648:AI302954
 R-HEMBA1007194//ESTs//9.0e-68:336:98//Hs.49760:AA741051
 R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.7e-62:332:95//Hs.3363:D86987
 R-HEMBA1007206//Human c-yes-1 mRNA//4.5e-49:390:80//Hs.75680:M15990
 R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//7.4e-98:471:97//Hs.27197:
 55 AB018340
 R-HEMBA1007251//ESTs//1.6e-78:377:99//Hs.98912:AA436864
 R-HEMBA1007256//ESTs//3.5e-20:127:79//Hs.137352:AA024934
 R-HEMBA1007267//Homo sapiens KIAA0395 mRNA, partial cds//8.8e-48:343:83//Hs.43681:AL022394

- R-HEMBA1007273//ESTs//1.0e-98:472:98//Hs.122610:AA807062
 R-HEMBA1007279//ESTs//3.3e-107:558:94//Hs.126480:AI221207
 R-HEMBA1007281//EST//0.074:244:63//Hs.29304:R73543
 R-HEMBA1007288//EST//9.4e-43:344:81//Hs.162112:AA524804
 5 R-HEMBA1007300//ESTs//0.096:371:57//Hs.102680:N52990
 R-HEMBA1007301
 R-HEMBA1007319//ESTs//7.7e-113:570:96//Hs.29263:AI337917
 R-HEMBA1007320//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//5.5e-15:311:64//Hs.142764:AA205569
 10 R-HEMBA1007322//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//5.7e-49:383:83//Hs.139107:K00629
 R-HEMBA1007327//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.9e-42:371:79//Hs.154069:U06452
 R-HEMBA1007341//EST//3.0e-17:291:68//Hs.150788:AI301848
 15 R-HEMBA1007342//EST//2.7e-11:263:67//Hs.145259:AI218684
 R-HEMBA1007347//Homo sapiens DEC-205 mRNA, complete cds//9.7e-47:368:82//Hs.153563:AF011333
 R-HEMBA1000005//ESTs, Weakly similar to putative p150 [H.sapiens]//3.3e-44:341:71//Hs.111730:AA604403
 R-HEMBA1000008//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//3.2e-40:292:83//Hs.129708:AF064090
 20 R-HEMBA1000018//H.sapiens mRNA for urea transporter//5.0e-49:311:87//Hs.66710:X96969
 R-HEMBA1000024//ESTs//7.5e-21:234:76//Hs.157049:AI345418
 R-HEMBA1000025//ESTs//2.2e-36:371:78//Hs.56562:AA056332
 R-HEMBA1000030//ESTs//3.2e-76:373:97//Hs.140190:AA701449
 R-HEMBA1000036//ESTs, Highly similar to HYPOTHETICAL 43.2 KD PROTEIN C34E10.1 IN CHROMOSOME
 25 III [Caenorhabditis elegans]//6.0e-92:477:95//Hs.4877:AA418465
 R-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//2.5e-92:467:97//Hs.20815:AF084928
 R-HEMBA1000039//ESTs//1.8e-43:361:71//Hs.108208:N64702
 R-HEMBA1000044//EST//7.6e-70:367:95//Hs.140860:R42954
 30 R-HEMBA1000048//EST//1.5e-45:262:91//Hs.157627:AI357802
 R-HEMBA1000050//ESTs//0.039:91:74//Hs.163189:AA236903
 R-HEMBA1000054//ESTs//3.0e-104:550:94//Hs.152395:AA533107
 R-HEMBA1000055//ESTs, Moderately similar to UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX SUB-UNIT VI REQUIRING PROTEIN [H.sapiens]//1.1e-72:350:99//Hs.116490:AA659584
 35 R-HEMBA1000059//ESTs//1.7e-10:200:70//Hs.163954:N57939
 R-HEMBA1000083//Homo sapiens mRNA for GCP170, complete cds//6.0e-41:337:80//Hs.4953:D63997
 R-HEMBA1000089//Human mRNA for KIAA0355 gene, complete cds//3.5e-39:487:70//Hs.153014:AB002353
 R-HEMBA1000099//ESTs//5.7e-37:353:75//Hs.22910:W18193
 R-HEMBA1000103//Homo sapiens mRNA for KIAA0640 protein, partial cds//6.5e-18:298:69//Hs.153026:AB014540
 40 R-HEMBA1000113//EST//8.2e-94:437:100//Hs.136893:AA805239
 R-HEMBA1000119//Homo sapiens ASMTL gene//1.2e-84:428:95//Hs.6315:Y15521
 R-HEMBA1000136//ESTs//0.043:262:59//Hs.61304:AA025692
 R-HEMBA1000141//ESTs//5.0e-38:254:79//Hs.141658:N77915
 45 R-HEMBA1000144//ESTs//9.6e-05:235:60//Hs.61700:AA033951
 R-HEMBA1000173//EST//9.6e-44:258:76//Hs.161917:AA483223
 R-HEMBA1000175//ESTs//4.8e-98:475:97//Hs.149740:AI199558
 R-HEMBA1000198//ESTs//1.0:123:62//Hs.116602:AA665965
 R-HEMBA1000215//Human mRNA for KIAA0355 gene, complete cds//2.2e-46:302:86//Hs.153014:AB002353
 50 R-HEMBA1000217//ESTs//2.2e-105:496:99//Hs.65973:AI339364
 R-HEMBA1000218//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//1.1e-48:292:79//Hs.133089:AF064019
 R-HEMBA1000226//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II [C.elegans]//5.1e-73:449:89//Hs.16803:AA843214
 55 R-HEMBA1000240//ESTs//1.1e-109:536:97//Hs.13528:AA523106
 R-HEMBA1000244//Small inducible cytokine A5 (RANTES)//9.5e-42:323:83//Hs.155464:AF088219
 R-HEMBA1000250//EST//8.8e-12:284:64//Hs.145960:AI276783
 R-HEMBA1000258//EST//4.5e-14:315:66//Hs.162551:AA584782

- R-HEMBB1000264
R-HEMBB1000266/ESTs, Weakly similar to similar to the beta transducin family [C.elegans]/2.7e-102:556:93//Hs.16079:AA083522
- 5 R-HEMBB1000272/ESTs/4.3e-91:480:94//Hs.107467:H11385
R-HEMBB1000274/Homo sapiens mRNA for KIAA0557 protein, partial cds//7.9e-24:198:72//Hs.101414:AB011129
R-HEMBB1000284/ESTs/4.8e-64:389:91//Hs.118043:N50458
R-HEMBB1000307/Human mRNA for KIAA0355 gene, complete cds//3.6e-43:288:87//Hs.153014:AB002353
- 10 R-HEMBB1000312/ESTs/6.0e-23:272:73//Hs.121354:AA758601
R-HEMBB1000317/ESTs/7.5e-90:424:99//Hs.150042:A1298034
R-HEMBB1000318/Small inducible cytokine A5 (RANTES)/3.3e-41:318:80//Hs.155464:AF088219
R-HEMBB1000335/ESTs/3.7e-15:324:65//Hs.85077:AA968576
R-HEMBB1000336/ESTs/6.4e-76:402:95//Hs.17207:H92480
R-HEMBB-1000337/ESTs/2.1e-80:391:97//Hs.118990:A1378084
- 15 R-HEMBB1000338/Small inducible cytokine A5 (RANTES)/4.0e-39:274:85//Hs.155464:AF088219
R-HEMBB1000339/EST/5.8e-41:336:79//Hs.151873:AA205736
R-HEMBB1000341/ESTs/3.8e-19:310:68//Hs.37573:H59651
R-HEMBB1000343/EST/1.1e-77:396:95//Hs.162664:AA605020
R-HEMBB1000354/Human mRNA for KIAA0186 gene, complete cds//1.7e-15:293:65//Hs.36232:D80008
- 20 R-HEMBB1000369/ESTs/1.6e-21:234:73//Hs.111583:AA463590
R-HEMBB1000374/Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487/2.3e-56:335:77//Hs.92381:AB007956
R-HEMBB1000376/H. sapiens mRNA for urea transporter//2.7e-50:525:74//Hs.66710:X96969
R-HEMBB1000391/ESTs/6.6e-50:316:88//Hs.142259:AA828840
- 25 R-HEMBB1000399/Homo sapiens mRNA for cell cycle checkpoint protein//3.8e-109:531:97//Hs.16184:AJ001642
R-HEMBB1000402/H. sapiens mRNA for MACH-alpha-2 protein//2.7e-35:369:72//Hs.19949:X98173
R-HEMBB1000404/ESTs/0.088:298:59//Hs.61607:AA032026
R-HEMBB1000420/EST//2.2e-78:376:98//Hs.160787:A1336591
R-HEMBB1000434/Human mRNA for KIAA0118 gene, partial cds//3.9e-50:302:89//Hs.154326:D42087
- 30 R-HEMBB1000438/ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]/0.30:214:63//Hs.142209:AA873303
R-HEMBB1000441/Human c-yes-1 mRNA//2.2e-46:280:90//Hs.75680:M15990
R-HEMBB1000449/ESTs/7.8e-59:332:92//Hs.87013:AA130221
R-HEMBB1000455/EST//4.8e-14:421:65//Hs.68832:AA088438
- 35 R-HEMBB1000472/ESTs/1.1e-104:505:98//Hs.132824:A1033396
R-HEMBB1000480/Human mRNA for KIAA0392 gene, partial cds//2.5e-49:295:90//Hs.40100:AB002390
R-HEMBB1000487/EST//0.78:87:68//Hs.134601:A1081506
R-HEMBB1000490/Small inducible cytokine A5 (RANTES)/4.0e-39:320:80//Hs.155464:AF088219
- 40 R-HEMBB1000491/Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.7e-50:312:76//Hs.113283:AF018080
R-HEMBB1000493/EST/7.1e-18:150:82//Hs.142068:AA176125
R-HEMBB1000510/EST//1.4e-45:139:97//Hs.152260:AA489703
R-HEMBB1000518/Human mRNA for KIAA0118 gene, partial cds//4.8e-50:415:78//Hs.154326:D42087
R-HEMBB1000523/Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.7e-57:497:78//Hs.113283:AF018080
- 45 R-HEMBB1000530/ESTs/2.7e-73:425:90//Hs.141254:A1334099
R-HEMBB1000550/EST//2.9e-11:113:79//Hs.161503:N68662
R-HEMBB1000554/Human huntingtin interacting protein (HIP1) mRNA, complete cds//8.2e-13:932:81//Hs.97206:AF052288
R-HEMBB1000556/ESTs/1.1e-94:529:92//Hs.33476:N36986
R-HEMBB1000564/ESTs/1.3e-19:128:91//Hs.142058:N34258
- 50 R-HEMBB1000573/ESTs/1.6e-86:494:90//Hs.120979:A160709
R-HEMBB1000575/ESTs/1.6e-45:232:74//Hs.141019:AA287618
R-HEMBB1000586/ESTs/5.1e-42:281:83//Hs.138852:AA284247
R-HEMBB1000589/ESTs/1.0e-10:184:71//Hs.142677:R95895
R-HEMBB1000591/ESTs/3.2e-40:406:75//Hs.138787:H73704
- 55 R-HEMBB1000592/ESTs/1.8e-97:455:99//Hs.94229:W65391
R-HEMBB1000598/Human anti secretory factor-1 mRNA, complete cds//1.8e-46:305:85//Hs.148495:AF050199
R-HEMBB1000623/ESTs/8.3e-47:277:92//Hs.6045:W67125
R-HEMBB1000630/ESTs/5.1e-106:538:96//Hs.13422:A1082249

R-HEMBB1000631//ESTs//5.1e-100:508:96//Hs.110379:N58152
 R-HEMBB1000632//ESTs//6.2e-44:371:80//Hs.132722:AA618531
 R-HEMBB1000637//Human mRNA for KIAA0080 gene, partial cds//6.4e-49:254:86//Hs.74554:D38522
 R-HEMBB1000638//EST//2.2e-38:371:76//Hs.162236:AA551582
 5 R-HEMBB1000643//ESTs//0.0049:191:62//Hs.55445:W31963
 R-HEMBB1000649//ESTs, Moderately similar to hTAFII68 [H.sapiens]//4.0e-76:399:95//Hs.124106:AA948100
 R-HEMBB1000652//ESTs//1.5e-14:271:64//Hs.163954:N57939
 R-HEMBB1000665//ESTs//4.2e-12:109:87//Hs.14107:W94988
 R-HEMBB1000671//ESTs//2.8e-68:439:87//Hs.140491:W52705
 10 R-HEMBB1000673//EST//0.58:46:82//Hs.142286:AA338293
 R-HEMBB1000684//ESTs//8.5e-20:307:72//Hs.122825:AA765454
 R-nnnnnnnnnnn//Homo sapiens neuroan1 mRNA, complete cds//6.5e-52:287:93//Hs.158300:AF040723
 R-HEMBB1000705//Small inducible cytokine A5 (RANTES)//4.6e-24:165:78//Hs.155464:AF088219
 R-HEMBB1000706//EST//1.2e-10:211:65//Hs.105524:AA521412
 15 R-HEMBB1000709//ESTs, Weakly similar to putative p150 [H.sapiens]//3.9e-50:245:99//Hs.111730:AA604403
 R-HEMBB1000725//Human mRNA for KIAA0308 gene, partial cds//0.11:350:59//Hs.10351:AB002306
 R-HEMBB1000726//EST//5.3e-49:303:88//Hs.149580:AI281881
 R-HEMBB1000773 8//Homo sapiens mRNA, clone:RES4-16//2.5e-49:302:89//Hs.121493:D25272
 R-HEMBB1000749//ESTs//1.6e-49:331:86//Hs.152788:AA630925
 20 R-HEMBB1000763//ESTs//9.7e-104:474:95//Hs.77480:AA100522
 R-HEMBB1000770//EST//1.0e-75:359:99//Hs.136564:AA642445
 R-HEMBB1000781//ESTs//5.3e-66:317:99//Hs.28827:AI125541
 R-HEMBB1000789//ESTs//5.9e-83:394:99//Hs.120842:AA435771
 R-HEMBB1000790//PLATELET GLYCOPROTEIN V PRECURSOR//1.3e-37:193:75//Hs.73734:Z23091
 25 R-HEMBB1000794//ESTs//7.1e-98:490:96//Hs.105743:AA532718
 R-HEMBB1000807//ESTs//2.6e-22:145:92//Hs.53913:AA908961
 R-HEMBB1000810//Small inducible cytokine A5 (RANTES)//1.8e-34:206:79//Hs.155464:AF088219
 R-HEMBB1000821//ESTs//2.4e-90:425:99//Hs.118659:AI052447
 R-HEMBB1000822//ESTs//1.7e-45:288:89//Hs.24130:R27124
 30 R-HEMBB1000826//Small inducible cytokine A5 (RANTES)//2.9e-51:245:82//Hs.155464:AF088219
 R-HEMBB1000827//EST//2.8e-40:295:84//Hs.149580:AI281881
 R-HEMBB1000831//ESTs//4.0e-59:291:98//Hs.62675:AA044176
 R-HEMBB1000835//ESTs//7.3e-21:124:82//Hs.102671:N52545
 R-HEMBB1000840//ATPase, Na⁺/K⁺ transporting, beta 2 polypeptide//1.3e-43:163:84//Hs.78854:AF007876
 35 R-HEMBB1000848//Homo sapiens mRNA for KIAA0565 protein, complete cds//9.5e-41:367:78//Hs.129740:AB011137
 R-HEMBB1000852//EST//1.2e-09:188:70//Hs.127869:AA968599
 R-HEMBB1000870//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1.0e-41:483:73//Hs.2379:U23942
 R-HEMBB1000876//EST//0.0022:211:63//Hs.125552:AA884141
 40 R-HEMBB1000883//ESTs//1.4e-65:343:95//Hs.98269:H27247
 R-HEMBB1000887//ESTs//4.0e-22:212:79//Hs.138965:AI004740
 R-HEMBB1000888//EST//8.2e-07:196:64//Hs.118276:W15258
 R-HEMBB1000890//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.1e-46:327:83//Hs.51048:X68830
 R-HEMBB1000893//EST//4.7e-34:242:85//Hs.149580:AI281881
 45 R-HEMBB1000908//EST//0.95:27:100//Hs.142568:AA285066
 R-HEMBB1000910//ESTs//1.9e-36:318:78//Hs.141140:AA715983
 R-HEMBB1000913//Human mRNA for KIAA0327 protein, complete cds//2.5e-33:367:73//Hs.149323:AB002325
 R-HEMBB1000915//ESTs//0.00018:188:61//Hs.44847:AI222742
 R-HEMBB1000917//Homo sapiens KIAA0414 mRNA, partial cds//3.7e-41:228:84//Hs.127649:AB007874
 50 R-HEMBB1000927//ESTs//2.2e-62:307:98//Hs.97044:AA365784
 R-HEMBB1000947//ESTs, Weakly similar to F26E4.13 [C.elegans]//3.3e-60:350:91//Hs.49163:AA532881
 R-HEMBB1000959//Human Line-1 repeat mRNA with 2 open reading frames//8.1e-84:546:86//Hs.23094:M19503
 R-HEMBB1000973//ESTs//6.8e-95:445:99//Hs.105859:AI419354
 R-HEMBB1000975//ESTs//1.2e-39:197:100//Hs.26176:AI032007
 55 R-HEMBB1000981//EST//7.7e-58:284:98//Hs.60179:AA007242
 R-HEMBB1000985//ESTs//1.2e-103:524:95//Hs.43102:AA131369
 R-HEMBB1000991//EST//0.99:58:72//Hs.100246:T23625
 R-HEMBB1000996//Homo sapiens LIM protein mRNA, complete cds//1.3e-41:482:70//Hs.154103:AF061258

- R-HEMBB1001004//ESTs//5.7e-70:362:95//Hs.6434:W27112
 R-HEMBB1001008//ESTs, Weakly similar to hypothetical L1 protein [H.sapiens]/2.3e-25:339:71//Hs.129992:H58762
- 5 R-HEMBB1001011//ESTs//4.0e-53:325:92//Hs.33268:AI191214
 R-HEMBB1001014//ESTs//1.3e-46:323:83//Hs.163980:AA715814
 R-HEMBB1001020//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.0e-46:305:76//Hs.113283:AF018080
 R-HEMBB1001024//ESTs//8.5e-47:374:80//Hs.141602:N63562
 R-HEMBB1001037//ESTs//2.6e-47:282:91//Hs.155384:Z78385
 R-HEMBB1001047//EST//6.2e-33:232:74//Hs.160146:AI049975
- 10 R-HEMBB1001051//ESTs//7.7e-79:385:98//Hs.95290:AA046107
 R-HEMBB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.1e-87:497:91//Hs.15832:AB014518
 R-HEMBB1001058//Homo sapiens mRNA for KIAA0475 protein, complete cds//2.2e-26:125:81//Hs.5737:AB007944
- 15 R-HEMBB1001060//ESTs//1.9e-37:541:69//Hs.141534:N64785
 R-HEMBB1001063//ESTs//4.7e-42:269:88//Hs.55855:AA621381
 R-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.1e-107:512:97//Hs.12953:AF034803
 R-HEMBB1001096//Human HsLIM15 mRNA for HsLIM15, complete cds//1.2e-20:233:70//Hs.37181:D64108
 R-HEMBB1001102//Human mRNA for KIAA0355 gene, complete cds//9.1e-40:299:82//Hs.153014:AB002353
- 20 R-HEMBB1001105//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.8e-46:296:87//Hs.113283:AF018080
 R-HEMBB1001114//ESTs//6.2e-44:293:86//Hs.70279:AA757426
 R-HEMBB1001117//ESTs//1.1e-80:47:1:90//Hs.61935:T75092
 R-HEMBB1001119//ESTs//4.0e-38:213:84//Hs.109140:AI289942
 R-HEMBB1001126
- 25 R-HEMBB1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subunit mRNA, complete cds//1.6e-24:285:73//Hs.554:M25077
 R-HEMBB1001137//ESTs//4.6e-10:66:100//Hs.74924:AI332962
 R-HEMBB1001142//EST//6.4e-48:315:85//Hs.149580:AI281881
 R-HEMBB1001151
- 30 R-HEMBB1001153//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/1.3e-65:331:96//Hs.154179:AA579197
 R-HEMBB1001169//Oxytocin receptor//1.5e-25:165:73//Hs.2820:X64878
 R-HEMBB1001169//ESTs//3.5e-41:233:93//Hs.129218:AA991162
 R-HEMBB1001177
- 35 R-HEMBB1001182//ESTs//1.9e-86:455:95//Hs.6937:AA524349
 R-HEMBB1001199
 R-HEMBB1001208//ESTs//3.3e-43:216:99//Hs.121806:N71183
 R-HEMBB1001209//ESTs//6.7e-80:409:96//Hs.141185:R99549
 R-HEMBB1001210//ESTs//2.2e-46:290:88//Hs.103329:D11573
- 40 R-HEMBB1001218//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//3.1e-44:298:87//Hs.103458:X53795
 R-HEMBB1001221//ESTs//9.4e-75:353:100//Hs.151504:AA550817
 R-HEMBB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Gallus gallus]/3.8e-80:400:96//Hs.71873:AA148213
- 45 R-HEMBB1001242//ESTs//1.6e-63:404:87//Hs.25534:AA149560
 R-HEMBB1001249//ESTs//3.8e-34:360:70//Hs.150727:AI292236
 R-HEMBB1001253//EST//0.0011:84:77//Hs.124579:AA853987
 R-HEMBB1001254//ESTs//4.5e-95:444:99//Hs.161059:AI431268
 R-HEMBB1001267//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.3e-50:524:73//Hs.159897:AB007970
- 50 R-HEMBB1001271//Human mRNA for KIAA0118 gene, partial cds//4.0e-45:323:84//Hs.154326:D42087
 R-HEMBB1001282//EST//2.9e-78:401:96//Hs.72871:AA169412
 R-HEMBB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III [Caenorhabditis elegans]//2.6e-104:515:97//Hs.16606:W81021
 R-HEMBB1001289//ESTs//7.8e-45:440:75//Hs.44702:AI148840
- 55 R-HEMBB1001294//ESTs//1.9e-100:476:99//Hs.109017:AI057112
 R-HEMBB1001302
 R-HEMBB1001304//ESTs//4.0e-92:431:99//Hs.113750:AI091154

- R-HEMBB1001314//Interleukin 10//6.3e-41:334:79//Hs.2180:M57627
 R-HEMBB1001315//Interleukin 10//1.9e-43:285:87//Hs.2180:M57627
 R-HEMBB1001317//Human cytochrome P450-11B (h11B3) mRNA, complete cds//8.4e-45:357:81//Hs.110194:M29873
- 5 R-HEMBB1001326//ESTs//0.85:174:62//Hs.133487:AI393754
 R-HEMBB1001331//ESTs, Weakly similar to DFS70 [H.sapiens]//6.5e-61:313:96//Hs.43071:AA206222
 R-HEMBB1001335//EST//5.2e-80:381:99//Hs.116769:AA630365
 R-HEMBB1001337//ESTs//2.7e-84:404:99//Hs.148966:AI242639
 R-HEMBB1001339//ESTs//2.1e-97:485:96//Hs.88357:AA262470
- 10 R-HEMBB1001346
 R-HEMBB1001348//ESTs//1.1e-43:295:85//Hs.163604:R94354
 R-HEMBB1001356//EST//6.0e-11:89:88//Hs.152366:AA486721
 R-HEMBB1001364//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-12:129:79//Hs.9792:AA207055
- 15 R-HEMBB1001366//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:550:72//Hs.154326:D42087
 R-HEMBB1001367//ESTs//1.2e-19:165:82//Hs.146314:R99617
 R-HEMBB1001369//Small inducible cytokine A5 (RANTES)//1.9e-25:217:80//Hs.155464:AF088219
 R-HEMBB1001380//ESTs//4.0e-08:216:63//Hs.143763:AI174205
 R-HEMBB1001384//ESTs//6.6e-110:547:96//Hs.6671:AI341699
- 20 R-HEMBB1001387//ESTs//1.1e-104:497:98//Hs.87654:AA853970
 R-HEMBB1001394//ESTs//6.4e-73:428:89//Hs.139922:AA281350
 R-HEMBB1001410//Alcohol dehydrogenase 7 sigma subunit (class IV)//0.88:365:58//Hs.389:X76342
 R-HEMBB1001424//ESTs//1.3e-88:466:94//Hs.42174:AA194644
 R-HEMBB1001426//ESTs//2.2e-45:337:82//Hs.37573:H59651
- 25 R-HEMBB1001429//EST//3.8e-59:543:76//Hs.158803:AI376846
 R-HEMBB1001436//ESTs//3.7e-69:332:99//Hs.156518:AA724317
 R-HEMBB1001443//ESTs//4.8e-54:270:98//Hs.21898:AI088201
 R-HEMBB1001449//ESTs//3.2e-43:170:84//Hs.150727:AI292236
 R-HEMBB1001454//ESTs//9.1e-46:304:86//Hs.139190:N55515
- 30 R-HEMBB1001458//ESTs//3.2e-98:478:97//Hs.50144:N67293
 R-HEMBB1001463//Homo sapiens KIAA0421 mRNA, partial cds//4.3e-50:440:78//Hs.41742:AB007881
 R-HEMBB1001464//ESTs, Weakly similar to K01H12.1 [C.elegans]//0.25:222:61//Hs.13275:AI341468
 R-HEMBB1001482//ESTs, Moderately similar to zinc finger protein [R.norvegicus]//0.80:53:83//Hs.26799:W74481
 R-HEMBB1001500//EST//1.4e-13:310:67//Hs.162863:AA604515
- 35 R-HEMBB1001521//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.5e-29:186:92//Hs.17630:AB018280
 R-HEMBB1001527//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//4.7e-51:404:81//Hs.141429:AA631915
 R-HEMBB1001531//ESTs//3.3e-13:250:67//Hs.139158:AA226159
- 40 R-HEMBB1001535//H. sapiens mRNA for sigma 3B protein//1.9e-39:291:82//Hs.154782:X99459
 R-HEMBB1001536//Human mRNA for KIAA0355 gene, complete cds//5.0e-44:318:83//Hs.153014:AB002353
 R-HEMBB1001537//Homo sapiens KIAA0409 mRNA, partial cds//3.2e-47:318:80//Hs.5158:AB007869
 R-HEMBB1001555//ESTs//2.6e-13:182:71//Hs.112671:AI377274
 R-HEMBB1001562//ESTs//1.7e-43:316:83//Hs.151365:AA643962
- 45 R-HEMBB1001564//EST//1.3e-35:141:81//Hs.162197:AA53521
 R-HEMBB1001565//Human mRNA for KIAA0331 gene, complete cds//5.1e-18:152:85//Hs.146395:AB002329
 R-HEMBB1001585//ESTs//1.1e-32:190:84//Hs.33354:AA179944
 R-HEMBB1001586//ESTs//4.9e-94:447:99//Hs.124084:AA843219
 R-HEMBB1001588//EST//8.3e-27:363:69//Hs.141603:N66015
- 50 R-HEMBB1001603//ESTs//1.2e-101:482:99//Hs.12403:AI090184
 R-HEMBB1001618//ESTs//5.8e-35:437:70//Hs.136868:AA805044
 R-HEMBB1001619//EST//1.7e-38:476:70//Hs.139093:AA166888
 R-HEMBB1001630//Homo sapiens mRNA, clone:RES4-16//5.7e-41:193:90//Hs.121493:D25272
 R-HEMBB1001635//ESTs//9.5e-34:304:82//Hs.140444:AI002082
 R-HEMBB1001637//ESTs//1.0e-42:443:74//Hs.21978:AA009633
- 55 R-HEMBB1001641//EST//2.4e-06:67:86//Hs.162398:AA572813
 R-HEMBB1001653//ESTs//4.8e-80:381:99//Hs.140502:AA806438
 R-HEMBB1001665//ESTs//2.3e-44:372:79//Hs.132818:AI038577

- R-HEMBB1001668//ESTs//0.73:212.62//Hs.8928:N32572
 R-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//5.9e-117:573.97//Hs.24439:AB014546
- 5 R-HEMBB1001684//ESTs, Moderately similar to Tbcd [M.musculus]//5.4e-106:523.97//Hs.26939:AA804534
 R-HEMBB1001685//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.9e-43:292.86//Hs.96337:AA225358
 R-HEMBB1001695//ESTs//3.7e-101:539.94//Hs.78289:R60867
 R-HEMBB1001704//EST//0.96:248.57//Hs.163025:AA703038
 R-HEMBB1001706//ESTs//1.3e-39:308.81//Hs.141318:N171080
- 10 R-HEMBB1001707//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.9e-32:277.73//Hs.142764:AA205569
 R-HEMBB1001717//ESTs//1.6e-34:225.87//Hs.57883:AA218645
 R-HEMBB1001735//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.6e-11:158.71//Hs.141263:H64113
- 15 R-HEMBB1001736//ESTs//0.0035:223.60//Hs.21354:AA203403
 R-HEMBB1001747//EST//9.9e-55:293.81//Hs.112866:AA620488
 R-HEMBB1001749//ESTs//2.5e-13:95.91//Hs.139888:N25287
 R-HEMBB1001753//ESTs//2.6e-07:141.70//Hs.144604:AI052059
 R-HEMBB1001756//EST//2.6e-06:165.64//Hs.121195:AA757211
- 20 R-HEMBB1001760//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//1.3e-24:264.74//Hs.70008:L00352
 R-HEMBB1001762//ESTs//2.1e-81:447.93//Hs.152766:AA211369
 R-HEMBB1001785//ESTs//0.040:390.58//Hs.116651:AA993406
 R-HEMBB1001797//ESTs//2.1e-90:428.99//Hs.8958:AA169253
- 25 R-HEMBB1001802//Desmin//9.9e-95:497.93//Hs.119104:M63391
 R-HEMBB1001812//ESTs//1.2e-12:91.78//Hs.138852:AA284247
 R-HEMBB1001816//Human Line-1 repeat mRNA with 2 open reading frames//5.9e-13:143.76//Hs.23094:M19503
 R-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds//5.5e-106:499.98//Hs.159396:AF056209
- 30 R-HEMBB1001836//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//9.6e-39:288.73//Hs.67619:AB007957
 R-HEMBB1001839
 R-HEMBB1001850//EST//0.020:119.68//Hs.32767:H38125
 R-HEMBB1001863//ESTs//4.5e-17:226.72//Hs.157253:AI357539
- 35 R-HEMBB1001867//ESTs//2.3e-16:254.68//Hs.123664:AA806106
 R-HEMBB1001868//EST//9.8e-30:155.100//Hs.160572:AA888397
 R-HEMBB1001869//ESTs//2.8e-42:376.78//Hs.141973:N21434
 R-HEMBB1001872//EST//0.85:156.64//Hs.119501:AA487980
- 40 R-HEMBB1001874//EST//0.64:107.70//Hs.147482:AI215572
 R-HEMBB1001875//EST//0.079:199.59//Hs.121810:AA775240
 R-HEMBB1001880//Thromboxane A2 receptor//9.0e-47:297.88//Hs.89887:D38081
 R-HEMBB1001899//ESTs//6.3e-68:323.100//Hs.121538:AA609310
 R-HEMBB1001905//ESTs//4.4e-19:227.73//Hs.146173:AA906191
 R-HEMBB1001906//ESTs//1.6e-90:463.95//Hs.28266:H46725
- 45 R-HEMBB1001908//Homo sapiens EVI5 homolog mRNA, complete cds//3.7e-27:557.64//Hs.26929:AF008915
 R-HEMBB1001910//EST//6.0e-37:308.78//Hs.162197:AA535216
 R-HEMBB1001911//Homo sapiens tapasin (NGS-17) mRNA, complete cds//8.0e-58:367.79//Hs.5247:AF029750
 R-HEMBB1001915//ESTs//3.1e-73:395.93//Hs.17054:AI139897
- 50 R-HEMBB1001921//Human mRNA for KIAA0392 gene, partial cds//2.7e-50:323.88//Hs.40100:AB002390
 R-HEMBB1001922//H.sapiens mRNA for novel member of serine-arginine domain protein, SRP129//7.4e-38:531.70//Hs.153086:Y11251
 R-HEMBB1001925//Human mRNA for KIAA0327 protein, complete cds//9.5e-19:199.77//Hs.149323:AB002325
 R-HEMBB1001930//EST//1.9e-18:136.78//Hs.132635:AI032875
 R-HEMBB1001944//EST//0.034:228.57//Hs.93664:N23366
- 55 R-HEMBB1001945//ESTs//1.8e-83:439.95//Hs.7341:N57875
 R-HEMBB1001947//ESTs//5.6e-109:533.97//Hs.48855:AA134589
 R-HEMBB1001950//ESTs//1.5e-107:583.93//Hs.8033:N94998
 R-HEMBB1001952//ESTs//3.1e-40:283.85//Hs.146811:AA410788

- R-HEM BB1001953//Human mRNA for KIAA0080 gene, partial cds//6.2e-50:284.83//Hs.74554:D38522
 R-HEM BB1001957//EST//4.8e-50:382.81//Hs.149580:AI281881
 R-HEM BB1001962//ESTs//1.5e-20:143.88//Hs.11924:W26972
 5 R-HEM BB1001967//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.3e-61:296.88//Hs.153468:AB011147
 R-HEM BB1001973//ESTs//1.4e-48:303.88//Hs.132722:AA618531
 R-HEM BB1001983//ESTs//2.6e-72:374.95//Hs.141022:H06475
 R-HEM BB1001988//ESTs//2.0e-31:204.88//Hs.142531:N91572
 10 R-HEM BB1001990//ESTs//9.4e-115:574.96//Hs.44426:AA173223
 R-HEM BB1001996
 R-HEM BB1001997//ESTs//7.6e-78:380.98//Hs.32682:H37798
 R-HEM BB1002002//Human kpni repeat mma (cdna clone pcd-kpni-8), 3' end//3.0e-18:222.71//Hs.103948:K00627
 15 R-HEM BB1002005//EST//2.2e-41:339.80//Hs.160833:AI345334
 R-HEM BB1002009//EST//2.9e-44:245.94//Hs.28788:R66896
 R-HEM BB1002015//EST//0.0027:198.63//Hs.160868:AI359052
 R-HEM BB1002042//ESTs//1.1e-75:529.84//Hs.106919:AA523900
 R-HEM BB1002043//ESTs//7.9e-40:292.83//Hs.70279:AA757426
 R-HEM BB1002044//ESTs//2.1e-92:460.94//Hs.115897:AA156638
 20 R-HEM BB1002045//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-75:301.85//Hs.113283:AF018080
 R-HEM BB1002049//ESTs//3.8e-77:409.94//Hs.122624:R32638
 R-HEM BB1002050//ESTs//8.7e-45:330.82//Hs.44702:AI148840
 R-HEM BB1002068//ESTs//8.3e-70:333.99//Hs.134807:AI090671
 R-HEM BB1002069//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.5e-75:486.81//Hs.129735:AF010144
 25 R-HEM BB1002092//ESTs//6.5e-46:331.83//Hs.22910:W18193
 R-HEM BB1002094//EST//3.6e-45:280.88//Hs.149580:AI281881
 R-HEM BB1002115
 R-HEM BB1002139//ESTs//4.2e-45:318.85//Hs.107657:AA126814
 30 R-HEM BB1002142//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//1.4e-45:281.88//Hs.152531:AF068006
 R-HEM BB1002152//EST//4.3e-39:250.89//Hs.156552:AA833553
 R-HEM BB1002189//H. sapiens mRNA for translin associated protein X//1.4e-47:328.85//Hs.96247:X95073
 R-HEM BB1002190//ESTs//8.3e-05:122.70//Hs.41974:AF039185
 35 R-HEM BB1002193//Human sky mRNA for Sky, complete cds//8.9e-24:398.69//Hs.301:U18934
 R-HEM BB1002217//EST//6.6e-50:303.89//Hs.149580:AI281881
 R-HEM BB1002218//ESTs//2.3e-19:150.86//Hs.136031:W95841
 R-HEM BB1002232//ESTs//8.9e-47:445.77//Hs.163971:N27584
 R-HEM BB1002247//EST//6.6e-09:236.65//Hs.130578:AI004631
 40 R-HEM BB1002249//ESTs//5.2e-16:325.64//Hs.156253:AI334807
 R-HEM BB1002254//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-99:590.88//Hs.23094:M19503
 R-HEM BB1002255//Human mRNA for KIAA0365 gene, partial cds//5.6e-45:342.83//Hs.84123:AB002363
 R-HEM BB1002266//ESTs//4.4e-98:472.98//Hs.65366:AI189112
 R-HEM BB1002280//EST//2.9e-41:247.90//Hs.161917:AA483223
 45 R-HEM BB1002300//ESTs//8.4e-19:229.75//Hs.138463:N72305
 R-HEM BB1002306//Homo sapiens KIAA0432 mRNA, complete cds//0.0021:138.67//Hs.155174:AB007892
 R-HEM BB1002327//EST//0.042:249.61//Hs.121097:AA714637
 R-HEM BB1002329//ESTs//1.7e-94:453.99//Hs.7114:R24312
 R-HEM BB1002340//ESTs//5.8e-15:163.77//Hs.26378:H10228
 50 R-HEM BB1002342//Homo sapiens mRNA for putative thioredoxin-like protein//0.85e-46:84//Hs.42644:AJ010841
 R-HEM BB1002358//ESTs//2.0e-52:319.81//Hs.140255:AA708322
 R-HEM BB1002359//ESTs//2.7e-106:517.97//Hs.13634:AI051613
 R-HEM BB1002364//Human mRNA for KIAA0080 gene, partial cds//5.3e-37:360.65//Hs.74554:D38522
 R-HEM BB1002371//Catalase//3.3e-22:235.77//Hs.76359:X04085
 55 R-HEM BB1002381//Homo sapiens (JH8) mRNA, partial cds//1.0e-08:120.78//Hs.142296:AF072467
 R-HEM BB1002383//ESTs//3.5e-108:520.98//Hs.45140:D80055
 R-HEM BB1002387
 R-HEM BB1002415//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.3e-23:

- 168:77//Hs.133526:N21103
 R-HEMBB1002425//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)/3.2e-57.304.90//Hs.144563:AF057280
 R-HEMBB1002442//ESTs//2.7e-48:289.87//Hs.155243:N70293
 5 R-HEMBB1002453//Human mRNA for KIAA0355 gene, complete cds//6.2e-45:292.87//Hs.153014:AB002353
 R-HEMBB1002457//Human mRNA for KIAA0118 gene, partial cds//2.7e-46:546.71//Hs.154326:D42087
 R-HEMBB1002458//EST//1.8e-72:343.100//Hs.162006:AA508089
 R-HEMBB1002477//ESTs//1.6e-38:215.93//Hs.18240:AA460083
 10 R-HEMBB1002489//ESTs//1.2e-101:534.94//Hs.7981:H15176
 R-HEMBB1002492//ESTs//5.0e-14:350.62//Hs.99205:AA204969
 R-HEMBB1002495//ESTs//2.1e-19:147.86//Hs.163747:AA174017
 R-HEMBB1002500//ESTs, Weakly similar to p40 [H.sapiens]//1.2e-68:336.98//Hs.141515:T41142
 R-HEMBB1002509//ESTs//2.7e-97:459.99//Hs.127638:AI014615
 15 R-HEMBB1002510//ESTs, Weakly similar to located at OATL1 [H.sapiens]//2.2e-48:265.95//Hs.48827:AA873278
 R-HEMBB1002520//EST//7.2e-40:198.84//Hs.140493:AA804538
 R-HEMBB1002522//Human putative transmembrane receptor IL-1R α mRNA, complete cds//0.50:142.69//Hs.159301:U43672
 R-HEMBB1002531//EST//0.024:147.61//Hs.148305:AA909605
 R-HEMBB1002534//EST//3.1e-22:168.84//Hs.146794:AI149478
 20 R-HEMBB1002545//ESTs//9.2e-90:421.99//Hs.118317:AI033259
 R-HEMBB1002550//ESTs, Weakly similar to similar to S. cerevisiae LAG1 [C.elegans]//5.1e-22:210.81//Hs.11896:T68813
 R-HEMBB1002556//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.9e-45:344.82//Hs.51048:X68830
 R-HEMBB1002579//ESTs//4.6e-47:326.85//Hs.155184:AA573189
 25 R-HEMBB1002582//ESTs//0.00036:91.76//Hs.140039:AA047045
 R-HEMBB1002590//ESTs//1.0e-37:210.84//Hs.36658:N91138
 R-HEMBB1002596//Human mRNA for KIAA0118 gene, partial cds//2.2e-46:297.87//Hs.154326:D42087
 R-HEMBB1002600//EST//2.5e-17:147.84//Hs.121918:AA777424
 R-HEMBB1002601//ESTs//7.8e-68:358.95//Hs.101489:R66923
 30 R-HEMBB1002603//EST//1.1e-47:281.90//Hs.149580:AI281881
 R-HEMBB1002607//ESTs//5.4e-75:379.97//Hs.29438:H42896
 R-HEMBB1002610//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.2e-07:140.70//Hs.155456:AA707265
 R-HEMBB1002613//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//8.5e-47:278.83//Hs.159187:AB007977
 35 R-HEMBB1002614//ESTs//3.4e-81:383.99//Hs.13012:AI094150
 R-HEMBB1002617//Homo sapiens protease-activated receptor 4 mRNA, complete cds//7.4e-19:151.80//Hs.137574:AF055917
 R-HEMBB1002623//ESTs//1.6e-45:288.87//Hs.138852:AA284247
 40 R-HEMBB1002635//Small inducible cytokine A5 (RANTES)//5.5e-39:278.81//Hs.155464:AF088219
 R-HEMBB1002664//EST//8.9e-49:315.87//Hs.149580:AI281881
 R-HEMBB1002677//ESTs//0.65:159.62//Hs.163517:AI419775
 R-HEMBB1002683//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase//8.6e-54:543.75//Hs.2638:Z28339
 45 R-HEMBB1002684//ESTs//3.0e-18:148.87//Hs.158270:AA776646
 R-HEMBB1002686//ESTs//6.1e-80:419.96//Hs.103002:W02753
 R-HEMBB1002692//ESTs//3.3e-58:451.82//Hs.141254:AI334099
 R-HEMBB1002697//ESTs//6.2e-86:423.98//Hs.129812:AA769487
 R-HEMBB1002699//EST//5.6e-46:322.84//Hs.140231:AI054398
 50 R-HEMBB1002702//ESTs//5.6e-36:412.72//Hs.154993:AA142842
 R-HEMBB1002705//POLYPOSIS LOCUS PROTEIN 1//0.024:412.58//Hs.74646:M73547
 R-HEMBB1002712//ESTs//9.0e-96:451.99//Hs.136806:AA805682
 R-MAMMA1000009//ESTs//3.0e-78:392.96//Hs.163947:AA678701
 R-MAMMA1000019//Small inducible cytokine A5 (RANTES)//1.5e-47:247.87//Hs.155464:AF088219
 55 R-MAMMA1000020//Zinc finger protein 2 (A1-5)//4.9e-49:384.80//Hs.155533:X60152
 R-MAMMA1000025//Homo sapiens KIAA0441 mRNA, complete cds//4.7e-11:154.71//Hs.32511:AB007901
 R-MAMMA1000043//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.0e-58:277.84//Hs.93121:AB018304

- R-MAMMA1000045//ESTs//1.0e-38:225.92//Hs.142567:AA287165
 R-MAMMA1000055//EST//0.14:91:67//Hs.144061:AA996350
 R-MAMMA1000057//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//3.8e-77:545:83//Hs.69747:M35531
- 5 R-MAMMA1000069//ESTs//8.0e-108:546:96//Hs.44856:N37065
 R-MAMMA1000084//Homo sapiens clone 23632 mRNA sequence//7.3e-43:313:83//Hs.46918:AF052099
 R-MAMMA1000085//ESTs, Highly similar to PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C [Schizosaccharomyces pombe]//7.7e-104:546:94//Hs.7779:AA045241
 R-MAMMA1000092//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.2e-22:287:71//Hs.136063:U51713
- 10 R-MAMMA1000103//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//8.4e-49:334:86//Hs.70008:L00352
 R-MAMMA1000117//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.1e-08:96:80//Hs.115088:AA230172
 R-MAMMA1000129//EST//2.8e-64:310:99//Hs.136394:AA523577
 R-MAMMA1000133
- 15 R-MAMMA1000134//ESTs//1.1e-21:152:87//Hs.163747:AA174017
 R-MAMMA1000139//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.3e-40:288:78//Hs.159897:AB007970
 R-MAMMA1000143//EST//5.0e-52:314:89//Hs.149580:AI281881
 R-MAMMA1000155//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.5e-59:562:75//Hs.77579:AF013263
 R-MAMMA1000163//ESTs//2.8e-92:457:96//Hs.114413:AA884787
 R-MAMMA1000171//Homo sapiens mRNA for putative lipoic acid synthetase, partial//2.5e-39:173:83//Hs.53531:AJ224162
- 25 R-MAMMA1000173//ESTs, Highly similar to SRC SUBSTRATE P80/85 PROTEINS [Gallus gallus]//2.4e-07:63:90//Hs.90367:AI357069
 R-MAMMA1000175//EST//0.66:217:58//Hs.146444:AI127611
 R-MAMMA1000183//ESTs//6.7e-30:341:73//Hs.125254:AA872054
 R-MAMMA1000198//EST//2.8e-45:185:88//Hs.149580:AI281881
 R-MAMMA1000221//ESTs, Weakly similar to circadian clock protein [M.musculus]//1.4e-41:272:90//Hs.68398:AA421103
 R-MAMMA1000227//EST//2.4e-39:388:76//Hs.144175:H70425
 R-MAMMA1000241//EST//0.0027:263:61//Hs.37532:H57946
- 35 R-MAMMA1000251//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.3e-47:322:86//Hs.15519:AB018315
 R-MAMMA1000254//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//2.2e-43:315:83//Hs.129708:AF064090
 R-MAMMA1000257//EST//1.6e-62:330:93//Hs.141728:W73041
 R-MAMMA1000264//Von Hippel-Lindau syndrome//2.3e-31:141:81//Hs.78160:AF010238
 R-MAMMA1000266//ESTs//3.4e-34:150:81//Hs.163980:AA715814
 R-MAMMA1000270//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//2.7e-57:304:78//Hs.159187:AB007977
 R-MAMMA1000277//Thiopurine S-methyltransferase//3.7e-27:380:71//Hs.51124:AF019369
- 45 R-MAMMA1000278//ESTs//5.2e-99:504:95//Hs.8494:W72694
 R-MAMMA1000279//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//3.1e-58:295:83//Hs.92381:AB007956
 R-MAMMA1000284//EST//4.1e-10:151:73//Hs.60742:AA017066
 R-MAMMA1000287
- 50 R-MAMMA1000302//Homo sapiens KIAA0432 mRNA, complete cds//1.0:50:84//Hs.155174:AB007892
 R-MAMMA1000307//Human mRNA for KIAA0033 gene, partial cds//1.8e-48:468:76//Hs.22271:D26067
 R-MAMMA1000309//ESTs//1.7e-94:491:94//Hs.135106:AI335251
 R-MAMMA1000312//ESTs//8.9e-74:377:96//Hs.133163:AI051434
 R-MAMMA1000313//EST//8.3e-19:294:62//Hs.127400:AA954491
 R-MAMMA1000331//ESTs, Moderately similar to envelope protein [H.sapiens]//8.6e-54:278:97//Hs.139170:AA662998
 R-MAMMA1000339//EST//6.8e-44:169:89//Hs.149580:AI281881
 R-MAMMA1000340//Homo sapiens mRNA for KIAA0625 protein, partial cds//0.82:204:61//Hs.154919:AB014525

- R-MAMMA1000348//ESTs//3.3e-34:320:75//Hs.139158:AA226159
 R-MAMMA1000356//ESTs, Highly similar to URIDYLATE KINASE [Saccharomyces cerevisiae]//0.42:172:61//Hs.11463:AA535912
- 5 R-MAMMA1000360//Human mRNA for KIAA0118 gene, partial cds//3.8e-43:212:82//Hs.154326:D42087
 R-MAMMA1000361//ESTs//3.1e-17:188:68//Hs.164036:AA845659
 R-MAMMA1000372//ESTs//1.0e-46:307:85//Hs.145032:AA343523
 R-MAMMA1000385//ESTs//8.2e-97:467:98//Hs.152282:AA412065
 R-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//8.6e-14:106:92//Hs.32170:AB015132
- 10 R-MAMMA1000395//ESTs//1.9e-57:292:96//Hs.11365:AB01060
 R-MAMMA1000402//ESTs, Moderately similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//9.1e-47:316:81//Hs.138698:N38973
 R-MAMMA1000410//Archain//1.8e-40:443:74//Hs.33642:X81198
 R-MAMMA1000413//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.3e-27:304:72//Hs.119387:AB007958
- 15 R-MAMMA1000414//ESTs//2.9e-27:181:87//Hs.141254:AI334099
 R-MAMMA1000416//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//1.5e-58:282:82//Hs.97203:U83171
 R-MAMMA1000421//Thromboxane A2 receptor//4.9e-48:372:80//Hs.89687:D38061
- 20 R-MAMMA1000422//ESTs//0.077:240:62//Hs.123136:AA631067
 R-MAMMA1000423//Human mRNA for KIAA0392 gene, partial cds//1.3e-48:375:81//Hs.40100:AB002390
 R-MAMMA1000424//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.4e-44:418:75//Hs.154069:U06452
 R-MAMMA1000429//ESTs//3.9e-113:565:96//Hs.5076:N53461
- 25 R-MAMMA1000431//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//8.6e-68:302:85//Hs.97203:U83171
 R-MAMMA1000444//Calcium modulating ligand//5.5e-44:344:81//Hs.13572:AF068179
 R-MAMMA1000446//ESTs//1.0:236:60//Hs.126958:AI147447
 R-MAMMA1000458
- 30 R-MAMMA1000468//ESTs//4.4e-51:271:96//Hs.6839:AA055176
 R-MAMMA1000472//ESTs//5.4e-39:146:86//Hs.141581:AA315361
 R-MAMMA1000478//ESTs//2.3e-74:365:98//Hs.140591:AA828959
 R-MAMMA1000483//ESTs//9.9e-23:235:75//Hs.163592:AA280886
 R-MAMMA1000490//EST//2.1e-80:500:87//Hs.142137:AA213759
- 35 R-MAMMA1000500//Small inducible cytokine A5 (RANTES)/4.7e-43:283:86//Hs.155464:AF088219
 R-MAMMA1000501//ESTs//4.2e-37:250:86//Hs.141323:N80390
 R-MAMMA1000516//Human mRNA for KIAA0392 gene, partial cds//5.1e-46:459:75//Hs.40100:AB002390
 R-MAMMA1000522//ESTs//9.5e-16:226:70//Hs.116673:AA669267
 R-MAMMA1000559//ESTs//5.2e-34:244:84//Hs.150727:AI292236
- 40 R-MAMMA1000565//EST//2.7e-38:386:76//Hs.162404:AA573131
 R-MAMMA1000567//EST//0.33:49:79//Hs.147754:AI220561
 R-MAMMA1000576//ESTs//4.9e-57:348:89//Hs.108921:N31211
 R-MAMMA1000583//Homo sapiens KIAA0412 mRNA, partial cds//1.3e-52:373:77//Hs.6200:AB007872
 R-MAMMA1000585//ESTs//5.1e-40:337:78//Hs.130815:AA936548
- 45 R-MAMMA1000594//Small inducible cytokine A5 (RANTES)/3.0e-45:225:80//Hs.155464:AF088219
 R-MAMMA1000597//ESTs//2.0e-98:461:99//Hs.43212:AA993042
 R-MAMMA1000605//CD4 receptor (exons 1 and 2) [human, T-lymphocyte, mRNA, 3429 nt]//1.5e-50:500:73//Hs.116007:S79267
 R-MAMMA1000612//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.6e-108:559:94//Hs.29203:AI344105
- 50 R-MAMMA1000616//EST//0.071:169:60//Hs.144096:AI032180
 R-MAMMA1000621//ESTs//1.0e-90:477:94//Hs.26073:R96361
 R-MAMMA1000623
 R-MAMMA1000625//ESTs//3.4e-98:556:91//Hs.119482:AI361002
- 55 R-MAMMA1000643//EST//4.9e-74:379:96//Hs.137447:AA342203
 R-MAMMA1000664//Homo sapiens mRNA for putative lipolic acid synthetase, partial//3.2e-43:400:76//Hs.53531:AJ224162
 R-MAMMA1000669//EST//6.9e-53:368:84//Hs.149580:AI281881

- R-MAMMA1000670//ESTs, Highly similar to HYPOTHETICAL PROTEIN IN TONB 3'REGION [Klebsiella pneumoniae]/J.8.4e-98:464:98//Hs.31431:AI022065
- R-MAMMA1000672//ESTs/J.2.0e-80:382:99//Hs.106747:AI080476
- R-MAMMA1000684//ESTs/J.6.2e-72:357:98//Hs.67896:AA865212
- 5 R-MAMMA1000696//Human mRNA for KIAA0345 gene, complete cds/J.3.5e-52:216:75//Hs.98938:AB002343
- R-MAMMA1000707//EST/J.7.0e-11:195:68//Hs.147002:AI184644
- R-MAMMA1000713//Homo sapiens DEC-205 mRNA, complete cds/J.1.5e-45:485:74//Hs.153563:AF011333
- R-MAMMA1000714//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]/J.1.2e-29:158:79//Hs.142764:AA205569
- 10 R-MAMMA1000718//ESTs/J.3.1e-45:264:88//Hs.152413:AA780515
- R-MAMMA1000720//ESTs/J.7.4e-44:244:87//Hs.111742:R39329
- R-MAMMA1000723//Homo sapiens mRNA for alpha(L2)fucosyltransferase, complete cds/J.5.6e-52:350:82//Hs.46328:D87942
- R-MAMMA1000731//ESTs/J.1.1e-19:420:66//Hs.35036:H95267
- 15 R-MAMMA1000732//EST/J.2.9e-20:229:74//Hs.135400:AI056893
- R-MAMMA1000733//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]/J.1.2e-35:371:74//Hs.141429:AA631915
- R-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds/J.2.1e-58:253:98//Hs.31575:AF100141
- R-MAMMA1000738//ESTs, Weakly similar to similar to Achlya ambisexualis antheridial steroid receptor [C.elegans]/J.2.3e-116:557:98//Hs.71472:AA632288
- 20 R-MAMMA1000744//ESTs/J.0.015:143:67//Hs.135382:AI224205
- R-MAMMA1000746//Human Line-1 repeat mRNA with 2 open reading frames/J.2.3e-90:568:86//Hs.23094:M19503
- R-MAMMA1000752//Interleukin 10/J.2.8e-43:339:80//Hs.2180:M57627
- R-MAMMA1000760//EST/J.5.0e-44:306:86//Hs.162404:AA573131
- 25 R-MAMMA1000761//EST/J.5.0e-41:187:85//Hs.162335:AA564256
- R-MAMMA1000775//Human mRNA for KIAA0355 gene, complete cds/J.3.0e-46:465:76//Hs.153014:AB002353
- R-MAMMA1000776//ESTs/J.1.9e-43:429:73//Hs.141742:W22204
- R-MAMMA1000778//ESTs/J.1.8e-31:445:70//Hs.111723:H57439
- R-MAMMA1000782//EST/J.0.0019:102:68//Hs.120686:AA747150
- 30 R-MAMMA1000798//ESTs/J.1.4e-13:267:69//Hs.140156:AA704163
- R-MAMMA1000802//Clathrin, light polypeptide (Lcb)/J.1.5e-45:358:76//Hs.73919:X81637
- R-MAMMA1000831//ESTs/J.1.3e-1,04:510:97//Hs.17494:AA572675
- R-MAMMA1000839//EST/J.2.9e-51:307:89//Hs.149580:AI281881
- R-MAMMA1000841//ESTs/J.1.3e-34:412:72//Hs.121256:AA757902
- 35 R-MAMMA1000842//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/J.9.4e-44:363:79//Hs.96337:AA225358
- R-MAMMA1000843//ESTs/J.2.2e-106:525:97//Hs.152016:AA603097
- R-MAMMA1000845//ESTs/J.1.6e-66:327:98//Hs.156900:AA468955
- R-MAMMA1000851//ESTs/J.3.7e-14:115:86//Hs.140590:R76251
- 40 R-MAMMA1000855//Human mRNA for KIAA0392 gene, partial cds/J.5.7e-47:281:91//Hs.40100:AB002390
- R-MAMMA1000856//EST/J.1.8e-16:150:79//Hs.136811:AA789212
- R-MAMMA1000862//EST/J.3.2e-05:93:73//Hs.161205:AI419311
- R-MAMMA1000863//ESTs/J.1.0e-46:446:73//Hs.153432:AA098922
- R-MAMMA1000865//Homo sapiens clone 23632 mRNA sequence/J.3.0e-39:324:80//Hs.46918:AF052099
- 45 R-MAMMA1000870//ESTs/J.9.8e-16:193:76//Hs.152340:AA521399
- R-MAMMA1000875//EST/J.3.1e-24:301:72//Hs.132635:AI032875
- R-MAMMA1000876//ESTs/J.9.9e-48:246:97//Hs.112165:AA621243
- R-MAMMA1000877//ESTs/J.1.4e-38:324:79//Hs.141024:H07128
- 50 R-MAMMA1000880//Homo sapiens mRNA for KIAA0594 protein, partial cds/J.3.2e-40:542:68//Hs.154872:AB011166
- R-MAMMA1000883//ESTs/J.1.0:207:60//Hs.47199:N51107
- R-MAMMA1000897//ESTs/J.2.6e-78:383:97//Hs.41067:AI310215
- R-MAMMA1000905//Human mRNA for KIAA0331 gene, complete cds/J.9.7e-53:307:91//Hs.146395:AB002329
- R-MAMMA1000906//ESTs/J.8.0e-25:206:83//Hs.141825:AA017093
- 55 R-MAMMA1000908//ESTs/J.4.4e-32:176:96//Hs.38559:AA701634
- R-MAMMA1000914//ESTs/J.0.032:150:63//Hs.119162:AA399989
- R-MAMMA1000921//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds/J.7.7e-38:269:74//Hs.108966:U48696

- R-MAMMA1000931//ESTs//1.2e-80:457:91//Hs.122319:AA782335
 R-MAMMA1000940//ESTs//3.3e-43:329:82//Hs.35254:AI133727
 R-MAMMA1000941//ESTs//7.5e-55:306:84//Hs.163936:AA632281
 R-MAMMA1000942//ESTs//2.5e-83:405:98//Hs.116491:AA650428
 5 R-MAMMA1000943//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//9.3e-79:567:80//Hs.1361:M55053
 R-MAMMA1000958//EST//5.7e-53:256:100//Hs.162209:AA536178
 R-MAMMA1000957//Kangal 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody I44))//7.5e-49:340:85//Hs.103458:X53795
 10 R-MAMMA1000962//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.0e-48:216:85//Hs.153468:AB011147
 R-MAMMA1000968//EST//6.2e-46:302:86//Hs.149580:AI281881
 R-MAMMA1000975//ESTs//1.4e-85:428:96//Hs.141742:W22204
 R-MAMMA1000979//Homo sapiens mRNA for KIAA0761 protein, partial cds//8.0e-39:338:79//Hs.93121:AB018304
 15 R-MAMMA1000987//EST//2.8e-41:249:90//Hs.149580:AI281881
 R-MAMMA1000998//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//3.9e-50:445:77//Hs.77579:AF013263
 R-MAMMA1001003//Slalophorin (gpL115, leukosialin, CD43)//4.1e-51:282:82//Hs.80738:X52075
 20 R-MAMMA1001008//ESTs, Weakly similar to renin [H.sapiens]//1.9e-82:405:97//Hs.25863:AA630313
 R-MAMMA1001021//Homo sapiens DEC-205 mRNA, complete cds//3.0e-44:309:86//Hs.153563:AF011333
 R-MAMMA1001024//ESTs//6.8e-35:333:78//Hs.107657:AA126814
 R-MAMMA1001030//ESTs//1.6e-110:552:96//Hs.59483:AA524536
 R-MAMMA1001035//ESTs//1.0e-45:273:85//Hs.138856:HA7461
 25 R-MAMMA1001038//Human mRNA for KIAA0392 gene, partial cds//3.0e-50:298:91//Hs.40100:AB002390
 R-nnnnnnnnnnn//ESTs//3.6e-86:445:95//Hs.122625:R68650
 R-MAMMA1001050//EST//2.2e-54:387:85//Hs.149580:AI281881
 R-MAMMA1001059//ESTs, Moderately similar to RNA helicase [M.musculus]//1.7e-13:273:65//Hs.98738:AI015487
 30 R-MAMMA1001067//ESTs//1.3e-38:324:78//Hs.20190:AA525532
 R-MAMMA1001073//ESTs//5.2e-106:554:94//Hs.12336:W63748
 R-MAMMA1001074//Human mRNA for KIAA0355 gene, complete cds//1.2e-38:544:68//Hs.153014:AB002353
 R-MAMMA1001075//ESTs//2.0e-98:463:99//Hs.18341:N38944
 R-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-84:556:85//Hs.23094:M19503
 35 R-MAMMA1001082//ESTs//2.4e-71:356:97//Hs.152302:T90222
 R-MAMMA1001091//ESTs//4.7e-83:429:95//Hs.154412:AA310926
 R-MAMMA1001092//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//6.4e-34:262:82//Hs.129727:AF035587
 R-MAMMA1001105//Human putative RNA binding protein RNPL mRNA, complete cds//4.2e-27:232:76//Hs.61840:U28686
 40 R-MAMMA1001110//ESTs//1.6e-17:128:87//Hs.161314:AI421576
 R-MAMMA1001126//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//8.8e-53:462:78//Hs.116007:S79267
 R-MAMMA1001133//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.8e-59:460:81//Hs.5247:AF029750
 45 R-MAMMA1001139//ESTs//1.3e-62:341:94//Hs.18819:R01029
 R-MAMMA1001143//ESTs//3.0e-48:383:80//Hs.152340:AA521399
 R-MAMMA1001145//Calcium modulating ligand//5.1e-48:403:79//Hs.13572:AF068179
 R-MAMMA1001154//EST//6.8e-35:313:75//Hs.162404:AA573131
 R-MAMMA1001161//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.1e-58:409:84//Hs.5247:AF029750
 50 R-MAMMA1001162//ESTs, Highly similar to t-BOP [M.musculus]//2.1e-91:430:99//Hs.129982:AI420970
 R-MAMMA1001181//ESTs//5.0e-112:557:96//Hs.118181:W02251
 R-MAMMA1001186//ESTs//3.8e-85:410:99//Hs.163811:W44959
 R-MAMMA1001191//ESTs//0.018:57:87//Hs.141253:AA226519
 55 R-MAMMA1001198//ESTs, Weakly similar to involved in signaling by the epidermal growth factor receptor [M.musculus]//2.6e-80:358:96//Hs.163827:AA074202
 R-MAMMA1001202//ESTs//7.0e-43:230:95//Hs.79788:AA527348
 R-MAMMA1001203//Clathrin, light polypeptide (Lcb)//2.8e-65:348:79//Hs.73919:X81637
 R-MAMMA1001206//EST//0.098:84:72//Hs.162941:AA635148

- R-MAMMA1001215//ESTs//1.3e-43:156:86//Hs.155243:N70293
 R-MAMMA1001220//ESTs//8.9e-17:276:68//Hs.116518:AA653202
 R-MAMMA1001222//ESTs//0.49:112:66//Hs.24668:AA897315
 R-MAMMA1001243//EST//0.99:143:62//Hs.68522:C20701
 5 R-MAMMA1001244//ESTs//2.2e-06:79:83//Hs.123163:AA809619
 R-MAMMA1001249//ESTs//4.2e-68:343:97//Hs.147139:AI191307
 R-MAMMA1001256//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.7e-31:221:77//Hs.142764:AA205569
 R-MAMMA1001259//ESTs//1.3e-43:266:90//Hs.6193:AA045149
 10 R-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.0e-21:226:75//Hs.65238:AB014561
 R-MAMMA1001268//H.sapiens HCG II mRNA//2.4e-53:181:85//Hs.146333:X81001
 R-MAMMA1001271//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK [Mus musculus]//1.1e-108:546:95//Hs.18999:N30643
 15 R-MAMMA1001260//Homo sapiens mRNA for KIAA0572 protein, partial cds//4.4e-32:188:94//Hs.14409:AB011144
 R-MAMMA1001280//EST//0.0015:170:62//Hs.116770:AA630371
 R-MAMMA1001292//ESTs//5.6e-102:481:99//Hs.94810:AA811876
 R-MAMMA1001296//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.2e-27:348:70//Hs.15731:AB011135
 20 R-MAMMA1001298//ESTs//1.4e-44:375:79//Hs.70279:AA757426
 R-MAMMA1001305//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.0e-43:300:85//Hs.46468:U45984
 R-MAMMA1001322//Homo sapiens stress-activated protein kinase 4 mRNA, complete cds//8.8e-12:188:70//Hs.55771:AF004709
 25 R-MAMMA1001324//ESTs//5.3e-68:297:88//Hs.121228:AA709471
 R-MAMMA1001330//ESTs//1.6e-57:429:83//Hs.70279:AA757426
 R-MAMMA1001341//Homo sapiens 4F5S mRNA, complete cds//4.8e-27:285:75//Hs.32567:AF073519
 R-MAMMA1001343//ESTs//8.1e-51:273:93//Hs.162208:AA536127
 30 R-MAMMA1001346//ESTs//1.0:122:65//Hs.33028:AA482478
 R-MAMMA1001383//ESTs//1.4e-45:377:80//Hs.114671:N39322
 R-MAMMA1001388//EST//7.7e-47:361:80//Hs.162197:AA535216
 R-MAMMA1001397//EST//8.7e-48:337:83//Hs.149580:AI281881
 R-MAMMA1001408//EST//1.2e-38:251:87//Hs.162677:AA604831
 35 R-MAMMA1001411//ESTs//4.3e-93:435:99//Hs.105460:AA780275
 R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, complete cds//1.6e-19:117:96//Hs.19122:AF038957
 R-MAMMA1001420//ESTs//7.3e-96:507:95//Hs.55299:AI335267
 R-MAMMA1001435//ESTs//5.0e-97:459:99//Hs.144843:AI222168
 40 R-MAMMA1001442//ESTs//7.1e-28:167:83//Hs.141019:AA287618
 R-MAMMA1001446//Homo sapiens KIAA0432 mRNA, complete cds//6.2e-19:328:67//Hs.155174:AB007892
 R-MAMMA1001452//EST//5.6e-44:487:75//Hs.161476:N57542
 R-MAMMA1001465
 R-MAMMA1001476//Homo sapiens yeast sac permease-like molecule 3 (YSLP3) mRNA, complete cds//0.79:182:66//Hs.136529:AF058317
 45 R-MAMMA1001487//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-35:328:78//Hs.43681:AL022394
 R-MAMMA1001501//ESTs//4.6e-100:472:98//Hs.123660:AA813065
 R-MAMMA1001502//Human mRNA for KIAA0080 gene, partial cds//5.6e-15:220:69//Hs.74554:D38522
 R-MAMMA1001510
 50 R-MAMMA1001522//ESTs//3.2e-16:214:75//Hs.152816:AA634242
 R-MAMMA1001547//H.sapiens mRNA for urea transporter//2.3e-45:282:89//Hs.66710:X96969
 R-MAMMA1001551//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.9e-56:489:76//Hs.108966:U48696
 R-MAMMA1001575//ESTs//4.3e-92:440:98//Hs.162882:AA807140
 55 R-MAMMA1001576//ESTs, Highly similar to TUBULIN GAMMA CHAIN [Homo sapiens]//1.9e-111:549:96//Hs.21635:AI417305
 R-MAMMA1001590//ESTs//1.1e-63:324:96//Hs.142217:AA278441
 R-MAMMA1001600//ESTs//5.6e-15:159:78//Hs.138633:H98792

- R-MAMMA1001604
R-MAMMA1001606//ESTs, Weakly similar to finger protein kox1 [H.sapiens]/1.9e-97:488:96//Hs.143263:AI057616
- 5 R-MAMMA1001620//Homo sapiens mRNA, clone:RES4-16//5.4e-43:408:76//Hs.121493:D25272
R-MAMMA1001627//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.0e-49:472:76//Hs.15519:AB018315
R-MAMMA1001630//ESTs, Weakly similar to putative p150 [H.sapiens]/6.8e-15:168:73//Hs.115216:AA291074
R-MAMMA1001633//EST//5.1e-14:228:68//Hs.141456:N36377
R-MAMMA1001635//ESTs//3.4e-37:368:75//Hs.164033:AA769606
- 10 R-MAMMA1001649
R-MAMMA1001663//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.7e-54:272:81//Hs.129735:AF010144
R-MAMMA1001670//Small inducible cytokine A5 (RANTES)/5.7e-50:304:89//Hs.155464:AF088219
R-MAMMA1001671//EST//1.9e-14:312:65//Hs.137153:R46248
- 15 R-MAMMA1001679//H.sapiens mRNA for rho GDP-dissociation Inhibitor 1//0.066:196:62//Hs.159161:X69550
R-MAMMA1001683//ESTs//4.9e-94:447:98//Hs.134464:AI151081
R-MAMMA1001686//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-17:246:73//Hs.67619:AB007957
- 20 R-MAMMA1001692//Human mRNA for KIAA0063 gene, complete cds//2.1e-47:294:89//Hs.3094:D31884
R-MAMMA1001711//ESTs//2.4e-86:439:96//Hs.18498:N52088
R-MAMMA1001715//ESTs//1.2e-73:399:9311Hs.124620:AI082338
R-MAMMA1001730//ESTs//1.1e-85:403:99//Hs.125464:AI084596
R-MAMMA1001735//ESTs, Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]/3.7e-110:552:96//Hs.6923:AI161158
- 25 R-MAMMA1001740//ESTs//4.6e-45:342:82//Hs.37573:H59651
R-MAMMA1001743//EST//2.7e-58:412:85//Hs.149742:AI285666
R-MAMMA1001744
R-MAMMA1001745//EST//5.6e-54:374:84//Hs.137041:AA877817
R-MAMMA1001751//EST//3.5e-36:375:73//Hs.139715:N25041
- 30 R-MAMMA1001754//EST//0.18:144:66//Hs.71957:AA151413
R-MAMMA1001757//ESTs//1.0e-9:8:488:96//Hs.45184:C14904
R-MAMMA1001760//ESTs//8.7e-29:206:86//Hs.143310:AI142276
R-MAMMA1001764//ESTs//0.00012:434:58//Hs.120051:AA707847
R-MAMMA1001768//Human mRNA for KIAA0327 protein, complete cds//2.3e-41:299:85//Hs.149323:AB002325
- 35 R-MAMMA1001769//EST//1.7e-15:139:81//Hs.162399:AA572825
R-MAMMA1001771//ESTs, Moderately similar to semaphorin B [M.musculus]/7.6e-43:257:91//Hs.7634:AA481246
R-MAMMA1001783//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.6e-42:272:86//Hs.73614:U83460
- 40 R-MAMMA1001785//ESTs//1.5e-87:431:98//Hs.131065:AA972238
R-MAMMA1001788//EST//0.95:108:62//Hs.145881:AI274644
R-MAMMA1001790//ESTs//4.0e-41:340:80//Hs.158045:AA425744
R-MAMMA1001806//EST//1.4e-40:297:84//Hs.141240:H60313
R-MAMMA1001812//ESTs//2.4e-93:446:98//Hs.129034:AA776892
- 45 R-MAMMA1001815//EST//0.00053:371:59//Hs.133255:AI052659
R-MAMMA1001817//Human mRNA for KIAA0226 gene, complete cds//2.1e-46:325:87//Hs.44106:D86979
R-MAMMA1001818
R-MAMMA1001820//EST//1.9e-49:303:89//Hs.149580:AI281881
R-MAMMA1001824//Homo sapiens 4F5S mRNA, complete cds//4.3e-48:438:75//Hs.32567:AF073519
- 50 R-MAMMA1001836//ESTs//3.8e-06:128:71//Hs.143611:M78140
R-MAMMA1001837//Homo sapiens KIAA0395 mRNA, partial cds//3.8e-47:339:83//Hs.43681:AL022394
R-MAMMA1001848//ESTs//2.1e-16:125:85//Hs.161662:AA836811
R-MAMMA1001851//ESTs//4.5e-48:344:84//Hs.138856:H47461
R-MAMMA1001854//Small inducible cytokine A5 (RANTES)/2.6e-38:280:83//Hs.155464:AF088219
- 55 R-MAMMA1001858//ESTs//1.1e-44:331:83//Hs.44702:AI148840
R-MAMMA1001864//Homo sapiens mRNA for KIAA0475 protein, complete cds//7.8e-31:262:77//Hs.5737:AB007944
R-nnnnnnnnnnn//Homo sapiens antigen NY-CO-16 mRNA, complete cds//9.2e-06:450:58//Hs.132206:

- R-MAMMA1002230//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIP5K) mRNA, complete cds//9.1e-50.330.77//Hs.108966:U48696
R-MAMMA1002236
R-MAMMA1002243
- 5 R-MAMMA1002250//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.2e-44:299.87//Hs.113283:AF018080
R-MAMMA1002267//Homo sapiens mRNA, chromosome 1 specific transcript
KIAA0487//1.6e-54:207.81//Hs.92381:AB007956
R-MAMMA1002268//ESTs//2.9e-94:439.100//Hs.68061:AI042283
R-MAMMA1002269//ESTs//7.4e-05:170.65//Hs.140466:AA766772
- 10 R-MAMMA1002282//ESTs//7.8e-09:69.78//Hs.159502:AA225141
R-MAMMA1002292//ESTs//5.3e-64:334.94//Hs.113606:AI138751
R-MAMMA1002293//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//1.7e-39:203.81//Hs.154257:AI275982
R-MAMMA1002294//EST//8.1e-43:326.82//Hs.149580:AI281881
R-MAMMA1002297//ESTs//6.5e-45:323.63//Hs.155475:AA761454
R-MAMMA1002298//ESTs//1.7e-68:355.96//Hs.52683:H87153
R-MAMMA1002299//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//2.3e-58:346.91//Hs.140385:AA773359
R-MAMMA1002308
- 20 R-MAMMA1002310//Human melanoma antigen recognized by T-cells (MART-1) mRNA//2.2e-44:280.87//Hs.154069:U06452
R-MAMMA1002311//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-70:503.81//Hs.23094:M19503
R-MAMMA1002312//EST//1.7e-31:144.80//Hs.135936:N36094
R-MAMMA1002317//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)/4.3e-49:457.76//Hs.144563:AF057280
- 25 R-MAMMA1002319//ESTs//3.9e-38:297.70//Hs.140326:AA827183
R-MAMMA1002322//ESTs//1.1e-46:301.86//Hs.155498:W27084
R-MAMMA1002329//EST//2.6e-09:146.72//Hs.132366:AI026658
R-MAMMA1002332//Homo sapiens clone 23892 mRNA sequence//2.6e-45:387.70//Hs.91916:AF035317
R-MAMMA1002333//EST//1.8e-09:139.74//Hs.137800:AA868897
- 30 R-MAMMA1002339//ESTs//4.2e-47:310.76//Hs.138865:W57618
R-MAMMA1002347//ESTs//1.5e-44:326.83//Hs.111723:H57439
R-MAMMA1002351//ESTs//3.0e-112:545.97//Hs.26209:AI143127
R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2//1.5e-58:259.92//Hs.43628:Y15228
R-MAMMA1002353//Human mRNA for KIAA0392 gene, partial cds//4.5e-40:360.77//Hs.40100:AB002390
R-MAMMA1002355//ESTs//1.4e-29:307.75//Hs.3769:AI085367
R-MAMMA1002356//Clathrin, light polypeptide (Lcb)/4.9e-31:217.88//Hs.73919:X81637
R-MAMMA1002359//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-70:483.84//Hs.113283:AF018080
R-MAMMA1002360//ESTs//3.5e-19:301.69//Hs.124701:AA701475
- 40 R-MAMMA1002361//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//2.6e-30:244.81//Hs.129727:AF035587
R-MAMMA1002362//ESTs//2.3e-43:241.88//Hs.150727:AI292236
R-MAMMA1002380//ESTs//5.1e-36:322.79//Hs.136994:AA843542
R-MAMMA1002384//Small inducible cytokine A5 (RANTES)/1.8e-42:298.84//Hs.155464:AF088219
R-MAMMA1002385//ESTs//0.57:203.63//Hs.146303:AA579061
R-MAMMA1002392//Human mRNA for platelet-activating factor acetylhydrolase 2, complete cds//5.8e-41:305.83//Hs.86188:D87845
R-MAMMA1002411//ESTs//4.4e-68:385.92//Hs.53478:N92294
R-MAMMA1002413//Homo sapiens mRNA for small GTP-binding protein, complete cds//3.3e-14:138.75//Hs.115325:D84488
- 50 R-MAMMA1002417//ESTs//1.6e-98:475.98//Hs.96345:N22588
R-MAMMA1002427//ESTs//3.1e-39:274.79//Hs.141130:H28477
R-MAMMA1002428//ESTs//8.4e-11:215.66//Hs.141022:H06475
R-MAMMA1002434//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//2.5e-106:521.98//Hs.112152:AA487348
R-MAMMA1002446//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//4.7e-37:374.68//Hs.157142:U85996
R-MAMMA1002454//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0485//2.0e-60:323.81//Hs.

- 89121:AB007954
 R-MAMMA1002461//ESTs//4.7e-111:548:97//Hs.104281:AA147076
 R-MAMMA1002470//ESTs, Highly similar to HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION [Saccharomyces cerevisiae]/8.5e-104:544:93//Hs.94570:AI192106
- 5 R-MAMMA1002475//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/3.4e-31:263:79//Hs.38687:AA744496
 R-MAMMA1002480//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/1.0e-34:159:79//Hs.133526:N21103
- 10 R-MAMMA1002485//Homo sapiens stannocalcin-2 (STC-2) mRNA, complete cds//8.9e-116:560:97//Hs.155223:AF055460
 R-MAMMA1002494//ESTs//3.2e-47:303:88//Hs.155243:N70293
 R-MAMMA1002498//Human novel homeobox mRNA for a DNA binding protein//0.0043:331:58//Hs.37035:U07664
- 15 R-MAMMA1002524//ESTs//0.0039:354:61//Hs.125797:AA806277
 R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//3.9e-103:529:95//Hs.18858:AF065214
 R-MAMMA1002545//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.5e-50:317:88//Hs.153468:AB011147
- 20 R-MAMMA1002554//ESTs//2.3e-85:445:95//Hs.139140:AA218851
 R-MAMMA1002556//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/1.0e-12:280:65//Hs.12725:T65058
 R-MAMMA1002566//ESTs//2.3e-88:421:99//Hs.17602:AA705681
 R-MAMMA1002571//ESTs//5.1e-97:456:99//Hs.152834:AA595693
 R-MAMMA1002573//ESTs//3.1e-38:258:87//Hs.163989:R74433
- 25 R-MAMMA1002585//ESTs//7.8e-96:533:91//Hs.26009:H49371
 R-MAMMA1002590//ESTs//0.61:202:62//Hs.161190:AI419258
 R-MAMMA1002597//Cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6//2.9e-21:177:75//Hs.1360:M29874
 R-MAMMA1002598//ESTs//3.4e-113:544:97//Hs.20263:AA573737
- 30 R-MAMMA1002603//Thiopurine S-methyltransferase//7.6e-35:225:80//Hs.51124:AF019369
 R-MAMMA1002612//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//4.2e-46:424:75//Hs.1361:M55053
 R-MAMMA1002617//ESTs//1.1e-38:229:92//Hs.96987:W27389
- 35 R-MAMMA1002618//Landsteiner-Wiener blood group glycoprotein//1.3e-27:185:73//Hs.108287:L27670
 R-MAMMA1002619//ESTs//1.7e-95:480:96//Hs.54873:AA526306
 R-MAMMA1002622//Thromboxane A2 receptor//3.2e-46:298:87//Hs.89887:D38081
 R-MAMMA1002623//EST//4.3e-49:336:85//Hs.149580:AI281881
 R-MAMMA1002625//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]/2.3e-35:308:79//Hs.93332:AA811920
- 40 R-MAMMA1002629//Homo sapiens mRNA for small GTP-binding protein, complete cds//9.7e-57:283:86//Hs.115325:D84488
 R-MAMMA1002636//Human mRNA for KIAA0392 gene, partial cds//1.2e-49:303:89//Hs.40100:AB002390
 R-MAMMA1002637//ESTs//1.3e-55:391:85//Hs.95074:AI144421
 R-MAMMA1002646//ESTs//7.4e-36:182:80//Hs.163937:N69915
 R-MAMMA1002650//ESTs//1.6e-102:547:94//Hs.57841:W63776
 R-MAMMA1002655
- 45 R-MAMMA1002662//Homo sapiens KIAA0426 mRNA, complete cds//2.2e-46:462:75//Hs.97476:AB007886
 R-MAMMA1002665//Human mRNA for KIAA0118 gene, partial cds//9.1e-51:376:82//Hs.154326:D42087
 R-MAMMA1002671//ESTs, Weakly similar to coded for by C. elegans cDNA yk52e10.5 [C.elegans]/5.3e-108:544:96//Hs.16464:W19606
- 50 R-MAMMA1002673//EST//3.3e-35:169:79//Hs.140046:AA668213
 R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//4.6e-109:544:96//Hs.3363:D86987
 R-MAMMA1002685//EST//1.9e-31:223:86//Hs.112540:AA601385
 R-MAMMA1002698//ESTs//5.9e-43:292:85//Hs.144660:AA652675
- 55 R-MAMMA1002699//ESTs//3.2e-25:134:100//Hs.126049:F22510
 R-MAMMA1002701//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/6.9e-70:353:96//Hs.138404:R70986

- R-MAMMA1002708//ESTs//2.1e-76:413.94//Hs.57932:W69234
 R-MAMMA1002711//ESTs//1.9e-44:236.96//Hs.138575:H67858
 R-MAMMA1002721//Homo sapiens DEC-205 mRNA, complete cds//2.7e-43:273.89//Hs.153563:AF011333
 R-MAMMA1002727//ESTs//2.9e-84:395:100.11Hs.162826:AA679571
 5 R-MAMMA1002728//Small inducible cytokine A5 (RANTES)/3.4e-42:266.88//Hs.155464:AF088219
 R-MAMMA1002744//ESTs//4.2e-18:473.63//Hs.42826:AA846757
 R-MAMMA1002746//ESTs//1.8e-100:473.99//Hs.117558:AA779907
 R-MAMMA1002748//Human melanoma antigen recognized by T-cells (MART-1) mRNA//5.8e-40:330.80//Hs.154069:U06452
 10 R-MAMMA1002754//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-40:369.77//Hs.105292:AA504776
 R-MAMMA1002758
 R-MAMMA1002764//ESTs//4.2e-103:486.99//Hs.159909:AI393281
 R-MAMMA1002765//ESTs//1.6e-37:338.76//Hs.37573:H59651
 15 R-MAMMA1002769//ESTs//0.72:409.57//Hs.141376:AI301272
 R-MAMMA1002780//ESTs//1.6e-52:292.92//Hs.135985:AA342750
 R-MAMMA1002782//ESTs//1.0e-31:157.80//Hs.159510:AA297145
 R-MAMMA1002796//ESTs//3.8e-49:284.92//Hs.156479:AA513812
 R-MAMMA1002807//Archain//1.4e-39:315.80//Hs.33642:X81198
 20 R-MAMMA1002820//ESTs//5.0e-14:192.74//Hs.134635:AA226260
 R-MAMMA1002830//EST//4.0e-50:255.97//Hs.160674:AI248319
 R-MAMMA1002833//EST//1.2e-48:306.88//Hs.149580:AI281881
 R-MAMMA1002835
 R-MAMMA1002838//EST//2.7e-12:161.76//Hs.163252:AA828723
 25 R-MAMMA1002842//ESTs//1.7e-41:366.78//Hs.141899:N22395
 R-MAMMA1002843//Von Hippel-Lindau syndrome//8.8e-38:258.79//Hs.78160:AF010238
 R-MAMMA1002844//ESTs//3.5e-51:250.99//Hs.151445:AA351081
 R-MAMMA1002858//H.sapiens ERF-1 mRNA 3' end//9.0e-101:361.91//Hs.85155:X79067
 R-MAMMA1002868//ESTs//2.1e-38:301.80//Hs.132717:AA171941
 30 R-MAMMA1002871//EST//6.0e-88:413.99//Hs.149057:AI243592
 R-MAMMA1002880//ESTs//6.5e-100:506.96//Hs.163533:N52194
 R-MAMMA1002881//EST//1.1e-40:335.80//Hs.160895:AI365871
 R-MAMMA1002886//Small inducible cytokine A5 (RANTES)/3.4e-36:228.88//Hs.155464:AF088219
 R-MAMMA1002887//ESTs//4.7e-87:409.99//Hs.152155:AA424811
 35 R-MAMMA1002890//ESTs, Weakly similar to coded for by C. elegans cDNA CEESB82F [C.elegans]//4.2e-92:438:99//Hs.155871:AA533783
 R-MAMMA1002892//Homo sapiens EVI5 homolog mRNA, complete cds//4.9e-62:322.80//Hs.26929:AF008915
 R-MAMMA1002895//ESTs//2.7e-32:330.76//Hs.139132:AA211087
 R-MAMMA1002908//Calcium modulating ligand//4.6e-48:313.86//Hs.13572:AF068179
 40 R-MAMMA1002909//Human mRNA for KIAA0180 gene, partial cds//3.4e-09:132.76//Hs.90981:D80002
 R-MAMMA1002930//EST//4.9e-44:260.91//Hs.149580:AI281881
 R-MAMMA1002938
 R-MAMMA1002941//Human Line-1 repeat mRNA with 2 open reading frames//1.1e-83:556.85//Hs.23094:M19503
 R-MAMMA1002947//ESTs//7.0e-22:222.80//Hs.103395:T79243
 45 R-MAMMA1002964//Human mRNA for KIAA0355 gene, complete cds//1.6e-44:427.77//Hs.153014:AB002353
 R-MAMMA1002970//Thromboxane A2 receptor//7.9e-48:300.84//Hs.89887:D38081
 R-MAMMA1002972//ESTs, Weakly similar to KIAA0371 [H.sapiens]//9.6e-104:525.95//Hs.94396:AA399630
 R-MAMMA1002973//ESTs//4.4e-40:257.87//Hs.163580:U15835
 R-MAMMA1002982//ESTs//2.5e-28:115.87//Hs.141694:W15279
 50 R-MAMMA1002987//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//2.1e-41:402.67//Hs.133089:AF064019
 R-MAMMA1003003//Calcium modulating ligand//1.9e-45:380.79//Hs.13572:AF068179
 R-MAMMA1003004//ESTs//3.0e-07:378.60//Hs.61885:AI127857
 R-MAMMA1003007//ESTs//2.0e-47:404.80//Hs.146314:R99617
 55 R-MAMMA1003011//ESTs, Highly similar to HISTONE MACRO-H2A.1 [Rattus norvegicus]//1.4e-53:320.90//Hs.92023:AI022248
 R-MAMMA1003015//ESTs//1.5e-42:363.79//Hs.155184:AA573189
 R-MAMMA1003019//ESTs//4.8e-10:232.66//Hs.111341:AA251268

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- R-NT2RM4000290//ESTs//4.0e-87.435.96//Hs.162592:AA594128
 R-NT2RM4000324//ESTs//2.2e-80.413.96//Hs.12313:R43673
 R-NT2RM4000327//Small inducible cytokine A5 (RANTES)//3.2e-45:286.87//Hs.155464:AF088219
 R-NT2RM4000344//Clathrin, light polypeptide (Lcb)//8.6e-60:452.84//Hs.73919:X81637
 5 R-NT2RM4000349//ESTs, Weakly similar to KIAA0005 [H.sapiens]//2.5e-117:579.96//Hs.5216:AA534881
 R-NT2RM4000354//ESTs//2.1e-85:406.99//Hs.126774:AI224479
 R-NT2RM4000356//ESTs//7.9e-109:548.96//Hs.44278:AA418063
 R-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds//2.8e-113:577.95//Hs.8152:AB014542
 R-NT2RM4000368//ESTs//2.2e-61:310.97//Hs.143611:M78140
 10 R-NT2RM4000386//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//1.0e-93:521.92//Hs.41793:AA775879
 R-NT2RM4000395//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//1.9e-99:524.94//Hs.5249:U55977
 R-NT2RM4000414//EST//2.7e-06:196.64//Hs.136648:AA688285
 15 R-NT2RM4000421//ESTs, Weakly similar to No definition line found [C.elegans]//5.4e-75:470.90//Hs.69235:AA192359
 R-NT2RM4000425//H.sapiens mRNA for MACH-alpha-2 protein//0.17:112.69//Hs.19949:X98173
 R-NT2RM4000433//ESTs//2.7e-100:479.98//Hs.24553:AI150687
 R-NT2RM4000457//ESTs//5.1e-107:535.95//Hs.7579:AA775865
 20 R-NT2RM4000471//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//6.0e-99:492.96//Hs.21090:AA418587
 R-NT2RM4000486//ESTs, Moderately similar to unnamed protein product [H.sapiens]//2.2e-102:493.97//Hs.111279:W84558
 R-NT2RM4000496
 25 R-NT2RM4000511//EST//5.1e-43:326.81//Hs.157658:AI358465
 R-NT2RM4000514//ESTs//1.7e-112:552.96//Hs.6686:AA205496
 R-ntnnnnnnnnnn//ESTs, Weakly similar to HYPOTHETICAL 85.0 KD PROTEIN IN CPA2-ATP2 INTERGENIC REGION [Saccharomyces cerevisiae]//1.4e-60:343.93//Hs.16014:AA074879
 R-NT2RM4000520//ESTs//2.7e-55:266.100//Hs.99838:AA204731
 30 R-NT2RM4000531//ESTs//2.0e-88:502.91//Hs.13110:T67461
 R-NT2RM4000532//ESTs//0.47:290.58//Hs.148753:T91777
 R-NT2RM4000534//EST//0.00025:303.60//Hs.162809:AA632198
 R-NT2RM4000585//EST//0.28:63.77//Hs.150024:AI291981
 R-NT2RM4000590//ESTs//5.8e-65:320.98//Hs.116017:AA613437
 35 R-NT2RM4000595//Homo sapiens KIAA0431 mRNA, partial cds//0.99:189.64//Hs.16349:AB007891
 R-NT2RM4000603//ESTs//4.6e-68:356.96//Hs.48855:AA134589
 R-ntnnnnnnnnnn//ESTs//1.5e-89:431.97//Hs.26117:W16697
 R-NT2RM4000616//ESTs, Highly similar to ACETYL-COENZYME A SYNTHETASE [Escherichia coli]//1.4e-102:519.96//Hs.14779:N64822
 40 R-NT2RM4000674//ESTs//5.1e-78:398.97//Hs.8268:N70144
 R-NT2RM4000689//ESTs, Weakly similar to T01G9.4 [C.elegans]//2.9e-115:550.98//Hs.11820:AA205531
 R-NT2RM4000698//ESTs//2.0e-17:130.87//Hs.86420:AA927510
 R-ntnnnnnnnnnn
 R-NT2RM4000712//EST//0.99:103.65//Hs.114039:AA701128
 45 R-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//2.2e-103:519.95//Hs.6823:W18181
 R-NT2RM4000733//ESTs//8.7e-88:429.98//Hs.72185:AA465311
 R-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//3.6e-105:536.95//Hs.137168:AB018303
 50 R-NT2RM4000741//ESTs//0.99:266.58//Hs.142718:AA034046
 R-NT2RM4000751//ESTs//1.6e-20:351.66//Hs.43145:AA776988
 R-NT2RM4000764
 R-NT2RM4000778//EST//0.066:254.61//Hs.148232:AA904174
 R-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//9.3e-106:546.94//Hs.18586:AB007920
 55 R-NT2RM4000787//Human melanoma antigen recognized by T-cells (MART-1) mRNA//6.5e-40:424.73//Hs.154069:U06452
 R-NT2RM4000790//EST//9.0e-48:259.94//Hs.156964:AA17008

R-NT2RM4000795//Human mRNA for KIAA0067 gene, complete cds//1.0:203:63//Hs.20991:D31891
R-NT2RM4000796//ESTs//7.0e-106:506:98//Hs.43559:AI003520
R-NT2RM4000798//Human polymorphic epithelial mucin core protein mRNA, 3' end//2.5e-28:158:96//Hs.118249:M21868
5 R-NT2RM4000813
R-NT2RM4000820//ESTs, Weakly similar to hypothetical protein [H.sapiens]//1.3e-109:539:97//Hs.99636:AI219667
R-NT2RM4000833//ESTs, Moderately similar to ZK863.3 [C.elegans]//4.0e-112:448:99//Hs.20223:AA482031
10 R-NT2RM4000848//ESTs//8.1e-97:476:97//Hs.16036:AA883864
R-NT2RM4000852//ESTs//6.4e-94:467:97//Hs.11556:AI309597
R-NT2RM4000855//ESTs//2.9e-95:544:90//Hs.106525:AI283343
R-ntnnnnnnnnnn
R-NT2RM4000895//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//9.3e-96:450:99//Hs.142076:AA604514
15 R-NT2RM4000950//ESTs//2.6e-91:438:98//Hs.43827:AA455262
R-NT2RM4000971//EST//2.9e-96:461:99//Hs.139709:AA227887
R-NT2RM4000979//EST//1.6e-67:329:98//Hs.96927:AA349647
R-NT2RM4000996//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//1.7e-82:414:96//Hs.115342:AA650126
20 R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//3.8e-114:545:97//Hs.19542:AB018272
R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//2.5e-114:556:97//Hs.15711:AB014539
R-NT2RM4001032//ESTs//7.8e-17:132:84//Hs.138720:N53352
25 R-NT2RM4001047//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//0.42:133:67//Hs.32170:AB015132
R-NT2RM4001054//ESTs//1.7e-84:404:99//Hs.116407:AA815300
R-ntnnnnnnnnnn//ESTs//3.4e-91:439:99//Hs.103177:W2798
R-NT2RM4001092//ESTs//1.4e-86:517:8911Hs.132969:Z78324
30 R-NT2RM4001116//EST//5.2e-57:275:100//Hs.131115:AI016962
R-NT2RM4001140//ESTs//5.5e-96:461:98//Hs.86965:AA252276
R-NT2RM4001151//ESTs//0.40:263:58//Hs.113189:R08311
R-NT2RM4001155//ESTs//8.3e-105:544:94//Hs.29647:W60848
R-NT2RM4001160//EST//7.6e-25:380:68//Hs.147405:AI209085
35 R-NT2RM4001187//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//9.2e-43:273:91//Hs.109005:N31174
R-NT2RM4001191//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//3.1e-32:274:70//Hs.2379:U23942
R-NT2RM4001200//ESTs//4.5e-102:494:97//Hs.31844:N32849
R-NT2RM4001203
40 R-NT2RM4001204//ESTs//9.8e-88:468:93//Hs.4990:T65307
R-NT2RM4001217//ESTs//1.2e-75:396:94//Hs.25042:R72410
R-NT2RM4001256//ESTs//1.0:157:62//Hs.65377:AA994677
R-NT2RM4001258//ESTs//9.6e-41:260:88//Hs.27633:N76184
R-NT2RM4001309
45 R-NT2RM4001313//EST//0.0022:150:66//Hs.161573:W64857
R-NT2RM4001316//ESTs//3.5e-26:139:99//Hs.23100:AI128899
R-NT2RM4001320//ESTs//1.6e-97:308:99//Hs.112024:AI042352
R-NT2RM4001340//ESTs, Highly similar to UTR4 PROTEIN [Saccharomyces cerevisiae]//1.9e-105:522:97//Hs.18442:AI129307
50 R-NT2RM4001344//EST//1.1e-90:436:99//Hs.95900:AA160339
R-NT2RM4001347//EST//0.17:186:61//Hs.16751:T90476
R-NT2RM4001371//EST//0.0069:270:62//Hs.99239:AA450211
R-NT2RM4001382
R-NT2RM4001384//ESTs//9.6e-91:445:98//Hs.55000:AA805507
55 R-NT2RM4001410//EST//0.13:50:82//Hs.157675:AI358790
R-NT2RM4001411//ESTs, Weakly similar to lymphocyte specific adaptor protein Lnk [M.musculus]//4.0e-102:539:94//Hs.15744:AI055859
R-NT2RM4001412

- R-NT2RM4001414//ESTs//6.5e-35:226.88//Hs.121727:AA775895
 R-NT2RM4001437//EST//0.017:169.67//Hs.13207:F10054
 R-NT2RM4001444//ESTs, Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [S.cerevisiae]//7.4e-108:544.94//Hs.7558:AA526812
- 5 R-NT2RM4001454//ESTs//4.7e-108:517.98//Hs.32295:N32277
 R-NT2RM4001455//EST//9.6e-81:395.97//Hs.127978:AA969739
 R-NT2RM4001483//Human mRNA for KIAA0033 gene, partial cds//1.8e-58:324.85//Hs.22271:D26067
 R-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//7.0e-104:547.93//Hs.153121:AB014585
- 10 R-NT2RM4001519//Histatin 1//0.53:340.59//Hs.119101:M26664
 R-NT2RM40015227//Small inducible cytokine A5 (RANTES)/8.4e-55:306.80//Hs.155464:AF088219
 R-NT2RM40015577//ESTs, Weakly similar to F11A10.4 [C.elegans]//6.1e-21:165.83//Hs.29134:HA3072
 R-NT2RM4001565//ESTs//2.0e-103:483.99//Hs.121273:AA758027
 R-NT2RM4001566//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//2.7e-103:446.72//Hs.4943:Z98046
- 15 R-NT2RM4001569//ESTs//3.6e-37:186.100//Hs.86959:AA888009
 R-NT2RM4001582//ESTs//1.2e-96:459.98//Hs.114432:N52946
- 20 R-NT2RM4001594//ESTs//1.6e-83:404.98//Hs.134740:AA282171
 R-NT2RM4001597//ESTs//6.9e-111:558.96//Hs.11408:AI358871
 R-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//2.1e-112:565.95//Hs.23255:AB018334
- 25 R-NT2RM4001611//EST//5.9e-74:353.99//Hs.125318:AA837079
 R-NT2RM4001629//ESTs//6.1e-95:453.99//Hs.115765:AA485957
 R-NT2RM4001650
 R-NT2RM4001662
 R-NT2RM4001666//Homo sapiens mRNA for KIAA0469 protein, complete cds//3.6e-36:230.70//Hs.7764:AB007938
- 30 R-NT2RM4001682//EST//4.3e-68:393.90//Hs.157362:AI367496
 R-NT2RM4001710//ESTs//4.3e-48:235.99//Hs.7299:AA203440
 R-NT2RM4001714//ESTs//0.0014:568.58//Hs.50458:AA866686
 R-NT2RM4001731//ESTs, Weakly similar to No definition line found [C.elegans]//3.1e-108:563.94//Hs.16510:AA522887
- 35 R-NT2RM4001741//IT3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2930 nt]//0.083:124.68//Hs.120980:S83390
 R-NT2RM4001746//ESTs//6.1e-90:420.100//Hs.139003:AA948200
 R-NT2RM4001754//Human kpni repeat mma (cdna clone pcd-kpni-4), 3' end//5.4e-59:504.78//Hs.139107:K00629
 R-NT2RM4001758//ESTs//8.9e-27:140.100//Hs.149973:AI290740
 R-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//6.4e-24:236.80//Hs.39871:AB018270
 R-NT2RM4001783//ESTs//9.9e-30:156.99//Hs.115260:AA314956
 R-NT2RM4001810//ESTs//1.3e-65:346.95//Hs.131915:W22567
 R-NT2RM4001813//ESTs//5.7e-102:473.100//Hs.87574:AI089920
- 45 R-NT2RM4001823//ESTs//3.8e-62:324.95//Hs.124109:AA888339
 R-NT2RM4001828//ESTs//1.3e-119:563.98//Hs.102397:AA706551
 R-NT2RM4001836//ESTs//5.5e-16:92.100//Hs.26996:AA551070
 R-NT2RM4001841//ESTs//1.3e-99:540.94//Hs.42322:AA082619
- 50 R-NT2RM4001842//ESTs, Weakly similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]//4.1e-10:274.62//Hs.161959:AA493652
 R-NT2RM4001856//ESTs, Weakly similar to contains similarity to ATP/GTP-binding site motif [C.elegans]//3.0e-43:292.86//Hs.14202:N46000
 R-NT2RM4001857//ESTs//6.2e-104:495.98//Hs.118686:AA682280
- 55 R-NT2RM40018657//Homo sapiens mRNA for atopy related autoantigen CALC//1.6e-120:592.97//Hs.61628:Y17711
 R-NT2RM4001876//ESTs//2.9e-98:532.92//Hs.100734:AA158252
 R-NT2RM4001880//ESTs//2.5e-29:224.86//Hs.6193:AA045149

- R-NT2RM4001905//ESTs//5.6e-109:565:95//Hs.9536:AA114178
 R-NT2RM4001922//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-105:535:95//Hs.30991:AA994438
 R-NT2RM4001930//ESTs//4.1-84:425:96//Hs.80042:N63143
 5 R-NT2RM4001938//EST//0.00040:241:60//Hs.147235:AI205893
 R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//2.0e-110:556:95//Hs.118631:AF098162
 R-NT2RM4001953//ESTs//5.3e-65:338:96//Hs.33718:AA453268
 R-NT2RM4001965//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//5.7e-62:326:95//Hs.3385:N25917
 10 R-ntnnnnnnnnnn//ESTs, Weakly similar to IP63 protein [R.norvegicus]//1.9e-21:121:98//Hs.8772:AA521097
 R-NT2RM4001979//ESTs//1.4e-96:465:98//Hs.157103:W60265
 R-NT2RM4001984
 R-NT2RM4001987
 R-NT2RM4002013//EST//2.2e-14:110:90//Hs.160835:AI345528
 15 R-NT2RM4002018
 R-NT2RM4002034//Human mRNA for KIAA0118 gene, partial cds//9.4e-46:293:87//Hs.154326:D42087
 R-NT2RM4002044//ESTs//2.8e-107:537:96//Hs.24078:W44435
 R-NT2RM4002054//ESTs//3.7e-88:482:94//Hs.4243:T78226
 R-NT2RM4002062//ESTs//1.4e-55:377:85//Hs.152592:AA587887
 20 R-NT2RM4002063//Calcium modulating ligand//1.8e-43:385:78//Hs.13572:AF068179
 R-ntnnnnnnnnnn//Homo sapiens OPA-containing protein mRNA, complete cds//5.5e-42:554:68//Hs.85313:AF071309
 R-NT2RM4002067//Human kpni repeat mra (cdna clone pcd-kpni-4), 3' end//2.3e-43:468:73//Hs.139107:K00629
 R-NT2RM4002073//ESTs, Weakly similar to very-long-chain acyl-CoA synthetase [H.sapiens]//6.8e-57:290:96//Hs.109274:AA193416
 25 R-NT2RM4002075//EST//0.078:267:61//Hs.163563:AA641655
 R-NT2RM4002093//ESTs//1.2e-64:316:99//Hs.34956:AI052528
 R-ntnnnnnnnnnn//ESTs//1.0:95:69//Hs.25897:W65409
 R-NT2RM4002128//Homo sapiens mRNA for BCL9 gene//0.51:259:60//Hs.122607:Y13620
 30 R-NT2RM4002140//ESTs//5.5e-46:187:94//Hs.8737:W22712
 R-NT2RM4002145//ESTs//4.6e-70:374:94//Hs.141082:H18987
 R-NT2RM4002146//ESTs//1.9e-93:43:9:99//Hs.119295:AA442090
 R-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.5e-111:560:96//Hs.22464:AF084535
 R-NT2RM4002174//Homo sapiens LIM protein mRNA, complete cds//3.2e-46:552:72//Hs.154103:AF061258
 35 R-NT2RM4002189//ESTs//9.6e-75:352:100//Hs.98350:H15400
 R-NT2RM4002194//EST//0.22:68:72//Hs.149104:AI244343
 R-NT2RM4002205//EST//0.00028:103:72//Hs.130032:AA897678
 R-NT2RM4002213//ESTs//3.3e-15:160:78//Hs.63304:W22079
 R-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]
 40 //5.1e-112:569:95//Hs.23900:U82984
 R-NT2RM4002251//ESTs, Weakly similar to similar to alpha-1,3-mannosyl-glycoprotein beta-1, 2-N-acetylglucosaminyltransferase [C.elegans]//1.1e-100:544:93//Hs.27567:W72190
 R-NT2RM4002256//Small inducible cytokine A5 (RANTES)//1.0e-44:341:81//Hs.155464:AF088219
 R-NT2RM4002266//ESTs//2.6e-100:539:93//Hs.57976:AA535864
 45 R-NT2RM4002278//ESTs//1.8e-112:569:95//Hs.87281:AA1128263
 R-NT2RM4002281//ESTs//4.9e-20:187:80//Hs.141203:H52638
 R-NT2RM4002287//ESTs//7.9e-84:388:94//Hs.33977:N52461
 R-NT2RM4002294
 R-NT2RM4002301//ESTs//4.5e-111:556:96//Hs.85916:AA194164
 50 R-NT2RM4002323//ESTs//4.5e-102:498:97//Hs.85782:AA191498
 R-ntnnnnnnnnnn//ESTs//5.0e-59:283:100//Hs.125048:AA682913
 R-NT2RM4002344//V-akt murine thymoma viral oncogene homolog 2//0.29:153:66//Hs.155129:M77198
 R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//2.8e-122:593:97//Hs.26163:AB014549
 55 R-NT2RM4002374//ESTs//3.3e-40:505:70//Hs.95115:AA206594
 R-NT2RM4002383//ESTs//2.7e-93:455:97//Hs.134278:AA648884
 R-NT2RM4002390//ESTs//3.3e-93:481:95//Hs.48764:AA613328
 R-NT2RM4002409//ESTs, Weakly similar to coded for by C. elegans cDNA yk52e10.5 [C.elegans]//1.3e-97:473:

R-NT2RM4.16464/W19606
R-NT2RM4002438//ESTs/I/0.74:162:61//Hs.65377:AA994677
R-NT2RM4002446
R-NT2RM4002452//EST/I/1.0:164:60//Hs.116619:AA668142
R-NT2RM4002457
R-NT2RM4002460//ESTs/I/3.0e-74:385:96//Hs.6933:R07890
R-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.6e-103:507:97//Hs.
8765:AF083255
R-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//2.3e-32:172:98//Hs.94781:
AB014591
R-NT2RM4002493//ESTs//6.4e-73:366:97//Hs.157114:T58884
R-NT2RM4002499//ESTs/I/3.5e-61:307:97//Hs.117737:AIO88029
R-NT2RM4002504//ESTs/I/2.1e-55:308:94//Hs.10949:AA64464
R-nnnnnnnnnnnn/ESTs, Weakly similar to peroxisome targeting signal 2 receptor [H.sapiens]/1.4e-73:360:91//
Hs.31030:H50467
R-NT2RM4002532//ESTs//1.3e-21:191:78//Hs.146811:AAA10788
R-NT2RM4002534//ESTs/I/1.8e-99:512:95//Hs.13526:AI417057
R-NT2RM4002567//ESTs/I/7.6e-41:272:87//Hs.7114:R24312
R-NT2RM4002571//ESTs, Highly similar to POLYPEPTIDE N-ACETYLALCATOSAMINYLTRANSFERASE [Bos
taurus]/2.3e-89:435:97//Hs.15830:AA165698
R-NT2RM4002593//ESTs/I/2.3e-109:552:96//Hs.17424:AA190569
R-NT2RM4002623//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]
/9.9e-28:194:87//Hs.59346:AI126802
R-NT2RP2000001//ESTs/I/2.6e-80:386:99//Hs.105061:N45096
R-NT2RP2000006//Thromboxane A2 receptor 1f/2.2e-37:253:84//Hs.89887:D38081
R-NT2RP2000008/Zinc finger protein 37a (KIX 21)/5.2e-25:366:67//Hs.54488:X69115
R-NT2RP2000027//ESTs/I/9.5e-74:377:96//Hs.96557:AA286713
R-NT2RP2000040/Homo sapiens mRNA for KIAA0747 protein, partial cds//2.7e-42:223:96//Hs.8309:AB018290
R-NT2RP2000045/Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//
4.3e-64:309:98//Hs.6216:AF061749
R-NT2RP2000054//EST//1.2e-71:375:96//Hs.98835:AA435798
R-NT2RP2000056//EST//I/2.8e-28:342:69//Hs.135526:AI094910
R-NT2RP2000067//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]/2.3e-35:199:94//Hs.41793:
AA775879
R-NT2RP2000070//ESTs, Weakly similar to proto-cadherin 3 [R.norvegicus]/1.4e-78:383:98//Hs.58254:W72881
R-NT2RP2000076//EST//I/0.0014:227:63//Hs.136761:AA738097
R-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//1.1e-78:379:97//Hs.
54877:AF050078
R-NT2RP2000079//Homo sapiens RET finger protein-like 1 antisense transcript, partial//2.9e-21:232:75//Hs.
102576:AJ102030
R-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.8e-75:378:96//Hs.22926:AB018338
R-NT2RP2000091/Carcinoembryonic antigen gene family member 6//10.030:236:63//Hs.41:DN0064
R-NT2RP2000097//ESTs/I/4.2e-15:92:97//Hs.7432:AA281757
R-NT2RP2000098//ESTs/I/9.0e-53:279:94//Hs.87807:AA813827
R-NT2RP2000108//EST//I/1.5e-75:378:96//Hs.162105:AA524419
R-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//5.8e-76:386:95//Hs.17706:AB018356
R-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III
[C.elegans]/1.9e-19:153:86//Hs.5268:W22670
R-nnnnnnnnnnnn/ESTs/I/1.0e-55:293:95//Hs.14570:AI422099
R-nnnnnnnnnnnn/ESTs/I/0.24:354:59//Hs.157564:AI356513
R-NT2RP2000147//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [Mus musculus]/3.0e-
89:457:95//Hs.3832:AI208601
R-NT2RP2000153//EST//I/0.0039:93:68//Hs.140386:AA773548
R-NT2RP2000157//ESTs/I/1.0e-53:322:91//Hs.6877:AA040820
R-NT2RP2000161//ESTs//I/1.6e-99:492:97//Hs.21738:AI188190
R-NT2RP2000175//ESTs/I/1.4e-98:489:96//Hs.4849:AI143741
R-NT2RP2000183//ESTs/I/9.0e-72:358:96//Hs.4856:N51373
R-NT2RP2000195//ESTs/I/3.9e-92:439:98//Hs.145091:AA814510

- R-NT2RP2000205//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/1.4e-80:415:95//Hs.11807:T86897
- R-NT2RP2000224//RNA polymerase II, polypeptide C (33kD)/1.1e-57:306:94//Hs.79402:AC004382
- R-NT2RP2000232
- 5 R-NT2RP2000233//ESTs/1.1e-08:63:96//Hs.124861:AI090683
- R-NT2RP2000239//ESTs/5.3e-87:427:96//Hs.86211:AA604379
- R-NT2RP2000248//ESTs, Weakly similar to O-linked GlcNAc transferase [H.sapiens]/1.3e-95:454:99//Hs.102057:AA649005
- R-NT2RP2000257//ESTs/5.1e-58:282:99//Hs.122565:AI126840
- 10 R-NT2RP2000258//EST/1.0:67:68//Hs.61812:AA035649
- R-NT2RP2000270//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]/8.4e-59:298:96//Hs.16085:AI261382
- R-NT2RP2000274//ESTs/7.5e-61:296:98//Hs.86081:AA196635
- R-NT2RP2000288//ESTs/1.8e-56:305:93//Hs.7579:AA775865
- 15 R-NT2RP2000289
- R-NT2RP2000297//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]/9.8e-106:494:99//Hs.102951:AA574249
- R-NT2RP2000298//ESTs/2.1e-62:256:90//Hs.8737:W22712
- R-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds//2.8e-39:222:93//Hs.58218:U82381
- 20 R-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3-.41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two unknown genes. Contains ESTs and GSSs//2.9e-71:342:98//Hs.87684:AL022398
- 25 R-NT2RP2000329//ESTs, Highly similar to GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL [Bos taurus]/3.4e-69:371:94//Hs.43436:N32441
- R-NT2RP2000337//ESTs/5.2e-79:411:95//Hs.101799:AI276062
- R-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds//1.1e-47:262:94//Hs.76556:U83981
- 30 R-NT2RP2000369//ESTs/4.3e-102:531:94//Hs.15855:H98103
- R-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//8.4e-09:93:83//Hs.808:L28010
- R-NT2RP2000420//ESTs/8.2e-24:142:94//Hs.144893:AI222324
- R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.2e-20:140:90//Hs.5819:AF102265
- 35 R-NT2RP2000438//ESTs, Weakly similar to misato [D.melanogaster]/1.3e-65:362:93//Hs.22197:AI151425
- R-NT2RP2000448//ESTs, Highly similar to HYPOTHETICAL 51.6 KD PROTEIN IN PAP1-MRPL13 INTERGENIC REGION [Saccharomyces cerevisiae]/3.6e-75:435:92//Hs.21938:W81045
- R-NT2RP2000459//ESTs/2.8e-95:527:93//Hs.103422:AI352013
- R-NT2RP2000498//ESTs/2.3e-17:119:79//Hs.161714:AA229078
- 40 R-NT2RP2000503//ESTs/5.2e-91:438:98//Hs.152335:AI290215
- R-NT2RP2000510//Homo sapiens KIAA0436 mRNA, partial cds//0.13:455:58//Hs.110:AB007896
- R-ntnnnnnnnn//ESTs/9.9e-63:376:89//Hs.47546:AA181348
- R-NT2RP2000523
- R-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.5e-30:167:97//Hs.14409:AB011144
- 45 R-NT2RP2000617//ESTs/9.5e-103:493:98//Hs.9412:W72446
- R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//8.1e-66:335:96//Hs.7314:AB014514
- R-NT2RP2000644//ESTs/1.1e-18:372:63//Hs.82419:AA789222
- R-NT2RP2000656//ESTs/1.0e-10:128:80//Hs.23977:AA115275
- R-NT2RP2000658//ESTs/0.31:278:59//Hs.15661:W02396
- 50 R-NT2RP2000668//ESTs/8.2e-40:255:88//Hs.113310:R16767
- R-NT2RP2000678//ESTs/2.6e-53:271:9611Hs.23790:N99347
- R-NT2RP2000710//ESTs/0.49:190:63//Hs.145521:AI261368
- R-NT2RP2000715//EST/1.2e-87:418:9911Hs.139425:AA429279
- R-NT2RP2000731//EST/5.3e-65:322:97//Hs.136754:AA713965
- 55 R-NT2RP2000758//ESTs/1.0:187:61//Hs.10545:N62642
- R-NT2RP2000764//ESTs/5.8e-84:485:91//Hs.121816:AA775419
- R-NT2RP2000809
- R-NT2RP2000812//ESTs/1.2e-45:231:97//Hs.121028:AA902745

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- R-NT2RP2001427//EST//1.7e-1 1:107.84//Hs.148584:AI201728
 R-NT2RP2001436//ESTs. Weakly similar to F02D8.3 [C.elegans]//2.9e-114:558.97//Hs.7627:AI341556
 R-NT2RP2001440//EST//0.17:192.58//Hs.133442:AI061394
 R-NT2RP2001445//ESTs//1.1e-43:215.100//Hs.145497:AA501453
 5 R-NT2RP2001449//ESTs//4.1e-08:234.61//Hs.134067:AI076765
 R-NT2RP2001450//ESTs//9.5e-65:356.94//Hs.61829:AI079539
 R-NT2RP2001467//Small inducible cytokine A5 (RANTES)//1.2e-34:255.83//Hs.155464:AF088219
 R-NT2RP2001506//ESTs//2.9e-23:170.89//Hs.7147:T23513
 R-NT2RP2001511//ESTs//2.0e-08:59.100//Hs.57660:AA251146
 10 R-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1//6.7e-106:545.95//Hs.4277:Y14494
 R-NT2RP2001526//ESTs//3.7e-23:295.72//Hs.8514:AF039240
 R-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//1.9e-15:99.95//Hs.99742:AF035586
 15 R-NT2RP2001560//ESTs//2.2e-58:310.94//Hs.87454:AA732816
 R-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//2.0e-76:387.96//Hs.67619:AB007957
 R-NT2RP2001576//Human mRNA for KIAA0105 gene, complete cds//0.17:193.60//Hs.119:D14661
 R-NT2RP2001581//ESTs//5.1e-08:107.78//Hs.157114:T58884
 20 R-NT2RP2001597//EST//5.2e-22:151.88//Hs.158613:AI369995
 R-NT2RP2001601//ESTs//1.5e-78:373.99//Hs.137558:AI393767
 R-NT2RP2001613
 R-NT2RP2001628//EST//0.99:195.60//Hs.144238:W52294
 R-NT2RP2001663//ESTs//4.0e-37:282.84//Hs.12319:W56090
 25 R-NT2RP2001677//ESTs//1.4e-44:232.96//Hs.159387:AI370845
 R-NT2RP2001678//ESTs//0.91:124.60//Hs.10593:AI201336
 R-NT2RP2001699//EST//0.0033:230.61//Hs.146544:AI125323
 R-NT2RP2001720//ESTs//1.8e-52:255.99//Hs.101064:AA290579
 R-NT2RP2001721//ESTs//7.0e-101:479.99//Hs.129750:AA987538
 30 R-NT2RP2001740//ESTs//3.3e-76:379.96//Hs.144704:AI147100
 R-NT2RP2001748//ESTs//1.4e-44:352.81//Hs.142259:AA828840
 R-NT2RP2001762//Homo sapiens exonuclease 1a (EXO1a) mRNA, complete cds//2.1e-105:519.96//Hs.47504:AF091754
 R-NT2RP2001813//ESTs//6.3e-78:406.95//Hs.21902:R44037
 35 R-NT2RP2001861
 R-NT2RP2001869//EST//2.8e-21:173.82//Hs.130321:AI002941
 R-NT2RP2001876//ESTs//6.1e-102:526.95//Hs.4944:AA533088
 R-NT2RP2001883//ESTs. Weakly similar to No definition line found [C.elegans]//6.9e-110:556.95//Hs.23159:AA113849
 40 R-NT2RP2001900//ESTs//6.9e-85:442.95//Hs.154220:AA171724
 R-NT2RP2001907//ESTs//2.1e-82:432.94//Hs.142257:AA189423
 R-NT2RP2001926//EST//2.3e-24:299.71//Hs.135085:AI097268
 R-NT2RP2001936//ESTs//1.1e-45:265.92//Hs.112482:T66087
 R-NT2RP2001943//EST//1.4e-05:246.61//Hs.144096:AI032180
 45 R-NT2RP2001946//ESTs//3.6e-87:410.99//Hs.20242:W72594
 R-NT2RP2001947//ESTs//1.9e-55:338.88//Hs.55852:T72588
 R-NT2RP2001969
 R-NT2RP2001976//ESTs//1.2e-98:499.95//Hs.121028:AA902745
 R-NT2RP2001985//ESTs. Weakly similar to GTPASE-ACTIVATING PROTEIN SPA-1 [M.musculus]//8.3e-15:118.89//Hs.18760:AA166678
 50 R-NT2RP2002025//ESTs//2.1e-82:393.98//Hs.159488:AI378233
 R-NT2RP2002032//ESTs//4.4e-98:531.91//Hs.93836:AA813332
 R-NT2RP2002033//ESTs//3.5e-43:229.96//Hs.30563:AA102627
 R-NT2RP2002041
 55 R-NT2RP2002046//ESTs//1.6e-101:476.99//Hs.101107:AA825938
 R-NT2RP2002047//ESTs//9.1e-85:431.95//Hs.116750:AA629895
 R-NT2RP2002058//ESTs//1.3e-31:163.99//Hs.33085:AA258068
 R-NT2RP2002066//ESTs//1.9e-87:459.93//Hs.118871:AA846091

- R-NT2RP2002070//ESTs//4. 1e-63.332.96//Hs. 156446:T92265
 R-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//1.7e-26:178.87//Hs. 11039.AF052183
 R-NT2RP2002079//ESTs//1.2e-79:389.97//Hs. 135214:AI350524
 5 R-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein//1.5e-60:376.89//Hs. 155218:AJ007509
 R-NT2RP2002105//ESTs//8. 4e-54:313.90//Hs. 98702:AI123000
 R-NT2RP2002124//ESTs//6.6e-81:431.93//Hs. 127326:AA525134
 R-NT2RP2002137//Deoxycytidine kinase//0.29:183.62//Hs. 709:M60527
 R-NT2RP2002154//ESTs//9. 6e-97:539.91//Hs. 18624:AA523268
 10 R-NT2RP2002172//EST//0.69:53:75//Hs. 156238:AI334495
 R-NT2RP2002185//ESTs. Weakly similar to F15C11.2 [C.elegans]//1.4e-54:269.98//Hs. 107201:W52859
 R-NT2RP2002192//ESTs. Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.9e-15:245:71//Hs. 87578:AI125363
 R-NT2RP2002193//ESTs//3.5e-79:45.3.90//Hs. 76578:AI290672
 15 R-NT2RP2002208//ESTs//2.0e-72:347.99//Hs. 164028:AI003946
 R-NT2RP2002219//EST//0.039:229:63//Hs. 149830:AI287499
 R-NT2RP2002231//ESTs//3.3e-64:337.94//Hs. 79828:AA642341
 R-nnnnnnnnnnn//ESTs. Highly similar to co-repressor protein [M.musculus]//5.4e-48:238.99//Hs. 22583:AA188168
 20 R-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds//1.6e-15:131.83//Hs. 150595:AF005418
 R-NT2RP2002259//Human L-myc protein gene, complete cds//5.3e-99:548.91//Hs. 92137:M19720
 R-NT2RP2002270//ESTs. Weakly similar to AF-9 PROTEIN [H.sapiens]//4.8e-100:550.91//Hs. 4029:Z87373
 R-NT2RP2002292//ESTs. Weakly similar to F13B12.1 [C.elegans]//3.2e-92:482.93//Hs. 5570:AI377863
 25 R-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//4.1e-103:527.94//Hs. 24812:AF069532
 R-NT2RP2002316//ESTs//4.2e-91:425:100//Hs. 3350:AI368015
 R-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds//1.2e-112:567.95//Hs. 31034:AB015594
 30 R-NT2RP2002333//ESTs//1.9e-86:483.91//Hs. 155198:AA767372
 R-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds//1.2e-103:600.89//Hs. 109051:AF038958
 R-NT2RP2002394//ESTs//0.11:158.65//Hs. 28792:AI343467
 R-NT2RP2002408//ESTs//1.5e-51:278.93//Hs. 6044:W22815
 35 R-NT2RP2002426//Homo sapiens mRNA for KIAA0563 protein, complete cds//1.7e-33:285.80//Hs. 15731:AB011135
 R-NT2RP2002439//ESTs//3.2e-12:134.76//Hs. 32246:AA464020
 R-NT2RP2002457//ESTs//4.7e-52:282.94//Hs. 21968:H97521
 R-NT2RP2002464//ESTs//5.3e-27:148.98//Hs. 115660:AI362230
 40 R-NT2RP2002475//ESTs//3.9e-85:439.94//Hs. 9873:W27233
 R-nnnnnnnnnnn//Homo sapiens mRNA for ABC transporter 7 protein, complete cds//9.9e-115:605.92//Hs. 125856:AB005289
 R-NT2RP2002498//ESTs//6.3e-37:227.93//Hs. 108779:N73180
 R-NT2RP2002503//ESTs//1.9e-54:358.86//Hs. 57800:W60838
 45 R-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//8.5e-107:583.91//Hs. 23255:AB018334
 R-NT2RP2002520//ESTs//4.2e-99:509.94//Hs. 32368:AA205305
 R-NT2RP2002537//ESTs//4.2e-105:552.93//Hs. 154363:AA533090
 R-NT2RP2002546//Homo sapiens clone TUA8 Cri-du-chat region mRNA//2.6e-109:570.93//Hs. 49476:AF009314
 50 R-NT2RP2002549//DNA polymerase gamma//1.1e-35:189.86//Hs. 80961:U60325
 R-NT2RP2002591//ESTs. Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//7.5e-118:564.97//Hs. 94549:AA149547
 R-NT2RP2002595//EST//1.4e-15:101.95//Hs. 129528:AA994783
 R-NT2RP2002606//ESTs//4.5e-99:475.98//Hs. 45046:N40170
 55 R-NT2RP2002609//ESTs//1.9e-104:568.92//Hs. 9175:AI184220
 R-NT2RP2002618//ESTs//0.014:493.57//Hs. 96322:AA541615
 R-NT2RP2002621//EST//1.4e-36:252.84//Hs. 149580:AI281881
 R-NT2RP2002643//ESTs//6.9e-32:247.74//Hs. 33354:AA179944

- R-NT2RP20020672
 R-NT2RP2002701//N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB//0.99:184.63//Hs.50727:U43572
 R-NT2RP2002706//ESTs//2.8e-41:148.86//Hs.161917:AA483223
 R-NT2RP2002710//EST//0.34:105.71//Hs.136747:AA749210
 5 R-NT2RP2002727//ESTs//8.7e-68:368.94//Hs.14366:178626
 R-NT2RP2002736//ESTs//9.7e-98:457.99//Hs.74899:AA993300
 R-NT2RP2002740//Homo sapiens mRNA for KIAA0536 protein, partial cds//0.66:360.59//Hs.119139:AB011108
 R-NT2RP2002741//ESTs//3.1e-102:489.98//Hs.112024:AI042352
 R-NT2RP2002750//EST//0.3e-43:166.86//Hs.162404:AA573131
 10 R-NT2RP2002752//ESTs//5.0e-56:355.89//Hs.95867:M62042
 R-NT2RP2002753//ESTs//1.7e-49:262.96//Hs.49005:W69124
 R-NT2RP2002769//ESTs//1.3e-59:376.88//Hs.4046:H03587
 R-NT2RP2002778//Homo sapiens clone 24606 mRNA sequence//4.0e-65:341.94//Hs.17481:AF070537
 R-NT2RP2002800//ESTs//6.5e-08:79.84//Hs.153262:AA551124
 15 R-NT2RP2002839//ESTs. Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.6e-100:501.97//Hs.136202:AA206578
 R-NT2RP2002857//ESTs//4.3e-94:463.97//Hs.134292:AA603031
 R-NT2RP2002862//ESTs//2.3e-42:302.82//Hs.117969:H94870
 R-NT2RP2002880
 20 R-NT2RP2002891
 R-NT2RP2002925//ESTs//1.3e-103:564.92//Hs.142079:AA182894
 R-NT2RP2002928//ESTs//3.9e-108:502.99//Hs.29105:AA574143
 R-NT2RP2002929//ESTs//4.1e-106:499.99//Hs.44743:AA837096
 R-NT2RP2002954//ESTs//2.6e-88:417.99//Hs.100824:AI308771
 25 R-NT2RP2002959//ESTs//7.5e-101:489.97//Hs.32690:N57480
 R-NT2RP2002979//ESTs//5.4e-06:197.65//Hs.146726:AI147060
 R-NT2RP2002980//ESTs//1.0e-110:562.96//Hs.28444:AA083213
 R-NT2RP2002986//ESTs. Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//3.1e-119:578.97//
 Hs.106290:AI125291
 30 R-NT2RP2002987//Human mRNA for KIAA0331 gene, complete cds//1.0:78.74//Hs.146395:AB002329
 R-NT2RP2002993//ESTs. Weakly similar to DNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE [H.
 sapiens]//2.4e-98:467.98//Hs.86337:AA149311
 R-NT2RP2003000//ESTs//0.0070:400.61//Hs.138506:U85642
 R-NT2RP2003034//ESTs//9.3e-87:408.96//Hs.164042:H12594
 35 R-NT2RP2003073//Human transporter protein (g17) mRNA, complete cds//0.95:259.61//Hs.76460:U49082
 R-NT2RP2003099//Thromboxane A2 receptor//2.6e-42:328.81//Hs.89887:D38081
 R-NT2RP2003108//ESTs//2.3e-82:398.98//Hs.5105:AA115512
 R-NT2RP2003117//Human mRNA for KIAA0347 gene, complete cds//2.4e-49:336.86//Hs.101996:AB002345
 40 R-NT2RP2003121//ESTs//2.0e-75:380.96//Hs.133127:AA133355
 R-NT2RP2003125
 R-NT2RP2003129//EST//0.68:115.69//Hs.122196:AA780986
 R-NT2RP2003137//ESTs//2.1e-37:259.85//Hs.63169:N78506
 R-NT2RP2003161//ESTs//2.5e-88:451.96//Hs.29041:W37379
 R-NT2RP2003164//ESTs//4.3e-113:543.97//Hs.8980:AA629067
 45 R-NT2RP2003165//ESTs//6.9e-83:486.89//Hs.138632:H97952
 R-NT2RP2003177//ESTs//0.47:38.100//Hs.61790:AA421156
 R-NT2RP2003194//ESTs//4.7e-118:582.96//Hs.27266:AA053816
 R-NT2RP2003206//ESTs//0.032:388.58//Hs.122148:AA442074
 R-NT2RP2003230//ESTs//8.8e-103:478.99//Hs.40140:AI079253
 50 R-NT2RP2003237//ESTs//2.7e-76:392.96//Hs.106278:R37661
 R-NT2RP2003243//ESTs//3.6e-53:300.92//Hs.18793:AA192438
 R-NT2RP2003265//ESTs. Highly similar to protein NGD5 [M.musculus]//3.3e-110:557.96//Hs.24994:AA236937
 R-NT2RP2003272//ESTs. Weakly similar to F15C11.2 [C.elegans]//1.2e-34:228.89//Hs.107201:W52859
 R-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//1.4e-111:565.95//Hs.154919:
 55 AB014525
 R-NT2RP2003280//ESTs//2.6e-101:541.94//Hs.6982:AA622427
 R-NT2RP2003286//ESTs//1.2e-104:497.98//Hs.113052:AI222106
 R-NT2RP2003293//Human mRNA for KIAA0118 gene, partial cds//9.1e-44:458.74//Hs.154326:D42087

- R-NT2RP2003295//Protein serine/threonine kinase stk2//0.31:321:57//Hs.1087:L20321
 R-NT2RP2003297//ESTs//3.0e-15:118:87//Hs.16621:AA098874
 R-NT2RP2003308//ESTs. Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]//4.8e-109:553:96//Hs.26089:AA195126
- 5 R-NT2RP2003329//ESTs//0.99:208:62//Hs.143607:AI424948
 R-NT2RP2003339//ESTs//1.3e-85:441:96//Rs.24115:N32618
 R-NT2RP2003347//ESTs//1.5e-70:365:96//Hs.155773:AI312825
 R-NT2RP2003367//EST//5.8e-80:376:100//Hs.112500:AA599014
 R-NT2RP2003391//ESTs//2.8e-98:484:97//Hs.5842:AA534476
- 10 R-NT2RP2003393//ESTs//2.0e-96:510:93//Hs.75844:AA115502
 R-NT2RP2003394//EST//5.2e-06:264:63//Hs.144234:W52249
 R-NT2RP2003401//ESTs//6.1e-25:161:90//Hs.155360:AA984683
 R-NT2RP2003433//ESTs. Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.2e-106:508:98//Hs.131840:AI016073
- 15 R-NT2RP2003445//ESTs. Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.6e-21:161:70//Hs.43153:N22360
 R-NT2RP2003446//ESTs. Weakly similar to C27H6.4 [C.elegans]//6.0e-105:529:96//Hs.8055:W60903
 R-NT2RP2003456//ESTs//7.5e-96:449:99//Hs.25362:AI277332
 R-NT2RP2003480//ESTs//1.6e-116:583:96//Hs.59757:AA176121
- 20 R-NT2RP2003499//ESTs. Weakly similar to elastin like protein [D.melanogaster]//7.0e-71:365:95//Hs.101056:R52777
 R-NT2RP2003506//ESTs. Weakly similar to ORF YPL207w [S.cerevisiae]//2.3e-115:577:96//Hs.16277:N36831
 R-NT2RP2003511//ESTs//1.6e-22:182:85//Hs.28249:AA203733
 R-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//1.3e-108:566:94//Hs.78482:Y16270
- 25 R-NT2RP2003517//Platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)//4.9e-62:518:79//Hs.1976:M12783
 R-NT2RP2003522//ESTs//2.0e-97:462:99//Hs.24512:D60170
 R-NT2RP2003533//ESTs//4.4e-45:273:78//Hs.140225:AA704101
 R-NT2RP2003543//EST//1.0e-80:68//Hs.65646:F13684
- 30 R-NT2RP2003559//ESTs. Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.8e-58:316:94//Hs.28891:W72439
 R-NT2RP2003564//ESTs//3.2e-112:528:99//Hs.53940:N46696
 R-NT2RP2003581//ESTs//1.3e-88:506:93//Hs.16157:AA203719
 R-NT2RP2003596//ESTs. Weakly similar to No definition line found [C.elegans]//4.7e-101:495:98//Hs.34627:AA126463
- 35 R-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.7e-103:501:97//Hs.58488:U97067
 R-NT2RP2003629//EST//0.032:440:59//Hs.135297:AI038981
 R-NT2RP2003643//ESTs. Weakly similar to HYPOTHETICAL 14.1 KD PROTEIN IN MURZ-RPON INTERGENIC REGION [E.coli]//9.1e-62:359:92//Hs.12492:AA203188
- 40 R-NT2RP2003668//EST//9.4e-110:535:97//Hs.116279:AA628951
 R-NT2RP2003687//EST//5.9e-05:196:65//Hs.139064:AA135523
 R-NT2RP2003691//ESTs. Weakly similar to F59C6.9 [C.elegans]//1.0e-202:62//Hs.65539:AI148540
 R-NT2RP2003702//ESTs. Moderately similar to ovarian-specific protein [R.norvegicus]//4.3e-99:492:96//Hs.93332:AA811920
- 45 R-NT2RP2003704//ESTs//1.0e-155:63//Hs.104166:AA740246
 R-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.4e-47:265:93//Hs.78494:AB011097
 R-NT2RP2003713//EST//0.81:210:59//Hs.14551:T79401
 R-NT2RP2003714//ESTs//1.7e-99:495:96//Hs.158101:AI365003
- 50 R-ntnnnnnnnnnnnn//Human 19.8 kDa protein mRNA, complete cds//0.84:221:60//Hs.2384:U18914
 R-NT2RP2003737//ESTs. Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD [Caenorhabditis elegans]//2.4e-50:302:90//Hs.19196:W74577
 R-NT2RP2003751
 R-NT2RP2003760//ESTs//2.6e-101:548:93//Hs.115987:AA483808
- 55 R-NT2RP2003764//ESTs//8.2e-25:134:98//Hs.64036:AA127709
 R-NT2RP2003769//ESTs//1.7e-108:545:95//Hs.56847:AA541606
 R-NT2RP2003770//Homo sapiens sperm acrosomal protein mRNA, complete cds//6.0e-106:531:96//Hs.90436:AF047437

- R-NT2RP2003777//ESTs//2.6e-59:323.94//Hs.10101:AI381811
 R-NT2RP2003781//ESTs//2.0e-25:269.75//Hs.144951:N34836
 R-NT2RP2003793//ESTs//8.7e-94:466.97//Hs.93949:AA782955
 R-NT2RP2003840//ESTs//3.4e-97:533.93//Hs.16130:AA195077
 5 R-NT2RP2003857//H.sapiens mRNA for G9a//2.8e-23:351.65//Hs.75196:X69838
 R-NT2RP2003859//ESTs//3.0e-07:96.81//Hs.153262:AA551124
 R-NT2RP2003871//ESTs//1.9e-102:509.97//Hs.25726:AA430167
 R-NT2RP2003885//ESTs//1.0e-102:502.97//Hs.36353:AA702341
 R-NT2RP2003912//EST//1.2e-38:336.76//Hs.134975:AI094611
 10 R-NT2RP2003952//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//0.90:190.60//Hs.75875:U49278
 R-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//7.6e-116:568.97//Hs.35086:AB014458
 R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//3.6e-109:540.97//Hs.7302:AB007916
 15 R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//2.5e-115:568.96//Hs.7316:AB018347
 R-NT2RP2003984
 R-NT2RP2003986//ESTs//4.9e-36:272.82//Hs.158268:AA738087
 R-NT2RP2003988//ESTs, Weakly similar to reverse transcriptase [H.sapiens]//3.2e-110:519.99//Hs.36093:AI149968
 20 R-NT2RP2004014//ESTs//8.4e-102:483.99//Hs.22867:AI417478
 R-NT2RP2004041
 R-NT2RP2004042//ESTs//1.5e-105:466.97//Hs.7296:N29706
 R-ntnnnnnnnnnn//ESTs//1.4e-110:559.96//Hs.71916:AA219699
 25 R-NT2RP2004081//ESTs//3.7e-105:503.98//Hs.27542:AA977204
 R-NT2RP2004098//EST//1.7e-26:203.87//Hs.21897:R41461
 R-NT2RP2004124//ESTs//1.1e-83:435.95//Hs.43299:N23036
 R-NT2RP2004142//EST//1.3e-06:165.65//Hs.146742:AI147500
 R-NT2RP2004152//ESTs//7.0e-98:455.100//Hs.17731:AI342241
 30 R-NT2RP2004165//ESTs, Highly similar to DYNEIN BETA CHAIN, CILIARY [Anthracidaris crassispina]//1.0e-118:583.97//Hs.16520:AI224533
 R-NT2RP2004170//ESTs//6.7e-66:407.88//Hs.157138:AI348544
 R-NT2RP2004172//ESTs//1.5e-109:567.95//Hs.159091:AA033974
 R-NT2RP2004187//ESTs//3.6e-92:488.93//Hs.22954:W26589
 35 R-NT2RP2004194//ESTs//6.2e-114:585.95//Hs.18778:AA203167
 R-NT2RP2004196
 R-NT2RP2004207//ESTs//6.3e-102:488.98//Hs.22678:AA604756
 R-NT2RP2004226//ESTs//8.8e-18:252.71//Hs.11924:W26972
 R-NT2RP2004232//ESTs, Highly similar to protein kinase C mu [H.sapiens]//5.2e-105:499.98//Hs.143460:AA483305
 40 R-NT2RP2004239//ESTs//1.2e-16:171.80//Hs.16134:AA203116
 R-NT2RP2004240//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cds//3.4e-103:530.93//Hs.54900:AF039687
 R-NT2RP2004242//ESTs//1.3e-85:460.93//Hs.104535:AA211483
 45 R-NT2RP2004245//ESTs//6.4e-117:575.97//Hs.23744:AA035744
 R-NT2RP2004270//ESTs//1.0:95.69//Hs.141371:H92187
 R-NT2RP2004300//ESTs//4.4e-80:379.99//Hs.130874:AA905056
 R-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds//4.7e-110:544.96//Hs.61152:AF000416
 50 R-NT2RP2004321//ESTs//2.1e-18:104.99//Hs.107207:AA044788
 R-NT2RP2004339//EST//1.4e-47:309.86//Hs.161917:AA483223
 R-NT2RP2004347
 R-NT2RP2004364//ESTs//1.1e-113:566.96//Hs.25880:AI268173
 R-NT2RP2004365//ESTs//0.022:271.62//Hs.38897:AI129310
 55 R-NT2RP2004366//ESTs//9.5e-71:335.100//Hs.91867:AI218624
 R-NT2RP2004373//ESTs//4.2e-25:172.87//Hs.83243:N32192
 R-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.4e-11:108.82//Hs.30490:AA146916

R-NT2RP2004392//ESTs//3.4e-81:427.94//Hs.5827:AA581646
 R-NT2RP2004396//EST//5.6e-06:100.77//Hs.138623:H92473
 R-NT2RP2004399//EST//0.98:337.59//Hs.118446:N67900
 R-NT2RP2004400//ESTs//2.1e-90:422.100//Hs.152460:AA602921
 5 R-NT2RP2004412//ESTs//1.4e-105:503.98//Hs.15929:AA403121
 R-NT2RP2004425//EST//0.00017:225.60//Hs.146935:AI168124
 R-NT2RP2004476//ESTs//1.4e-88:477.94//Hs.4859:N29695
 R-NT2RP2004490//Homo sapiens 3-phosphoinositide dependent protein kinase-1 (PKD1) mRNA, complete cds//
 8.6e-34:143.98//Hs.154729:AF017995
 10 R-NT2RP2004512//ESTs//2.6e-91:426.100//Hs.94133:AI270700
 R-NT2RP2004523//ESTs//1.6e-74:377.97//Hs.14217:R61320
 R-NT2RP2004538//Thromboxane A2 receptor//1.4e-45:279.89//Hs.89887:D38081
 R-NT2RP2004551//ESTs//0.47:147.66//Hs.131519:AI024347
 R-NT2RP2004568//ESTs//1.3e-107:567.94//Hs.65234:AA195470
 15 R-NT2RP2004580//ESTs//5.9e-29:156.98//Hs.147801:AI221661
 R-NT2RP2004587//ESTs//1.0e-102:495.97//Hs.91662:AA781126
 R-NT2RP2004594//ESTs//4.1e-56:298.95//Hs.24641:AA954666
 R-NT2RP2004600//ESTs//4.8e-67:374.93//Hs.49762:N69862
 R-NT2RP2004602//ESTs. Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-07:
 20 149.76//Hs.12845:N28835
 R-NT2RP2004614//ESTs//1.0e-111:557.96//Hs.37892:N53497
 R-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//2.4e-118:587.96//Hs.5198:AJ006291
 R-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds//5.9e-107:520.96//Hs.29956:
 AB007929
 25 R-NT2RP2004675//ESTs//2.7e-82:407.97//Hs.116113:F18930
 R-NT2RP2004681//NUCLEOLIN//0.34:387.58//Hs.79110:M60858
 R-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds//5.0e-120:600.96//Hs.154919:
 AB014525
 R-NT2RP2004709//ESTs//1.1e-106:511.98//Hs.38034:AI149793
 30 R-NT2RP2004710//ESTs//9.9e-87:477.93//Hs.6834:AA203433
 R-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds//1.3e-118:594.96//Hs.4236:
 AB007947
 R-NT2RP2004743//ESTs//2.1e-48:327.88//Hs.43635:AA447015
 R-NT2RP2004767//EST//4.0e-57:328.81//Hs.142796:N51423
 35 R-NT2RP2004775//ESTs//9.4e-60:326.94//Hs.115339:AA136774
 R-NT2RP2004791//ESTs//3.2e-82:367.96//Hs.141911:N64013
 R-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//
 8.0e-116:564.96//Hs.40820:AF058953
 40 R-NT2RP2004802//ESTs//6.5e-111:586.94//Hs.90375:W74579
 R-NT2RP2004816//Homo sapiens H beta 16 homolog mRNA, complete cds//8.7e-120:584.97//Hs.67052:
 AF054179
 R-NT2RP2004841//EST//3.8e-31:323.74//Hs.147714:AI219906
 R-NT2RP2004861//EST//0.92:147.63//Hs.23064:R20803
 R-NT2RP2004897//ESTs//1.7e-46:390.80//Hs.139225:H96567
 45 R-NT2RP2004936//EST//0.97:176.63//Hs.137436:AA280529
 R-ntnnnnnnnnnn//ESTs//0.059:137.64//Hs.144109:AI345543
 R-NT2RP2004961//ESTs//1.8e-87:409.100//Hs.138297:AA781941
 R-NT2RP2004962//ESTs//0.0021:292.59//Hs.145917:AI275458
 R-NT2RP2004967//Human mRNA for KIAA0118 gene, partial cds//7.4e-51:506.75//Hs.154326:D42087
 50 R-NT2RP2004978//ESTs//0.95:138.63//Hs.13619:W93496
 R-NT2RP2004982//ESTs//7.8e-95:468.97//Hs.22545:R43910
 R-NT2RP2004985
 R-NT2RP2004999//ESTs//2.9e-94:450.98//Hs.128766:AI419902
 R-NT2RP2005000
 55 R-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//9.6e-113:577.95//Hs.155972:
 AB014515
 R-NT2RP2005003//EST//1.3e-75:387.96//Hs.140843:R42235
 R-ntnnnnnnnnnn//Homo sapiens SEC63 (SEC63) mRNA, complete cds//3.1e-116:568.97//Hs.31575:AF100141

- R-NT2RP2005018//ESTs//7.5e-46:280.90//Hs.126857:AA932161
 R-NT2RP2005020//ESTs//1.6e-105:554.94//Hs.14846:AA148507
 R-NT2RP2005031//EST//3.1e-79:379.99//Hs.139709:AA227887
 R-NT2RP2005037//ESTs//5.3e-102:551.93//Hs.26516:AA195220
 5 R-NT2RP2005038//ESTs//5.8e-101:566.92//Hs.46964:N49757
 R-NT2RP2005108
 R-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//2.7e-105:518.97//Hs.22616:AB014564
 R-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//4.6e-69:464.85//Hs.100555:X98743
 10 R-NT2RP2005139//ESTs//1.0e-108:545.95//Hs.21006:AA523383
 R-NT2RP2005140//ESTs//4.3e-90:422.99//Hs.62180:AI341261
 R-NT2RP2005144//ESTs//0.91:162.62//Hs.52399:AI075744
 R-NT2RP2005147//ESTs//4.6e-100:502.96//Hs.27931:AA633438
 15 R-NT2RP2005159//ESTs//7.5e-105:533.95//Hs.109819:AI357582
 R-NT2RP2005162//ESTs//6.6e-83:419.96//Hs.113998:U50648
 R-NT2RP2005168//Homo sapiens mRNA for EIB-55kDa-associated protein//2.4e-101:513.95//Hs.155218:AJ007509
 R-NT2RP2005204//ESTs, Weakly similar to UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG [H.sapiens]//1.9e-115:577.96//Hs.7600:H98166
 20 R-NT2RP2005227//Homo sapiens UM protein mRNA, complete cds//1.0e-45:359.82//Hs.154103:AF061258
 R-NT2RP2005239//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//1.0e-47:245.97//Hs.21090:AA418587
 R-NT2RP2005254//ESTs//3.3e-111:581.94//Hs.22549:AA524503
 25 R-NT2RP2005270//ESTs, Highly similar to HYPOTHETICAL 67.6 KD PROTEIN ZK637.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.1e-79:412.95//Hs.23047:N66596
 R-NT2RP2005276//ESTs//4.6e-85:426.96//Hs.24550:AA316272
 R-NT2RP2005287//ESTs//1.7e-109:565.94//Hs.61976:AI279001
 R-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.4e-125:594.98//Hs.27007:AF060219
 30 R-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//4.9e-112:545.96//Hs.44766:AJ007590
 R-NT2RP2005293//ESTs//5.1e-116:538.99//Hs.62180:AI341261
 R-NT2RP2005315//ESTs//1.4e-82:415.97//Hs.155829:AA018338
 R-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds//2.5e-45:272.91//Hs.1569:U11701
 35 R-NT2RP2005336//ESTs//1.9e-93:444.99//Hs.110966:AA151699
 R-NT2RP2005344//Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA, complete cds//0.011:463:58//Hs.150926:AF017445
 R-NT2RP2005354//ESTs//7.2e-22:148.91//Hs.153783:H14544
 40 R-NT2RP2005360//ESTs//0.048:225.60//Hs.7602:AA099247
 R-NT2RP2005393//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.9e-41:248.82//Hs.93121:AB018304
 R-NT2RP2005407//ESTs, Weakly similar to OSH1 PROTEIN [Saccharomyces cerevisiae]//2.5e-75:461.88//Hs.70849:AA121697
 R-NT2RP2005436//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II [C.elegans]//8.1e-96:491.95//Hs.7194:AI185631
 45 R-NT2RP2005441//ESTs//1.1e-110:548.96//Hs.5209:AA780068
 R-NT2RP2005453//ESTs//0.94:352.58//Hs.25870:H14423
 R-NT2RP2005457//ESTs//2.1e-46:236.97//Hs.19522:AA975096
 R-NT2RP2005464//ESTs//1.8e-72:349.99//Hs.44045:N51307
 50 R-NT2RP2005465//ESTs//0.0058:322.58//Hs.127009:AI378936
 R-NT2RP2005472//ESTs//0.47:309.60//Hs.144838:AI222019
 R-NT2RP2005476//ESTs//5.1e-40:205.9811//Hs.101577:AI168526
 R-NT2RP2005490//ESTs//L3e-70:364.96//Hs.134382:AA083573
 R-NT2RP2005491//EST//0.012:220.60//Hs.144448:AA812455
 55 R-NT2RP2005495//ESTs//1.2e-86:501.91//Hs.99445:R93540
 R-NT2RP2005496//ESTs//3.2e-34:263.81//Hs.70279:AA757426
 R-NT2RP2005498//ESTs, Highly similar to PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, NEURONAL ISOFORM [Oryctolagus cuniculus]//2.3e-45:284.88//Hs.85752:AI138993

R-NT2RP2005501//ESTs//2.5e-84:404:98//Hs.143812:AI141755
 R-NT2RP2005509//ESTs. Highly similar to HYPOTHETICAL 37.2 KD PROTEIN C12C2.09C IN CHROMOSOME
 I [Schizosaccharomyces pombe]//8.2e-36:215:92//Hs.5298:AA725071
 R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//3.2e-110:
 570:9411Hs.119023:AF092563
 R-NT2RP2005525//ESTs. Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.3e-84:
 433:95/Hs.36942:AA524535
 R-NT2RP2005531//EST//0.98:64:70//Hs.146573:AI139856
 R-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.8e-108:560:94//Hs.159597:
 AJ012449
 R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.7e-115:583:96//Hs.62515:
 AB007963
 R-NT2RP2005549//EST//0.61:111:62//Hs.147482:AI215572
 R-NT2RP2005555//ESTs//6.6e-108:507:99//Hs.68613:AI357567
 R-NT2RP2005557//ESTs//3.1e-105:495:99//Hs.105985:AA885169
 R-NT2RP2005581//ESTs//1.7e-79:445:92//Hs.138152:H03240
 R-NT2RP2005600//ESTs//1.3e-38:192:100//Hs.48329:W92733
 R-NT2RP2005605//ESTs//7.6e-87:409:99//Hs.45005:AA975060
 R-NT2RP2005620//ESTs//2.9e-96:463:97//Hs.7407:AI376788
 R-NT2RP2005622//ESTs//1.8e-104:497:98//Hs.22595:AA394229
 R-NT2RP2005637//EST//2.5e-20:163:71//Hs.161164:AI418211
 R-NT2RP2005640//ESTs//5.0e-99:473:98//Hs.23467:AA708740
 R-NT2RP2005645//ESTs//9.5e-23:231:77//Hs.5534:AA195173
 R-NT2RP2005651//ESTs. Highly similar to XF1N PROTEIN [Xenopus laevis]//2.9e-103:525:96//Hs.70589:
 AA868470
 R-NT2RP2005654//Insulin-like growth factor binding protein 2//0.94:223:60//Hs.162:X16302
 R-NT2RP2005669//Homo sapiens nitrilase 1 (VIII) mRNA, complete cds//2.7e-14:87:100//Hs.146406:AF069887
 R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//5.8e-91:434:98//
 Hs.25664:AF089814
 R-NT2RP2005683//ESTs//1.5e-98:494:96//Hs.22595:AA394229
 R-NT2RP2005690//ESTs//4.8e-43:286:86//Hs.150727:AI292236
 R-NT2RP2005694//EST//3.1e-82:386:100//Hs.149391:AI273643
 R-NT2RP2005701//ESTs. Highly similar to BUTYROPOLIN PRECURSOR [Bos taurus]//2.8e-68:376:93//Hs.
 9095:AA532630
 R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//1.3e-105:503:98//Hs.61638:
 AB018342
 R-NT2RP2005719//ESTs. Weakly similar to GPI-anchored protein p137 precursor [H.sapiens]//5.4e-105:500:98//
 Hs.14298:AI417523
 R-NT2RP2005722//EST//6.5e-76:395:94//Hs.142150:AA223982
 R-NT2RP2005723//ESTs//1.5e-84:452:93//Hs.91753:R44455
 R-NT2RP2005726//ESTs//3.5e-64:500:82//Hs.100526:AI223153
 R-NT2RP2005741//ESTs//4.7e-60:333:93//Hs.107242:R40258
 R-NT2RP2005748//ESTs//3.4e-102:498:97//Hs.82660:N78064
 R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//4.3e-42:223:96//
 Hs.159651:AF068868
 R-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//1.2e-104:494:98//Hs.
 26285:AF082516
 R-NT2RP2005763//ESTs//1.1e-97:456:99//Hs.65412:AI362163
 R-NT2RP2005767//ESTs//8.0e-38:204:96//Hs.18460:AA193463
 R-NT2RP2005773//ESTs. Highly similar to PYRROLINE-5-CARBOXYLATE REDUCTASE [Homo sapiens]//5.4e-
 112:559:96//Hs.14214:AI189379
 R-NT2RP2005775//ESTs. Highly similar to NEUROLYSIN PRECURSOR [Sus scrofa]//3.0e-108:544:96//Hs.
 22151:AI214321
 R-NT2RP2005781//ESTs//1.7e-43:217:99//Hs.144391:AA365664
 R-NT2RP2005784//EST//0.0071:217:60//Hs.117332:AA699724
 R-NT2RP2005804//ESTs//8.8e-107:512:98//Hs.15496:W44398
 R-NT2RP2005812//ESTs//9.0e-76:359:99//Hs.113937:AI298746
 R-NT2RP2005815//ESTs//5.5e-76:363:99//Hs.136230:AA594981

- R-NT2RP2005835//ESTs//1.5e-100.541.94//Hs.86813:N25122
 R-NT2RP2005841//ESTs//2.8e-105.556.92//Hs.69993:AA628403
 R-NT2RP2005853//EST//2.0e-13.219.70//Hs.134016:AI076062
 R-NT2RP2005857//ESTs//1.0e-115.576.96//Hs.30663:AI338462
 5 R-NT2RP2005859//ESTs//7.3e-116.571.97//Hs.85986:AA195105
 R-NT2RP2005868//EST//0.00023.320.61//Hs.149689:AI284133
 R-NT2RP2005890//ESTs//1.0e-96.466.98//Hs.122579:AA766315
 R-NT2RP2005901//ESTs//8.3e-116.548.98//Hs.66296:AI125268
 R-NT2RP2005908//ESTs, Weakly similar to weakly similar to gastrula zinc finger protein [C.elegans]//2.4e-73.397:
 10 94//Hs.16667:T92427
 R-NT2RP2005933//ESTs, Highly similar to nucleoporin p54 [R.norvegicus]//2.8e-114.560.97//Hs.9082:AA873170
 R-NT2RP2005942//ESTs//5.6e-117.582.96//Hs.146123:AI338419
 R-NT2RP2005980//ESTs//6.9e-101.478.98//Hs.43145:AA776988
 R-NT2RP2006023//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.5e-51.398.80//Hs.113283:AF018080
 15 R-NT2RP2006038//ESTs//0.025.284.59//Hs.97852:AA404347
 R-NT2RP2006043//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II [C.elegans]//1.2e-50.278.94//Hs.7194:AI185631
 R-NT2RP2006052//ESTs//5.0e-52.272.95//Hs.99545:AA461492
 R-NT2RP2006069//ESTs//1.8e-90.495.93//Hs.43654:AA522714
 20 R-NT2RP2006071//ESTs//1.5e-38.218.94//Hs.107882:W72093
 R-NT2RP2006098//ESTs//2.9e-105.540.95//Hs.26860:N56918
 R-NT2RP2006100//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.031.254.62//
 Hs.46440:U21943
 R-NT2RP2006103//ESTs//1.5e-86.416.98//Hs.152114:AA401365
 25 R-NT2RP2006141//ESTs//5.3e-88.432.98//Hs.77480:AA100522
 R-NT2RP2006166//Homo sapiens LIM protein mRNA, complete cds//2.8e-17.255.72//Hs.154103:AF061258
 R-NT2RP2006184//ESTs//8.4e-101.487.98//Hs.58009:W69435
 R-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//6.1e-110.553.95//Hs.109299:
 AB014554
 30 R-NT2RP2006196//Human clone 23960 mRNA sequence//0.0037.48.100//Hs.151293:U79276
 R-NT2RP2006200//ESTs//6.5e-77.398.96//Hs.163953:R01398
 R-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//1.2e-94.532.90//Hs.153910:X96484
 R-NT2RP2006237//ESTs//1.2e-57.305.95//Hs.86149:AI341312
 R-NT2RP2006238//ESTs, Highly similar to rA8 [R.norvegicus]//1.5e-29.183.91//Hs.4048:AA404253
 35 R-NT2RP2006258//ESTs//3.2e-87.462.94//Hs.141556:N49928
 R-NT2RP2006261//ESTs//3.4e-57.3.26.92//Hs.22523:W02999
 R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//4.7e-96.481.97//Hs.3404:AF035262
 R-NT2RP2006320//EST//3.4e-21.335.65//Hs.141603:N66015
 R-NT2RP2006321//ESTs, Moderately similar to karyopherin beta 3 [H.sapiens]//1.9e-89.460.96//Hs.21889:
 40 N78664
 R-NT2RP2006323//ESTs//3.5e-91.439.98//Hs.61697:AI081771
 R-NT2RP2006333//ESTs//4.9e-38.301.82//Hs.155999:AA196412
 R-NT2RP2006334//EST//3.1e-45.264.91//Hs.149599:AI282321
 R-NT2RP2006365//ESTs//2.9e-81.417.95//Hs.11814:W44411
 45 R-NT2RP2006393//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//3.9e-48.403:
 77//Hs.1361:M55053
 R-NT2RP2006436//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.4e-27.155.76//Hs.
 115325:D84488
 R-NT2RP2006441//ESTs//6.0e-108.529.97//Hs.101282:N45092
 50 R-NT2RP2006454//ESTs//9.2e-20.110.99//Hs.144687:AI341146
 R-NT2RP2006456//ESTs//7.1e-91.508.92//Hs.12488:W63595
 R-NT2RP2006464//Homo sapiens mRNA for AND-1 protein//2.1e-109.524.97//Hs.72160:AJ006266
 R-NT2RP2006467//EST//0.9e-140.61//Hs.146958:AI174478
 R-NT2RP2006472//ESTs//3.3e-92.473.95//Hs.29216:AA916679
 55 R-NT2RP2006534//ESTs//1.2e-83.394.99//Hs.162116:AA524947
 R-NT2RP2006554//ESTs//1.0e-87.460.95//Hs.47095:AA181474
 R-NT2RP2006565//ESTs//3.2e-24.129.100//Hs.13499:AI299886
 R-NT2RP2006571//ESTs//2.6e-56.306.94//Hs.98370:AA316622

- R-nnnnnnnnnnn/ESTs//2.0e-112:533.98//Hs.18685:AI393829
 R-NT2RP2006598//ESTs, Weakly similar to retinoid X receptor interacting protein [M.musculus]/4.1e-109:542:97//Hs.7889:AI337112
 R-NT2RP3000002//ESTs//1.3e-08:399.59//Hs.126044:AI301598
 5 R-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21)/1.9e-116:560:97//Hs.6764:AJ011972
 R-NT2RP3000046//Small inducible cytokine A5 (RANTES)/1.9e-57:312.85//Hs.155464:AF088219
 R-NT2RP3000047//EST//0.91:130.66//Hs.140208:AA702213
 R-NT2RP3000050//ESTs, Weakly similar to putative p150 [H.sapiens]/3.1e-41:249:90//Hs.156155:AI222202
 10 R-NT2RP3000055//ESTs//2.4e-19:146.86//Hs.160497:AI255095
 R-NT2RP3000072//ESTs//2.2e-82:424.96//Hs.21542:N49574
 R-NT2RP3000080//ESTs//2.1e-29:186.89//Hs.153372:AA424029
 R-NT2RP3000085//ESTs//4.5e-101:482.98//Hs.47649:AA838715
 R-NT2RP3000109//ESTs//9.5e-97:455.99//Hs.17731:AI342241
 15 R-NT2RP3000134//EST//4.7e-106:497.99//Hs.125531:AA884000
 R-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.2e-116:578:96//Hs.13273:AB011164
 R-NT2RP3000149//ESTs//7.7e-62:361.90//Hs.6649:N93418
 R-NT2RP3000186
 20 R-NT2RP3000197//ESTs//1.5e-75:436.91//Hs.140931:R51882
 R-NT2RP3000207//ESTs//1.3e-98:468.98//Hs.126908:AA933091
 R-NT2RP3000220//ESTs//2.2e-27:144.99//Hs.108961:R61306
 R-NT2RP3000233//EST//1.7e-87:368.99//Hs.49075:N64817
 R-NT2RP3000235//ESTs//0.43:82.74//Hs.132828:AI032819
 25 R-NT2RP3000247//EST//2.2e-97:459.99//Hs.127928:AA969239
 R-NT2RP3000251
 R-NT2RP3000252//ESTs, Weakly similar to Lpg15p [S.cerevisiae]/2.0e-108:532:97//Hs.111086:AI379177
 R-NT2RP3000255//EST//0.67:93.67//Hs.120579:AA743073
 R-NT2RP3000267//ESTs//8.5e-108:542.95//Hs.24984:AA534446
 30 R-NT2RP3000299//ESTs, Weakly similar to enhancer of filamentation 1 [H.sapiens]/3.6e-103:516:96//Hs.4894:AI191323
 R-NT2RP3000312//ESTs//1.3e-100:493.97//Hs.29379:AI094117
 R-NT2RP3000320//ESTs//3.2e-95:538.91//Hs.118793:AA192438
 R-NT2RP3000324
 35 R-NT2RP3000333//ESTs//6.0e-39:194.100//Hs.119238:AA476267
 R-NT2RP3000341//ESTs//0.51:251.61//Hs.94090:AA777689
 R-NT2RP3000348//EST//1.8e-80:389.98//Hs.145944:AI276225
 R-NT2RP3000350//ESTs, Weakly similar to Lpg15p [S.cerevisiae]/3.1e-110:556:96//Hs.111086:AI379177
 R-NT2RP3000359//EST//4.9e-61:340.92//Hs.126495:AA913741
 40 R-NT2RP3000361//ESTs, Weakly similar to PRE-MRNA SPLICING FACTOR PRP6 [S.cerevisiae]/4.8e-91:439:97//Hs.31334:AI144423
 R-NT2RP3000366//EST//0.20:392.57//Hs.149652:AI283303
 R-NT2RP3000397//EST//8.7e-26:150.94//Hs.124617:AA855106
 R-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds//4.2e-111:529:98//Hs.28307:AF071185
 45 R-NT2RP3000418//EST//3.3e-09:202.67//Hs.117189:AA682947
 R-NT2RP3000433
 R-NT2RP3000439//ESTs//3.1e-79:426.92//Hs.26548:W26340
 R-NT2RP3000441//ESTs//6.3e-84:420.97//Hs.137482:AA421254
 50 R-NT2RP3000449//ESTs//4.9e-93:435.99//Hs.54617:AI379102
 R-NT2RP3000451//ESTs//2.3e-89:439.97//Hs.9196:AA748492
 R-NT2RP3000456//Homo Sapiens (clone B3B3E13) chromosome 4p16.3 DNA fragment//1.8e-23:347:70//Hs.114963:L34408
 R-NT2RP3000484//Heparin cofactor II//0.98:166.62//Hs.1478:M58600
 55 R-NT2RP3000487//ESTs//0.012:384.60//Hs.86684:AA885141
 R-NT2RP3000512//Homeo box B3//2.0e-69:377.93//Hs.49931:X16667
 R-NT2RP3000526//ESTs//1.6e-91:432.99//Hs.38042:AA187151
 R-NT2RP3000527//ESTs//1.2e-100:518.94//Hs.104557:AI078161

- R-NT2RP3000531//ESTs, Weakly similar to TH1 protein [D.melanogaster]/0.95:85.71//Hs.5184:AA709151
 R-NT2RP3000542//ESTs/2.6e-53:375.84//Hs.44158:N30180
 R-NT2RP3000561//EST//1.1e-13:170.75//Hs.148421:AI198036
 R-NT2RP3000562//Human mRNA for KIAA0233 gene, complete cds/0.97:141.68//Hs.79077:D87071
 5 R-NT2RP3000578//ESTs/2.6e-68:324:100//Hs.5445:AA779447
 R-NT2RP3000582//ESTs/2.1e-25:131:80//Hs.152465:AA563785
 R-NT2RP3000584//ESTs/1.8e-97:460.99//Hs.120698:AI241511
 R-NT2RP3000590//ESTs/2.0e-97:453:100//Hs.105355:AA953817
 R-NT2RP3000592//ESTs/2.8e-91:432.99//Hs.144304:AI190916
 10 R-NNNNNNNNNN//Human mRNA for KIAA0314 gene, partial cds/1.5e-09:447:58//Hs.155045:AB002312
 R-NT2RP3000599//ESTs/3.8e-93:437.99//Hs.23971:AA829880
 R-NT2RP3000605//ESTs/4.2e-111:554:96//Hs.40780:AA422049
 R-NT2RP3000622//ESTs/2.0e-100:473.99//Hs.11387:AI127394
 R-NT2RP3000624//ESTs, Weakly similar to KIAA0256 [H.sapiens]/5.4e-115:545.98//Hs.4857:AI090739
 15 R-NT2RP3000628//Homo sapiens mRNA for KIAA0772 protein, complete cds/4.3e-49:397.80//Hs.15519:AB018315
 R-NT2RP3000632//ESTs, Moderately similar to cyclin-selective ubiquitin carrier protein [H.sapiens]/6.3e-92:434:99//Hs.152517:AA719022
 R-NT2RP3000644//ESTs/1.0e-44:306.84//Hs.155498:W27084
 20 R-NT2RP3000661//ESTs/3.1e-95:470.97//Hs.126069:W76185
 R-NT2RP3000665//ESTs/3.3e-95:503.94//Hs.34313:W81185
 R-NT2RP3000685//ESTs/2.7e-99:515.94//Hs.9711:R60873
 R-NT2RP3000690//ESTs/3.3e-88:414.99//Hs.1465.89:AI085578
 R-NT2RP3000736
 25 R-NT2RP3000742//ESTs, Highly similar to 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODI-
 ESTERASE DELTA 1 [Rattus norvegicus]/1.8e-07:114.75//Hs.136065:W21960
 R-NT2RP3000753//ESTs/3.1e-99:461:100//Hs.150901:AI310447
 R-NT2RP3000759//ESTs/2.0e-74:384.95//Hs.104222:AA207243
 R-NT2RP3000815//ESTs/8.5e-97:455.99//Hs.158897:AI378583
 30 R-NT2RP3000825//EST//0.0089:343.59//Hs.42897:N20810
 R-NT2RP3000826//EST//3.4e-33:342.74//Hs.162236:AA551582
 R-NT2RP3000836//ESTs/6.8e-24:181.84//Hs.134464:AI151081
 R-NT2RP3000841//ESTs/4.5e-93:491.93//Hs.23618:H98082
 R-NT2RP3000845//ESTs/2.4e-88:473.93//Hs.8312:AA813022
 35 R-NT2RP3000847//ESTs/9.3e-89:460.95//Hs.154106:AI051657
 R-NT2RP3000850
 R-NT2RP3000852//Fibrillin 2//0.55:237.63//Hs.79432:U03272
 R-NT2RP3000859//ESTs/1.4e-96:509.94//Hs.7187:AA576895
 R-NT2RP3000865//EST//4.8e-23:461.66//Hs.162088:AA505741
 40 R-NT2RP3000868//ESTs/5.4e-78:430.93//Hs.102796:N70837
 R-NT2RP3000869//ESTs/8.5e-77:397.94//Hs.84848:AI014673
 R-NT2RP3000875//Mevalonate kinase/3.8e-78:531.84//Hs.75138:M88468
 R-NT2RP3000901//ESTs/2.1e-95:466.97//Hs.10647:AA428217
 R-NT2RP3000904//ESTs/1.6e-79:380.99//Hs.100850:AA479385
 45 R-NT2RP3000917//ESTs, Highly similar to mouse Dhml protein [M.musculus]/9.5e-113:566.96//Hs.5900:AA035728
 R-NT2RP3000919
 R-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A/1.5e-25:375.71//Hs.2953:X84407
 R-NT2RP3000980//ESTs/3.3e-72:364.96//Hs.9536:AA114178
 50 R-NT2RP3000994//ESTs/3.5e-111:537.97//Hs.21146:AA683542
 R-NT2RP3001004//ESTs/9.6e-91:456.96//Hs.58974:W87405
 R-NT2RP3001007//ESTs/6.7e-89:482.97//Hs.117737:AI088029
 R-NT2RP3001055//ESTs/0.0012:294.60//Hs.66479:AA863044
 R-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN HF.12 [Homo sapiens]/5.6e-102:486.99//Hs.145956:AA007349
 55 R-NT2RP3001081//Retinal pigment epithelium-specific protein (65kD)/0.0012:447.58//Hs.2133:U18991
 R-NT2RP3001084//ESTs/4.3e-102:528.96//Hs.25277:W87874
 R-NT2RP3001096//ESTs/1.1e-110:540.96//Hs.42824:AA873182

- R-NT2RP3001107//ESTs//7.6e-100:478:98//Hs.99669:AA287832
 R-nnnnnnnnnnnn/DNA polymerase gamma//0.0014:50:100//Hs.80961:U60325
 R-NT2RP300111//ESTs, Weakly similar to Trf-proximal protein [D.melanogaster]//3.2e-104:543:95//Hs.93796: C06063
- 5 R-NT2RP3001113//ESTs//3.3e-100:467:99//Hs.97757:AA401575
 R-NT2RP3001115//Oxytocin receptor//7.9e-30:505:67//Hs.2820:X64878
 R-NT2RP3001116//ESTs//4.6e-41:229:96//Hs.58412:W74779
 R-NT2RP3001119//ESTs//6.9e-88:478:92//Hs.19469:AA203180
 R-NT2RP3001120//ESTs//3.1e-82:430:93//Hs.110956:AI190166
- 10 R-NT2RP3001126//ESTs//4.4e-52:264:96//Hs.25264:R78188
 R-NT2RP3001133//ESTs//4.7e-105:541:94//Hs.73239:AA573761
 R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//2.6e-115:549:97//Hs.5378:AB018305
 R-NT2RP3001147//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster] //9.6e-113:552:97//Hs.23900:U82984
- 15 R-NT2RP3001150//ESTs//2.9e-90:444:97//Hs.99601:AA760717
 R-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//9.4e-118:563:98//Hs.72160:AJ006266
 R-NT2RP3001176//ESTs//1.8e-110:534:98//Hs.58650:AI074460
 R-NT2RP3001214//ESTs//1.7e-109:545:96//Hs.24481:AA573139
 R-NT2RP3001216//EST//0.00098:128:66//Hs.160493:AI254963
- 20 R-NT2RP3001221//EST//0.010:106:66//Hs.147774:AI221196
 R-NT2RP3001232//ESTs//1.5e-101:518:94//Hs.21630:AA778399
 R-NT2RP3001236//ESTs, Highly similar to KIAA0377 [H.sapiens]//2.8e-89:462:95//Hs.116793:AA779588
 R-NT2RP3001239//ESTs, Moderately similar to NEURAXIN [Rattus norvegicus]//5.2e-82:466:91//Hs.66048: AA524416
- 25 R-NT2RP3001245//EST//0.53:237:62//Hs.161131:AI417631
 R-NT2RP3001253//ESTs//1.7e-105:535:96//Hs.42315:AI222997
 R-NT2RP3001260//EST//0.16:144:62//Hs.126856:AA932135
 R-NT2RP3001268//Human Aac11(aac11) mRNA, complete cds//0.12:494:59//Hs.151031:U83857
 R-NT2RP3001272//ESTs//1.4e-92:436:99//Hs.149831:AI383965
- 30 R-NT2RP3001274//ESTs//3.9e-81:424:95//Hs.1113184:N25651
 R-NT2RP3001281//EST//3.1e-60:298:98//Hs.149230:AI247332
 R-NT2RP3001307//EST//0.42:215:62//Hs.126165:AA868691
 R-NT2RP3001318//ESTs//4.1e-74:363:97//Hs.130832:H92571
 R-NT2RP3001325//ESTs//1.7e-106:534:96//Hs.21214:H88989
- 35 R-NT2RP3001338//Human protein tyrosine phosphatase sigma mRNA, complete cds//0.22:199:63//Hs.159534: U35234
 R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//3.9e-114:566:96//Hs.18586: AB007920
- 40 R-NT2RP3001340//ESTs//1.1e-72:411:92//Hs.21135:W81653
 R-NT2RP3001355//ESTs//9.0e-103:521:95//Hs.99486:AA776798
 R-NT2RP3001374//ESTs//2.7e-82:395:98//Hs.117102:AA993090
 R-NT2RP3001383//ESTs//3.6e-10:118:78//Hs.111055:AA169778
 R-NT2RP3001384//ESTs, Weakly similar to A-kinase anchor protein 95, AKAP95 [R.norvegicus]//5.7e-92:522:90// Hs.96200:AA218942
- 45 R-NT2RP3001392//ESTs//5.9e-62:296:100//Hs.125034:AA907375
 R-NT2RP3001396//ESTs//3.7e-111:528:98//Hs.22612:AA152232
 R-NT2RP3001398//ESTs//2.6e-94:449:99//Hs.146332:AI276628
 R-NT2RP3001399//ESTs//2.6e-82:401:97//Hs.7932:AI041186
 R-NT2RP3001407//ESTs//2.2e-101:488:97//Hs.71573:AA498898
- 50 R-NT2RP3001420//EST//7.4e-44:394:79//Hs.137041:AA877817
 R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequence//3.6e-106:550:94//Hs.6957:AF052158
 R-NT2RP3001427//ESTs//1.3e-87:374:97//Hs.5457:H05692
 R-nnnnnnnnnnnn/Neurotrophic tyrosine kinase, receptor, type 1//4.7e-96:533:91//Hs.85844:X66397
 R-NT2RP3001432//ESTs//1.9e-102:523:95//Hs.132978:AI041374
- 55 R-NT2RP3001447//ESTs, Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//5.1e-101:482:98//Hs.124135:AA910560
 R-NT2RP3001449//ESTs//2.2e-99:502:96//Hs.7834:N45994
 R-NT2RP3001453//Small inducible cytokine A5 (RANTES)//8.1e-45:295:85//Hs.155464:AF088219

- R-NT2RP3001457//ESTs//1.5e-52:256.99//Hs.117982:AA644658
 R-NT2RP3001459//ESTs//3.4e-62:299.99//Hs.146098:AA167280
 R-NT2RP3001472//ESTs//4.8e-108:540:96//Hs.69594:N37009
 R-NT2RP3001490//ESTs//3.5e-91:549:88//Hs.6606:AA211783
 5 R-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds//1.4e-61:338:93//Hs.519:U13395
 R-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds//
 6.8e-112:549:9711Hs.28285:AF064801
 R-NT2RP3001527//ESTs//4.4e-105:543:95//Hs.158761:AA631047
 R-NT2RP3001529//Homo sapiens tapasin (NGS-17) mRNA, complete cds//7.9e-59:427:83//Hs.5247:AF029750
 10 R-NT2RP3001538//ESTs//1.6e-94:521:92//Hs.6846:AA209463
 R-NT2RP3001554//ESTs. Moderately similar to NEURAXIN [Rattus norvegicus]//2.8e-76:392:95//Hs.66048:
 AA524416
 R-NT2RP3001580//ESTs//3.7e-82:398:98//Hs.23490:N49477
 R-NT2RP3001587//Homa sapiens mRNA for HRIHFB2115, partial cds//1.8e-09:86:88//Hs.4311:AB015337
 15 R-NT2RP3001589//ESTs//0.0029:243:62//Hs.158924:AA605194
 R-NT2RP3001607//EST//0.00096:76:78//Hs.140319:AA748328
 R-NT2RP3001608//ESTs//3.8e-105:525:96//Hs.144655:AI279798
 R-NT2RP3001621//ESTs//3.3e-108:535:97//Hs.47378:AI193598
 R-NT2RP3001629
 20 R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//2.7e-109:541:96//Hs.9899:AF099149
 R-NT2RP3001642//ESTs//6.0e-105:525:96//Hs.3376:AA915989
 R-NT2RP3001646//ESTs//4.8e-95:523:92//Hs.64036:AA127709
 R-NT2RP3001671//ESTs//0.0013:367:60//Hs.106090:AA457030
 R-NT2RP3001672//ESTs//3.4e-37:191:98//Hs.57475:AI382189
 25 R-NT2RP3001676//ESTs//1.5e-81:408:97//Hs.142547:N67648
 R-NT2RP3001678//ESTs//4.3e-85:405:99//Hs.121915:AI268225
 R-NT2RP3001679//ESTs//3.4e-100:545:93//Hs.5943:AI222558
 R-NT2RP3001688//Human mRNA for KIAA0392 gene, partial cds//8.6e-46:301:87//Hs.40100:AB002390
 R-NT2RP3001690//ESTs//3.3e-111:542:97//Hs.86149:AI341312
 30 R-NT2RP3001708//ESTs//1.4e-96:349:95//Hs.17975:AA868618
 R-NT2RP3001712//ESTs//9.3e-14:102:92//Hs.78041:N29669
 R-NT2RP3001716//ESTs. Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]
 //4.1e-80:444:91//Hs.6823:W18181
 R-NT2RP3001724//ESTs//1.8e-109:547:96//Hs.14570:AI422099
 35 R-NT2RP3001730//ESTs//4.1e-98:528:92//Hs.155115:AA669923
 R-NT2RP3001739//ESTs//4.4e-87:444:94//Hs.27239:W27810
 R-NT2RP3001752//ESTs//6.1e-93:490:94//Hs.4210:AA740440
 R-NT2RP3001753//ESTs//2.5e-82:395:99//Hs.126435:AA912968
 40 R-NT2RP3001764//ESTs. Weakly similar to protein-tyrosine phosphatase [H.sapiens]//1.2e-87:450:96//Hs.20281:
 N92517
 R-NT2RP3001777//ESTs//1.1e-86:360:97//Hs.100530:H06725
 R-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//4.2e-113:549:97//Hs.28169:
 AB007928
 R-NT2RP3001792//ESTs. Weakly similar to F35C12.2 [C.elegans]//1.1e-21:119:99//Hs.44268:AA455900
 45 R-NT2RP3001799//OX40L RECEPTOR PRECURSOR//2.8e-45:374:79//Hs.129780:XT5962
 R-NT2RP3001819//ESTs//2.6e-87:432:96//Hs.10414:AI291292
 R-NT2RP3001844//ESTs//0.024:128:67//Hs.25131:N50117
 R-NT2RP3001854//ESTs//1.4e-92:490:92//Hs.15165:N52900
 R-NT2RP3001855//ESTs//1.9e-66:361:93//Hs.10043:D81792
 50 R-NT2RP3001896//ESTs//1.4e-96:343:97//Hs.24809:N73642
 R-NT2RP3001898//ESTs//4.1e-90:515:91//Hs.4867:AA521180
 R-NT2RP3001915//ESTs//4.4e-32:175:95//Hs.24641:AA954666
 R-NT2RP3001926//ESTs. Highly similar to NUCLEOLYSIN TIA-1 [Homo sapiens]//1.0e-40:202:100//Hs.24709:
 AI123300
 55 R-NT2RP3001929//ESTs//6.6e-84:449:94//Hs.26962:AA682781
 R-NT2RP3001931//ESTs//1.0e-41:214:99//Hs.32360:AA534737
 R-NT2RP3001938//ESTs. Highly similar to SPORULATION-SPECIFIC PROTEIN 1 [Saccharomyces cerevisiae]
 //1.3e-95:483:96//Hs.5771:W74591

- R-NT2RP3001943//ESTs//1.2e-23:169.88//Hs.103930:AA160990
 R-NT2RP3001944//ESTs//2.0e-90:439.97//Hs.103380:AI291325
 R-NT2RP3001969//ESTs//0.95:133.65//Hs.131669:AI025889
 R-NT2RP3001989//ESTs, Weakly similar to C01A2.4 [C.elegans]//8.9e-64:310.99//Hs.11449:AI201540
 5 R-NT2RP3002002//ESTs//2.1e-95:562.89//Hs.5997:AA897088
 R-NT2RP3002004//H.sapiens mRNA for FAST kinase//1.6e-42:335.82//Hs.75087:X86779
 R-NT2RP3002007//ESTs//0.12:184.66//Hs.94030:AA846729
 R-NT2RP3002014//Small inducible cytokine A5 (RANTES)//6.8e-47:291.89//Hs.155464:AF088219
 R-NT2RP3002033
 10 R-NT2RP3002045//ESTs//1.0e-92:555.88//Hs.106411:W29081
 R-NT2RP3002054//EST//0.45:155.63//Hs.5656:D20426
 R-NT2RP3002056//ESTs//1.4e.95:504.93//Hs.17428:AI365221
 R-NT2RP3002057//Human mRNA for KIAA0152 gene, complete cds//0.69:127.66//Hs.90438:D63486
 R-NT2RP3002062
 15 R-ntnnnnnnnnnn//ESTs//2.1e-113:552.97//Hs.9591:AA069657
 R-NT2RP3002081//ESTs//5.5e-43:212.100//Hs.124852:AA969139
 R-NT2RP3002097//EST//2.3e-10:80.91//Hs.102717:N59148
 R-NT2RP3002102
 R-NT2RP3002108
 20 R-NT2RP3002146//ESTs//5.5e-58:296.97//Hs.65328:AA625385
 R-NT2RP3002147//EST//2.5e-53:387.81//Hs.147928:M249703
 R-NT2RP3002151//ESTs, Highly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [Homo sapiens]//6.2e-107:534.96//Hs.59523:AA602837
 R-NT2RP3002163//ESTs//2.7e-106:520.97//Hs.21258:AA412293
 25 R-NT2RP3002165//ESTs//7.4e-93:479.95//Hs.27299:AI074024
 R-NT2RP3002166//ESTs//1.0:261.59//Hs.132817:AA593713
 R-NT2RP3002173//ESTs//2.7e-93:512.92//Hs.23648:H07120
 R-NT2RP3002181//ESTs//1.0e-84:435.96//Hs.47378:AI193598
 R-NT2RP3002244//ESTs//2.7e-11:97.89//Hs.9412:W72446
 30 R-NT2RP3002248//ESTs//4.3e-90:459.95//Hs.9848:AA130588
 R-NT2RP3002255//ESTs//1.3e-45:289.88//Hs.9100:AA431672
 R-NT2RP3002273//ESTs//2.3e-100:489.97//Hs.8258:AA744743
 R-NT2RP3002276//ESTs//1.2e-50:306.91//Hs.16160:AA778171
 R-NT2RP3002303//ESTs//1.1e-67:323.99//Hs.129761:AA836898
 35 R-NT2RP3002304//ESTs//2.8e-86:405.99//Hs.29643:AA418500
 R-NT2RP3002330//ESTs, Weakly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [H.sapiens] //1.8e-19:136.87//Hs.106928:AI041737
 R-NT2RP3002343//ESTs//1.0e-42:260.93//Hs.7797:W25667
 R-NT2RP3002351//Homo sapiens 9G8 splicing factor mRNA, complete cds//0.0048:221.64//Hs.556:L41887
 40 R-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene//5.8e-105:516.94//Hs.6483:Y16355
 R-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//1.5e-103:524.95//Hs.12707:AB014578
 R-NT2RP3002484//Human APRT gene for adenine phosphoribosyltransferase//0.54:108.71//Hs.28914:Y00486
 45 R-NT2RP3002501//ESTs//2.7e-96:489.95//Hs.27335:N74185
 R-NT2RP3002512//ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III [C.elegans]//3.2e-90:526.90//Hs.8083:AA521436
 R-NT2RP3002529//ESTs, Highly similar to PUTATIVE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN C2G11.03C [Schizosaccharomyces pombe]//3.8e-101:497.96//Hs.6650:AA843246
 50 R-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.1e-83:438.94//Hs.19542:AB018272
 R-NT2RP3002549//ESTs//3.8e-98:493.96//Hs.7358:AA191673
 R-NT2RP3002566//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.14:184.63//Hs.89230:AF031815
 R-NT2RP3002587//Homo sapiens KIAA0420 mRNA, complete cds//2.0e-18:138.78//Hs.129883:AB007880
 55 R-NT2RP3002590//ESTs//2.9e-51:290.93//Hs.162942:AI243850
 R-NT2RP3002602//Homo sapiens stannin mRNA, complete cds//5.5e-06:58.100//Hs.76691:AF070673
 R-NT2RP3002603
 R-NT2RP3002631//ESTs//4.8e-54:367.85//Hs.13109:AA192514

- R-NT2RP3002659//ESTs//5.3e-30:229.85//Hs.152114:AA401365
 R-NT2RP3002660//ESTs//1.9e-88:452.95//Hs.120146:AA708573
 R-NT2RP3002663//ESTs//3.2e-89:469.95//Hs.105767:AA525172
 R-NT2RP3002671//ESTs, Highly similar to ELONGATION FACTOR 2 [*Drosophila melanogaster*]/5.9e-109:537:97//Hs.19348:AA151678
 R-NT2RP3002682//ESTs//2.3e-98:541.91//Hs.75844:AA115502
 R-NT2RP3002687//ESTs//5.5e-103:498.97//Hs.72782:AA910871
 R-NT2RP3002688//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]/5.0e-101:524.95//Hs.32580:AI123601
 R-NT2RP3002701//EST//0.87:131.63//Hs.161916:AA483169
 R-NT2RP3002713//ESTs//4.7e-106:542.95//Hs.14479:AA160945
 R-NT2RP3002763//ESTs//1.3e-54:290.94//Hs.142031:AA809159
 R-NT2RP3002770//ESTs//0.047:275.61//Hs.122984:AA526973
 R-NT2RP3002785//ESTs//2.4e-52:255.99//Hs.132959:AI376958
 R-NT2RP3002799//EST//8.2e-61:321.94//Hs.140992:R71377
 R-NT2RP3002810//EST//0.19:116.68//Hs.121810:AA775240
 R-NT2RP3002818//ESTs//1.3e-109:531.98//Hs.58924:AI348080
 R-NT2RP3002861//ESTs//2.5e-84:429.95//Hs.23920:AA909678
 R-NT2RP3002869//EST//0.00011:116.71//Hs.161606:AA019641
 R-NT2RP3002876//ESTs//0.0024:182.63//Hs.117306:AA687262
 R-NT2RP3002877//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//8.1e-14:146.72//Hs.129727:AF035587
 R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.5e-110:570.95//Hs.6162:AB018314
 R-NT2RP3002911//ESTs//3.6e-92:436.99//Hs.143917:AI206286
 R-NT2RP3002948//EST//1.0:102.65//Hs.144730:AI191975
 R-NT2RP3002953//ESTs//1.8e-107:513.98//Hs.119693:AI201698
 R-NT2RP3002955//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.23:563.56//Hs.127338:AB007961
 R-NT2RP3002969//ESTs, Weakly similar to LONG-CHAIN-FATTY-ACID--COA LIGASE 1 [*Saccharomyces cerevisiae*]/12.0e-56:387.86//Hs.144597:W20143
 R-NT2RP3002972//ESTs//1.7e-97:502.96//Hs.7274:AA476850
 R-NT2RP3002978//ESTs//8.6e-104:498.98//Hs.118923:AA252116
 R-NT2RP3002988//EST//1.2e-59:315.94//Hs.157743:AI360553
 R-NT2RP3003008//ESTs//1.4e-97:515.94//Hs.6544:AA524423
 R-NT2RP3003032//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [*Mus musculus*]/3.0e-100:528.94//Hs.90353:N98551
 R-NT2RP3003059//ESTs//1.7e-76:398.95//Hs.102971:W05355
 R-NT2RP3003061//ESTs//4.9e-82:414.96//Hs.99603:AI141912
 R-NT2RP3003068//ESTs, Weakly similar to M18.3 [*C.elegans*]/5.9e-83:392.99//Hs.101364:AA534439
 R-NT2RP3003071//ESTs//6.3e-85:399.99//Hs.109755:AA180809
 R-NT2RP3003078//ESTs//1.0e-98:471.99//Hs.7995:AI359466
 R-NT2RP3003101//EST//0.032:235.60//Hs.147920:AI202441
 R-NT2RP3003121//ESTs//3.0e-47:238.97//Hs.43559:AI003520
 R-NT2RP3003133//EST//1.5e-77:395.96//Hs.142150:AA223982
 R-NT2RP3003138//ESTs, Highly similar to KINESIN-LIKE PROTEIN KIF4 [*Mus musculus*]/3.3e-107:535.96//Hs.27437:AA004208
 R-NT2RP3003139//ESTs//2.5e-106:504.98//Hs.106795:AI271632
 R-NT2RP3003150//ESTs//1.6e-99:539.91//Hs.46500:AA129774
 R-NT2RP3003157//ESTs//1.5e-114:563.97//Hs.58608:AA081007
 R-NT2RP3003185//ESTs//3.9e-93:443.98//Hs.9741:AI131226
 R-NT2RP3003193//ESTs//2.0e-37:428.71//Hs.33354:AA179944
 R-NT2RP3003197//ESTs//5.8e-56:312.94//Hs.7016:AA215796
 R-NT2RP3003203//EST//0.0073:212.63//Hs.161355:AI422634
 R-NT2RP3003204//ESTs//7.4e-52:253.99//Hs.120146:AA708573
 R-NT2RP3003212//ESTs//1.8e-76:401.95//Hs.29067:N26107
 R-NT2RP3003230//ESTs, Highly similar to CORONIN [*Dictyostelium discoideum*]/2.0e-40:229.93//Hs.17377:AI078151
 R-NT2RP3003242//ESTs//8.3e-97:458.99//Hs.23057:AI290343

R-NT2RP3003251//ESTs//1.5e-60:320.95//Hs.36495:AA151628
 R-NT2RP3003264//ESTs//2.1e-103:521.95//Hs.4094:AA173960
 R-NT2RP3003278//ESTs//8.2e-109:536.96//Hs.23788:AA524061
 R-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//2.4e-102:550.93//Hs.11702:L36983
 R-NT2RP3003290//EST//4.3e-27:372.70//Hs.159131:AI384035
 R-NT2RP3003301//ESTs//4.4e-56:285.97//Hs.95370:AA601055
 R-NT2RP3003302//EST//7.2e-10:395.63//Hs.162554:AA584818
 R-NT2RP3003311//ESTs//4.2e-110:538.97//Hs.62180:AI341261
 R-NT2RP3003313//ESTs//2.1e-106:531.96//Hs.22630:C05931
 R-NT2RP3003327//ESTs//4.3e-102:518.95//Hs.120355:AA625445
 R-NT2RP3003330//ESTs//8.6e-104:497.97//Hs.72071:AI125289
 R-NT2RP3003344//ESTs//2.5e-105:494.99//Hs.112188:AA672993
 R-NT2RP3003346//ESTs//1.0:123.69//Hs.116029:AA813102
 R-NT2RP3003353//EST//0.0014:162.68//Hs.149191:AI246155
 R-NT2RP3003377//EST//4.5e-15:119.85//Hs.148129:AA885567
 R-NT2RP3003384//EST//0.0057:86.74//Hs.127735:AA962272
 R-NT2RP3003385//ESTs//0.64:347.59//Hs.5646:W72721
 R-NT2RP3003403//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//2.2e-24:418.67//Hs.139488:AI124095
 R-NT2RP3003409//ESTs//5.3e-98:479.97//Hs.155198:AA767372
 R-NT2RP3003411//ESTs//4.8e-86:416.97//Hs.129059:AA126041
 R-NT2RP3003427//ESTs//7.4e-103:510.96//Hs.25303:AA641023
 R-NT2RP3003433//ESTs//3.5e-85:405.99//Hs.63131:AA664156
 R-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//3.6e-97:479.96//Hs.14934:AF004828
 R-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//4.1e-102:527.93//Hs.26450:AB018268
 R-NT2RP3003491//ESTs, Weakly similar to No definition line found [C.elegans]//4.0e-106:549.94//Hs.7886:AI057529
 R-NT2RP3003500//Human RP3 mRNA, complete cds//0.66:401.60//Hs.75307:U02556
 R-NT2RP3003543//Human clone A9A2BRB7 (CAC)n(GTC)n repeat-containing mRNA//4.1e-33:217.88//Hs.8068:U00952
 R-NT2RP3003552//ESTs//3.1e-106:546.94//Hs.101754:AI123430
 R-NT2RP3003555//ESTs//3.4e-106:537.95//Hs.85550:AA187681
 R-NT2RP3003564
 R-NT2RP3003572//ESTs//1.2e-20:122.88//Hs.8253:N48721
 R-NT2RP3003576//ESTs//2.7e-71:394.94//Hs.151136:R99944
 R-NT2RP3003589//EST//0.58:242.59//Hs.130804:AA894759
 R-NT2RP3003625//ESTs//7.6e-41:349.80//Hs.140608:N53448
 R-NT2RP3003656//Human LIM protein (LPP) mRNA, partial cds//0.26:222.60//Hs.17217:U49957
 R-NT2RP3003659//ESTs//2.0e-113:547.97//Hs.23389:AA769310
 R-NT2RP3003665//ESTs//1.6e-80:415.95//Hs.141084:H11714
 R-NT2RP3003672
 R-NT2RP3003686//ESTs//6.8e-114:552.97//Hs.43299:N23036
 R-NT2RP3003701//ESTs//2.1e-16:282.66//Hs.115512:AI208768
 R-NT2RP3003716//ESTs//2.1e-45:195.91//Hs.41296:N71923
 R-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//5.6e-103:492.97//Hs.48513:AB018300
 R-NT2RP3003746//ESTs//1.9e-85:411.98//Hs.54835:AI050863
 R-NT2RP3003795//EST//6.2e-97:459.99//Hs.134769:AI089747
 R-NT2RP3003799//ESTs//2.8e-62:337.94//Hs.124023:H18913
 R-NT2RP3003800//PROTO-ONCOGENE TYRO SINE-PROTEIN KINASE SRC//8.9e-108:551.95//Hs.115742:AF077754
 R-NT2RP3003805//ESTs//2.2e-103:490.99//Hs.9412:W72446
 R-NT2RP3003809//ESTs, Highly similar to SAV PROTEIN [Sulfolobus acidocaldarius]//3.4e-89:456.95//Hs.5555:AI285198
 R-NT2RP3003819//Interleukin 10//3.3e-43:173.89//Hs.2180:M57627
 R-NT2RP3003825//ESTs//1.6e-66:485.80//Hs.7405:W27761

- R-NT2RP3003828//ESTs, Weakly similar to unknown.[H.sapiens]/9.6e-98.511:95//Hs.26955.A133224
 R-NT2RP3003831//ESTs/2.2e-38.317:79//Hs.142173:AA757743
 R-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//5.2e-110.541:97//Hs.25300:AF070611
- 5 R-NT2RP3003842//EST//9.9e-44:506:70//Hs.139093:AA166888
 R-NT2RP3003846//ESTs/4.6e-10:66:100//Hs.74924:A1332962
 R-NT2RP3003870//ESTs/3.4e-82:449:92//Hs.122691:AA152298
 R-NT2RP3003876//ESTs/1.9e-89:449:96//Hs.45046:N40170
 R-NT2RP3003914//ESTs/1.3e-99:470:98//Hs.118966:AA926726
- 10 R-NT2RP3003918//ESTs/1.3e-79:417:94//Hs.5005:W25933
 R-NT2RP3003932//ESTs/6.0e-83:427:94//Hs.93581:H50221
 R-NT2RP3003989//ESTs/4.8e-76:403:93//Hs.127243:W80409
 R-NT2RP3003992//ESTs/2.4e-88:508:90//Hs.134200:D19593
 R-NT2RP3004013//ESTs/3.7e-111:551:97//Hs.105108:AA781142
- 15 R-NT2RP3004016//ESTs/1.7e-81:394:98//Hs.63368:AA613714
 R-NT2RP3004041
 R-NT2RP3004051//ESTs/3.5e-69:386:93//Hs.51347:T72820
 R-NT2RP3004070//ESTs/5.5e-108:552:9511Hs.23392:A1310139
 R-NT2RP3004078//ESTs/3.3e-82:443:93//Hs.26407:W4537
- 20 R-NT2RP3004093//ESTs/4.4e-83:426:94//Hs.140832:A1262104
 R-NT2RP3004095//ESTs/0.00013:93:78//Hs.36567:AA262045
 R-NT2RP3004110//ESTs, Weakly similar to similar to oxysterol-binding proteins: partial CDS [C.elegans]/3.5e-76:402:95//Hs.55847:W31092
 R-NT2RP3004125//ESTs/9.3e-74:363:97//Hs.32988:C01696
- 25 R-NT2RP3004145//ESTs/2.6e-96:451:99//Hs.59584:AA587334
 R-NT2RP3004148//ESTs/1.3e-10:77:92//Hs.135890:A183425
 R-NT2RP3004155//ESTs/1.7e-110:558:96//Hs.27003:A1279093
 R-NT2RP3004206//ESTs, Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]/1.8e-40:200:100//Hs.26089:AA195126
- 30 R-NT2RP3004207//ESTs, Weakly similar to gene SEZ-6 [M.musculus]/1.1e-41:266:89//Hs.6314:AA522619
 R-NT2RP3004209//ESTs, Highly similar to PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C [Schizosaccharomyces pombe]/3.7e-112:547:97//Hs.99819:A1346680
 R-NT2RP3004215//ESTs/1.1e-103:541:95//Hs.124918:N64794
 R-NT2RP3004242//ESTs/4.5e-105:524:96//Hs.29724:N46252
- 35 R-NT2RP3004246//EST//1.9e-07:67:91//Hs.125687:AA884827
 R-NT2RP3004253//EST//2.9e-88:454:94//Hs.127713:AA961628
 R-NT2RP3004258//ESTs, Weakly similar to PRE-MRNA SPLICING FACTOR SRP75 [Homo sapiens]/1.6e-89:468:95//Hs.5117:AA831530
 R-NT2RP3004262//ESTs/4.1e-86:443:96//Hs.101393:T87623
- 40 R-NT2RP3004334//EST//0.00057:206:63//Hs.149388:A1273630
 R-NT2RP3004341//EST//0.00042:151:68//Hs.148498:A1200264
 R-NT2RP3004348//Homo sapiens LIM protein mRNA, complete cds//5.9e-61:299:85//Hs.154103:AF061258
 R-NT2RP3004349//EST//3.6e-42:175:88//Hs.161917:AA483223
 R-NT2RP3004378//ESTs/0.27:294:60//Hs.66479:AA863044
- 45 R-NT2RP3004399//ESTs/5.8e-99:479:98//Hs.120234:AA732224
 R-NT2RP3004424//EST, Highly similar to F21G4.6 [C.elegans]/0.30:253:58//Hs.97184:AA385934
 R-NT2RP3004428//ESTs/2.8e-48:279:91//Hs.106826:W25985
 R-NT2RP3004451//ESTs/4.8e-101:509:96//Hs.29725:W74621
 R-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//9.3e-108:526:98//Hs.27349:AB007917
- 50 R-NT2RP3004466//ESTs/0.25:51:90//Hs.7776:AA195616
 R-NT2RP3004470//EST//0.032:70:71//Hs.147925:A1249332
 R-NT2RP3004472//ESTs/0.0069:430:59//Hs.116651:AA993406
 R-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//5.0e-107:521:97//Hs.5003:AB007925
 R-NT2RP3004480
- 55 R-NT2RP3004490//ESTs/4.7e-68:354:95//Hs.163721:H42504
 R-NT2RP3004498//ESTs, Moderately similar to ORF2: function unknown [H.sapiens]/3.4e-100:508:95//Hs.47393:AA218858

R-NT2R2P3004503/ESTs/1.6e-90:478:93/Hs.133998:AA994735
1.8e-83:465:92/Hs.137064:AA318257
R-NT2R2P3004507/ESTs/1.5e-98:495:96/Hs.128905:AI051971
R-NT2R2P3004527/ESTs/1.6e-109:535:97/Hs.149481:AI279865
R-nnnnnnnnnnnn
R-NT2R2P3004544/EST/0.035:226:60/Hs.99195:AA449232
R-NT2R2P3004566/ESTs/4.1e-86:455:95/Hs.13110:T67461
R-NT2R2P3004569/ESTs/2.9e-94:493:94/Hs.24948:AA977674
R-NT2R2P3004572/ESTs/1.1e-92:437:99/Hs.24846:AI420493
R-NT2R2P3004578/ESTs/0.9e-166:64/Hs.124593:AA854456
R-NT2R2P3004594/EST/5.8e-89:426:98/Hs.134213:AI080213
R-NT2R2P3004617/ESTs/1.4e-40:226:85/Hs.15921:R71157
R-NT2R2P3004618/ESTs/1.8e-38:229:90/Hs.125153:AA453723
R-NT2R2P3004670/Homo sapiens GN6ST mRNA for long form of N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete cds/1.2e-57:291:95/Hs.8788:AB014680
R-NT2R2P4000008/ESTs/8.9e-119:561:98/Hs.25035:AI123335
R-NT2R2P4000023/EST/1.2e-34:271:80/Hs.98300:AA418560
R-NT2R2P4000035/Small inducible cytokine A5 (RANTES)/2.1e-68:320:82/Hs.155464:AF088219
R-NT2R2P4000049/Homo sapiens TRAIL receptor 2 mRNA, complete cds/6.7e-60:289:82/Hs.51233:AF016266
R-NT2R2P4000051/ESTs, Weakly similar to protein B [H. sapiens]/8.3e-98:462:99/Hs.10114:AI345945
R-NT2R2P4000078/ESTs/0.00068:367:60/Hs.106090:AA457030
R-NT2R2P4000102/ESTs/9.7e-50:256:97/Hs.142666:R28287
R-NT2R2P4000109/Homo sapiens mRNA for MEGF5, partial cds/1.1e-107:536:96/Hs.57929:AB011538
R-NT2R2P4000129/Homo sapiens mRNA for KIAA0483 protein, partial cds/3.5e-112:554:97/Hs.64691:AB007952
R-NT2R2P4000147/ESTs/3.9e-11:122:80/Hs.25584:AA632014
R-NT2R2P4000150/EST/1.4e-84:510:88/Hs.144238:W52294
R-NT2R2P4000151/ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III [C.elegans]/5.7e-93:515:92/Hs.8083:AA521436
R-NT2R2P4000159/ESTs/0.0019:209:65/Hs.161816:AA400295
R-NT2R2P4000167/ESTs/2.1e-113:549:97/Hs.10944:1.N66569
R-NT2R2P4000185/ESTs/0.65:232:59/Hs.144445:AA807257
R-NT2R2P4000210/Homo sapiens mRNA for KIAA0700 protein, partial cds/1.5e-100:505:96/Hs.13999:AB014600
R-NT2R2P4000212/ESTs/8.5e-14:169:75/Hs.8520:AA081788
R-NT2R2P4000214/Human mRNA for KIAA0392 gene, partial cds/6.2e-43:272:90/Hs.440010:AB002390
R-NT2R2P4000218/ESTs/6.1e-10:335:64/Hs.105658:AA978185
R-NT2R2P4000243/Homo sapiens mRNA for cartilage-associated protein (CASP)/2.9e-70:354:96/Hs.155481:AJ006470
R-NT2R2P4000246/ESTs/7.1e-26:154:94/Hs.14838:AA502757
R-NT2R2P4000259/Homo sapiens clone 683 unknown mRNA, complete sequence/9.3e-79:379:99/Hs.43728:AF091092
R-NT2R2P4000263
R-nnnnnnnnnnnn/ESTs, Weakly similar to similar to Achlya ambisexualis antheridial steroid receptor [C.elegans]/4.7e-104:525:96/Hs.152069:AA548972
R-NT2R2P4000312/ESTs/8.2e-66:319:99/Hs.35091:AI271631
R-NT2R2P4000321/Homo sapiens clone 24455 mRNA sequence/1.3e-109:513:99/Hs.13410:AF070524
R-NT2R2P4000323/ESTs/7.7e-109:534:97/Hs.34790:AA192760
R-NT2R2P4000355/ESTs/3.1e-44:320:83/Hs.141323:N80390
R-NT2R2P4000360/Homo sapiens mRNA for KIAA0738 protein, complete cds/7.6e-111:520:99/Hs.107479:AB018281
R-NT2R2P4000367/Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds/2.8e-110:527:98/Hs.31323:AF044195
R-NT2R2P4000370/ESTs/8.9e-32:166:98/Hs.70488:AI301130
R-NT2R2P4000376/ESTs/6.8e-99:465:99/Hs.27182:AA604448
R-NT2R2P4000381/ESTs/3.0e-50:280:93/Hs.8395:W27376
R-NT2R2P4000415/ESTs, Weakly similar to coded for by C. elegans cDNA vk30b3.5 [C.elegans]/3.9e-87:499:

91//Hs.26156:AA630975
 R-NT2RP4000417//ESTs, Moderately similar to HYPOTHETICAL 91.2 KD PROTEIN IN RPS7A-SCH9 INTER-
 GENIC REGION [Saccharomyces cerevisiae]/8.9e-95:468:96//Hs.93871:AI191318
 R-NT2RP4000424//ESTs/3.7e-98:473:93//Hs.24945:AI189011
 5 R-NT2RP4000448//ESTs/2.6e-79:446:91//Hs.25159:R60955
 R-NT2RP4000449//ESTs/3.6e-98:468:98//Hs.31176:AI037953
 R-NT2RP4000455//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, com-
 plete cds/0.35:153.63//Hs.113286:U77783
 10 R-ntnnnnnnnnnn//ESTs/4.5e-89:455:96//Hs.62638:AA127740
 R-NT2RP4000480//ESTs/4.9e-92:431:99//Hs.121072:AI204167
 R-ntnnnnnnnnnn
 R-NT2RP4000500//ESTs, Weakly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III
 [C.elegans]/1.2e-40:125:97//Hs.56124:AI424792
 R-NT2RP4000515//EST/6.7e-30:183:90//Hs.150710:AI122713
 15 R-NT2RP4000517//Aldehyde dehydrogenase 7//7.5e-28:183:76//Hs.83155:U10868
 R-NT2RP4000518//EST/0.091:178:58//Hs.133031:AI049874
 R-NT2RP4000519
 R-NT2RP4000524//ESTs, Highly similar to rsec8 [R.norvegicus]/3.4e-93:496:93//Hs.107394:H07126
 R-NT2RP4000528//EST/0.84:130:66//Hs.140208:AA702213
 20 R-NT2RP4000541//EST/15.2e-63:337:94//Hs.156337:AI337328
 R-NT2RP4000556//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.norvegicus]/8.2e-92:448:98//Hs.
 25597:H93026
 R-NT2RP4000588//ESTs/3.8e-94:445:98//Hs.44077:N28840
 R-NT2RP4000614//ESTs/6.5e-18:159:83//Hs.24549:N57263
 25 R-NT2RP4000638//ESTs/2.5e-46:296:87//Hs.132722:AA618531
 R-NT2RP4000648//ESTs/2.6e-103:559:93//Hs.23794:W80393
 R-NT2RP4000657//ESTs/1.0:189:60//Hs.87073:AA972704
 R-NT2RP4000704//ESTs/2.8e-101:509:96//Hs.84824:AA935651
 R-NT2RP4000724//ESTs/1.5e-93:442:94//Hs.142114:AA205615
 30 R-NT2RP4000728//ESTs/0.84:61:75//Hs.145334:AI251399
 R-NT2RP4000739//ESTs/8.8e-80:418:94//Hs.42959:N21211
 R-NT2RP4000781//ESTs/1.4e-79:376:99//Hs.135458:AI081312
 R-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds/3.1e-106:550:94//Hs.25132:
 AB007939
 35 R-NT2RP4000833//ESTs/5.8e-46:309:85//Hs.163979:AA828834
 R-NT2RP4000837//ESTs/1.7e-112:539:97//Hs.97718:AI334028
 R-NT2RP4000855//ESTs/1.1e-95:486:95//Hs.5345:AA988104
 R-NT2RP4000865//EST/6.2e-68:412:89//Hs.142196:AA258356
 40 R-NT2RP4000878//ESTs/1.9e-80:417:95//Hs.104716:AI023185
 R-NT2RP4000879//ESTs/1.8e-42:211:99//Hs.89991:AI374617
 R-ntnnnnnnnnnn//ESTs/1.2e-89:453:97//Hs.100182:N92594
 R-ntnnnnnnnnnn/EST/9.4e-06:197:63//Hs.145970:AI277106
 R-NT2RP4000925//ESTs, Weakly similar to KIAA0405 [H.sapiens]/5.9e-17:134:85//Hs.14146:W92235
 R-ntnnnnnnnnnn/ESTs/4.3e-14:84:100//Hs.155360:AA984683
 45 R-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds/8.2e-108:548:95//
 Hs.24812:AF069532
 R-NT2RP4000929//ESTs/1.3e-119:567:98//Hs.62717:AA044905
 R-NT2RP4000955//ESTs/3.5e-10:119:78//Hs.42946:N21111
 R-NT2RP4000973//ESTs/2.8e-05:93:69//Hs.155126:AA563986
 50 R-NT2RP4000975//ESTs/4.4e-58:324:95//Hs.126070:AA045179
 R-NT2RP4000979//ESTs/3.5e-42:468:73//Hs.106210:AI193017
 R-NT2RP4000984//Homo sapiens clone 23770 mRNA sequence/8.7e-120:570:98//Hs.12457:AF052123
 R-NT2RP4000989//ESTs/1.3e-122:581:98//Hs.10499:AA528018
 R-NT2RP4000996//ESTs/9.2e-113:579:94//Hs.23762:N26620
 55 R-NT2RP4000997//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds/1.1e-28:439:68//Hs.
 129735:AF010144
 R-NT2RP4001004//ESTs/3.6e-78:389:98//Hs.156290:AI016769
 R-NT2RP4001006//ESTs, Moderately similar to ORF2: function unknown [H.sapiens]/6.6e-124:574:99//Hs.

- 47393:AA218858
 R-NT2RP4001010//EST//2.8e-31:194.90//Hs.161186:AI418635
 R-NT2RP4001029//ESTs//4.4e-111:523.99//Hs.28423:AI336292
 R-NT2RP4001041//ESTs. Highly similar to LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC [Saccharomyces cerevisiae]//3.6e-114:569.96//Hs.6762:AA088424
- 5
 R-NT2RP4001057//Homo sapiens KIAA0399 mRNA, partial cds//2.0e-51:282.94//Hs.100955:AB007859
 R-NT2RP4001064//ESTs. Weakly similar to protein B [H.sapiens]//2.1e-103:485.99//Hs.10114:AD45945
 R-NT2RP4001078
 R-NT2RP4001079//Homo sapiens mRNA for putative Ca²⁺-transporting ATPase, partial/1.7e-119:596.98//Hs.106778:AJ010953
- 10
 R-NT2RP4001080//ESTs//7.6e-10:65:100//Hs.131694:AA927668
 R-ntnnnnnnnnnn/Homo sapiens mRNA for KIAA0592 protein, partial cds//5.9e-121:548.95//Hs.13273:AB011164
 R-NT2RP4001095//ESTs//1.5e-113:563.96//Hs.118732:AI344055
 R-NT2RP4001100//ESTs//2.0e-46:413.79//Hs.146314:R99617
- 15
 R-NT2RP4001117//EST//1.7e-51:294.92//Hs.7260:T23737
 R-NT2RP4001122//ESTs//5.4e-109:509.99//Hs.16390:AI052357
 R-NT2RP4001126//EST//0.97:169.61//Hs.148107:AA693476
 R-NT2RP4001138//ESTs//3.0e-110:543.97//Hs.57655:AI056890
 R-NT2RP4001143//ESTs. Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//5.4e-113:573.96//Hs.5249:U55977
- 20
 R-NT2RP4001148//ESTs//3.1e-103:490.98//Hs.121282:AI091453
 R-NT2RP4001149//EST//1.7e-50:281.93//Hs.101727:H16171
 R-NT2RP4001150//ESTs//1.9e-90:422.100//Hs.125490:AI138884
 R-NT2RP4001159
- 25
 R-NT2RP4001174//ESTs//2.5e-110:526.98//Hs.116555:AA639278
 R-ntnnnnnnnnnn/ESTs//1.1e-25:140.97//Hs.83756:AI002822
 R-NT2RP4001207//ESTs//4.4e-70:432.89//Hs.13109:AA192514
 R-NT2RP4001210//ESTs//1.4e-108:509.99//Hs.27021:AI359495
 R-NT2RP4001213//ESTs. Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]//4.4e-123:624.95//Hs.22744:AI379892
- 30
 R-NT2RP4001219//ESTs//0.0043:142.65//Hs.6733:AI160750
 R-NT2RP4001228//ESTs//4.9e-101:482.98//Hs.62684:AA806103
 R-NT2RP4001235//ESTs//3.7e-105:571.93//Hs.37706:AA005120
 R-NT2RP4001256//ESTs//1.1e-12:189.74//Hs.20621:W28255
- 35
 R-NT2RP4001260//EST//6.9e-05:313.61//Hs.116438:AA648430
 R-NT2RP4001274//EST//0.0020:246.63//Hs.149955:AI289933
 R-ntnnnnnnnnnn/ESTs//2.9e-34:213.91//Hs.43100:AA186588
 R-NT2RP4001313
 R-NT2RP4001315//EST//6.1e-38:217.93//Hs.97832:AA400892
- 40
 R-NT2RP4001339//ESTs//3.8e-91:430.99//Hs.34840:AI279612
 R-NT2RP4001345//ESTs//5.3e-89:443.96//Hs.6770:AA92732
 R-NT2RP4001351//ESTs//6.0e-78:394.97//Hs.102796:N70837
 R-NT2RP4001353//ESTs//4.8e-06:90.82//Hs.7778:AA195616
 R-NT2RP4001372
- 45
 R-NT2RP4001373//ESTs. Weakly similar to HYPOTHETICAL 48.8 KD PROTEIN IN TRK2-MRS4 INTERGENIC REGION [Saccharomyces cerevisiae]//1.7e-108:546.96//Hs.32271:AA203680
 R-NT2RP4001375//ESTs//2.4e-19:155.87//Hs.62119:AA043299
 R-NT2RP4001379//EST//4.4e-29:288.72//Hs.157848:AI362501
 R-NT2RP4001389//ESTs. Highly similar to HYPOTHETICAL 51.6 KD PROTEIN IN PAP1-MRPL13 INTERGENIC REGION [Saccharomyces cerevisiae]//3.8e-79:438.93//Hs.21938:W81045
- 50
 R-NT2RP4001407//ESTs//8.3e-112:541.97//Hs.22587:AA743132
 R-NT2RP4001414//ESTs//8.6e-118:117.90//Hs.90789:W27649
 R-NT2RP4001433//ESTs. Moderately similar to PROHIBITIN [H.sapiens]//1.6e-102:498.97//Hs.62386:AA512948
 R-NT2RP4001442//ESTs//8.8e-104:489.99//Hs.101619:AI339433
 R-NT2RP4001447
- 55
 R-NT2RP4001474
 R-NT2RP4001483//ESTs//2.1e-100:528.92//Hs.17860:AA706655
 R-NT2RP4001498//ESTs//1.1e-97:470.98//Hs.95744:AI392846

- R-NT2RP4001502//ESTs//6.7e-73:382.96//Hs.11874:N93511
 R-NT2RP4001507//ESTs//2.6e-57:302.96//Hs.65328:AA625385
 R-NT2RP4001524//ESTs. Weakly similar to F13B12.1 [C.elegans]//2.9e-107:546.96//Hs.5570:AI377863
 R-NT2RP4001529//ESTs//3.3e-112:524.99//Hs.28423:AI336292
 5 R-NT2RP4001547//ESTs. Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Paramecium tetraurelia]//2.8e-120:566.98//Hs.108530:AA523928
 R-nnnnnnnnnnn//ESTs. Weakly similar to CELL DIVISION CONTROL PROTEIN 68 [S.cerevisiae]//1.4e-26:184:88//Hs.136189:AA133224
 R-NT2RP4001555//ESTs//1.1e-95:445.100//Hs.134403:AA677552
 10 R-NT2RP4001567//ESTs//2.8e-106:506.98//Hs.102708:AA292285
 R-NT2RP4001568//ESTs//6.4e-55:300.94//Hs.57442:N63437
 R-NT2RP4001571//ESTs//1.3e-114:556.97//Hs.30340:AA521251
 R-NT2RP4001574//ESTs//0.0035:120.67//Hs.96339:AA225906
 R-NT2RP4001575
 15 R-NT2RP4001592//ESTs. Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL[S.cerevisiae]//8.7e-112:557.97//Hs.7558:AA526812
 R-NT2RP4001610//ESTs//6.2e-77:382.96//Hs.21543:AA166776
 R-NT2RP4001614//ESTs//2.8e-117:565.98//Hs.9591:AA069657
 R-NT2RP4001634//ESTs//2.0e-39:213.96//Hs.32360:AA534737
 20 R-NT2RP4001638//Homo sapiens clone 23967 unknown mRNA, partial cds//1.7e-116:559.97//Hs.5332:AF007151
 R-NT2RP4001644//ESTs. Moderately similar to MNK1 [H.sapiens]//5.3e-36:192.97//Hs.5662:AA868361
 R-NT2RP4001656//ESTs. Highly similar to HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II [Caenorhabditis elegans]//1.1e-104:525.96//Hs.20472:W28734
 25 R-NT2RP4001677//ESTs//1.8e-106:522.97//Hs.106390:AA156805
 R-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence//5.7e-118:583.96//Hs.15562:U96629
 R-NT2RP4001725//ESTs//2.0e-11:141.74//Hs.117589:N25941
 R-nnnnnnnnnnn//ESTs. Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRE-CURSOR [D.melanogaster]//3.4e-73:382.97//Hs.152332:AI141922
 30 R-NT2RP4001739//ESTs//6.6e-59:340.91//Hs.122293:AA843692
 R-NT2RP4001753//Zinc finger protein 3 (A8-51)//5.6e-113:552.96//Hs.2481:X78926
 R-NT2RP4001760//ESTs//2.5e-94:453.98//Hs.122579:AA766315
 R-NT2RP4001790//ESTs. Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//2.0e-62:326.94//Hs.110839:W28098
 35 R-NT2RP4001803
 R-NT2RP4001822//ESTs//4.4e-98:526.92//Hs.96908:AI161133
 R-NT2RP4001823//ESTs//1.7e-72:357.97//Hs.144900:AI218434
 R-NT2RP4001828//ESTs//3.3e-101:536.92//Hs.18851:AA857826
 40 R-NT2RP4001838//ESTs//4.2e-58:344.90//Hs.48723:N66663
 R-NT2RP4001849//EST//0.24:105.71//Hs.136747:AA749210
 R-NT2RP4001889//Human mRNA for KIAA0118 gene, partial cds//3.4e-34:212.88//Hs.154326:D42087
 R-NT2RP4001893//ESTs//3.0e-58:321.95//Hs.158787:W79602
 R-NT2RP4001896//EST//3.8e-15:108.92//Hs.160835:AI345528
 45 R-NT2RP4001901//ESTs//1.2e-110:536.97//Hs.31443:AI018606
 R-NT2RP4001927//ESTs//2.1e-105:546.93//Hs.73291:AI417099
 R-NT2RP4001938//ESTs//2.8e-40:235.78//Hs.163641:R61848
 R-NT2RP4001946//ESTs//1.3e-29:175.93//Hs.43703:AA088436
 R-NT2RP4001950//ESTs//4.6e-95:458.98//Hs.150890:AI341793
 50 R-NT2RP4001953//Clathrin, light polypeptide (Lcb)//2.3e-62:310.82//Hs.73919:X81637
 R-NT2RP4001966//ESTs. Weakly similar to tenascin-like protein [D.melanogaster]//8.3e-87:457.94//Hs.41793:AA775879
 R-NT2RP4001975//ESTs//1.9e-52:281.94//Hs.7704:W58252
 R-NT2RP4002018
 55 R-NT2RP4002047//ESTs. Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]//4.7e-09:90.86//Hs.41127:AA555184
 R-NT2RP4002052//ESTs//0.054:353.60//Hs.117510:AA903738
 R-NT2RP4002058//EST//1.7e-26:151.94//Hs.124617:AA855106

R-NT2RP4002071//ESTs/6.9e-99:475.98//Hs.29216:AA916679
R-NT2RP4002075//ESTs/0.67:121.65//Hs.153939:AI284198
R-NT2RP4002078//ESTs, Highly similar to ZINC FINGER PROTEIN 35 [Homo sapiens]//1.6e-61:464.82//Hs.144228:N99507
R-nnnnnnnnnnn//ESTs, Weakly similar to HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN CHROMOSOME II [C.elegans]//2.3e-56:271.100//Hs.6185:AA428565
R-NT2RP4002083//ESTs/2.0e-108:548:96//Hs.6120:W80407
R-NT2RP4002408//ESTs/2.6e-77:391.96//Hs.14014:AA745592
R-NT2RP4002791//ESTs/7.9e-101:527.93//Hs.22394:N32555
R-NT2RP4002888//ESTs, Highly similar to ENV POLYPROTEIN [Avian spleen necrosis virus]//1.9e-65:373.92//Hs.31532:H18272
R-NT2RP4002905//ESTs/1.5e-107:517.98//Hs.40460:N36090
R-AB0071000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//2.8e-115:605.94//Hs.108258:AB007934
R-OVARC1000004
R-OVARC1000006//ESTs/1.5e-19:139.89//Hs.143034:AI126929
R-OVARC1000013//ESTs/5.9e-98:531.93//Hs.16470:AA121635
R-OVARC1000014//ESTs/0.24:243.60//Hs.19569:AA464273
R-OVARC1000017
R-OVARC1000035//ESTs/0.035:252.63//Hs.134123:AI078286
R-OVARC1000058//H.sapiens mRNA for translin associated protein X//3.8e-46:331.83//Hs.96247:X95073
R-OVARC1000060//EST//2.8e-28:348.71//Hs.141728:W73041
R-OVARC1000068//ESTs/3.0e-83:491.90//Hs.29397:N15367
R-OVARC1000071//ESTs/2.5e-60:321.96//Us.25010:R6787
R-OVARC1000085//Proteasome component C5//8.6e-67:366.92//Hs.75748:AL031259
R-nnnnnnnnnnn//ESTs/1.0e-111:526.98//Hs.129020:AI380703
R-OVARC1000091//ESTs, Weakly similar to HOST CELL FACTOR CI [H.sapiens]//3.9e-112:596.94//Hs.20597:W58370
R-OVARC1000092//ESTs/5.1e-18:144.82//Hs.109140:AI289942
R-OVARC1000106
R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//8.3e-102:495.97//Hs.3688:AF069250
R-OVARC1000114//H.sapiens mRNA for phosphoinositide 3-kinase//1.7e-45:489.74//Hs.101238:Y11312
R-OVARC1000133//EST//0.00028:284.61//Hs.30547:H05482
R-OVARC1000145//EST//3.9e-40:201.99//Hs.156148:AI333214
R-OVARC1000148//EST//0.79:150.62//Hs.100078:T05090
R-OVARC1000151
R-OVARC1000168//EST//1.7e-19:142.90//Hs.38441:H66023
R-OVARC1000191//EST//0.0072:292.63//Hs.132492:AA922629
R-OVARC1000198//Homo sapiens LIM protein mRNA, complete cds//6.1e-44:339.81//Hs.154103:AF061258
R-OVARC1000209//ESTs, Moderately similar to ZINC FINGER PROTEIN 93 [H.sapiens]//1.1e-32:196.92//Hs.64322:AA142864
R-OVARC1000212//EST//0.20:178.61//Hs.133031:AI049874
R-OVARC1000240//ESTs/9.0e-64:314.98//Hs.42300:AA204958
R-OVARC1000241//EST//0.00018:115.68//Hs.150728:AI123130
R-OVARC1000288//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROTEIN IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]//3.3e-74:403.93//Hs.108117:AI097079
R-OVARC1000302//EST//4.0e-14:102.90//Hs.136617:AA630476
R-OVARC1000304//ESTs, Highly similar to PUTATIVE GTP-BINDING PROTEIN MOV10 [Mus musculus]//2.9e-37:191.98//Hs.20725:AI027777
R-OVARC1000309//ESTs/3.6e-66:348.94//Hs.9547:AA532449
R-OVARC1000321//ESTs/3.6e-87:454.95//Hs.110445:AA044743
R-OVARC1000326//ESTs, Moderately similar to lamina associated polypeptide 1C [R.norvegicus]//1.3e-98:488.96//Hs.125749:AI377682
R-OVARC1000335//ESTs/3.0e-115:565.97//Hs.54835:AI050863
R-OVARC1000347//EST//0.0018:145.65//Hs.136945:AA765672
R-OVARC1000384//ESTs/2.8e-38:253.89//Hs.15093:AA203423
R-OVARC1000408//ESTs//2.6e-98:515.94//Hs.119808:C05928

R-*OVARC*1000411//ESTs//3.2e-82;395.98/Hs.104747:AA406291
R-*OVARC*1000414//Landsteiner-Wiener blood group glycoprotein//1.5e-27;.211.79/Hs.108287.L27670
R-*OVARC*1000042//EST//2.8e-38;255.74/Hs.138525.R99237
R-*OVARC*1000427//EST//2.6e-58;302.96/Hs.122914:AA767034
5 R-*OVARC*1000431//ESTs//4.9e-108;551.96/Hs.11668:A123246
R-*OVARC*1000437
R-*OVARC*1000440//ESTs//2.9e-91;456.96/Hs.93701:A1018671
R-*OVARC*10000442//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.3e-45;320.84/
Hs.73614.U83462
10 R-*OVARC*1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.6e-79;418.94/Hs.12334:
AB014583
R-*OVARC*1000461//ESTs//3.1e-62;342.93/Hs.23241.R46582
R-*OVARC*1000465//ESTs//1.7e-67;349.95/Hs.127238:AA47576
R-*OVARC*1000466//ESTs//1.9e-66;337.95/Hs.5212.A1421211
15 R-*OVARC*1000473//ESTs//5.4e-89;320.99/Hs.29173:AA134926
R-*OVARC*1000479//ESTs, Highly similar to TIP120 [R.norvegicus]//1.1e-102;514.96/Hs.11833:A1299947
R-*OVARC*1000486//ESTs//3.9e-78;405.95/Hs.98312:AA424983
R-*OVARC*10000496
R-*OVARC*1000520//ESTs//1.2e-20;145.88/Hs.87456:AA434484
20 R-*OVARC*1000526//Small inducible cytokine A5 (RANTES)//8.9e-47;217.87/Hs.155464:AF088219
R-*OVARC*1000533//ESTs, Moderately similar to integrase [H.sapiens]//8.5e-48;264.92/Hs.49860:AA702248
R-*OVARC*1000543//ESTs//5.7e-74;410.94/Hs.62817:AA047021
R-*OVARC*1000556//H.sapiens mRNA for ribosomal S6 kinase//9.5e-27;202.85/Hs.90859:X85106
25 R-*OVARC*1000557//EST//2.8e-18;169.79/Hs.149101:A1244285
R-*OVARC*1000564//EST//2.3e-34;199.92/Hs.146637:A141587
R-*OVARC*1000573//Interleukin 10//4.7e-42;300.83/Hs.2180:M57627
R-*OVARC*1000578//Small inducible cytokine A5 (RANTES)//5.2e-58;392.84/Hs.155464:AF088219
R-*OVARC*1000588//EST//1.8e-41;174.85/Hs.163333:AA879053
R-*OVARC*10000605
30 R-*OVARC*1000622//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.4e-47;417.77/Hs.
159897:AB007970
R-*OVARC*1000640//H.sapiens mRNA for translin associated protein X//1.9e-28;366.72/Hs.96247:X95073
R-*OVARC*1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//5.1e-31;162.100/Hs.111862:
AB011162
35 R-*OVARC*1000678//EST//0.92;199.60/Hs.122025:AA778480
R-nnnnnnnnnnnn//ESTs//0.94;416.59/Hs.130754:AA279522
R-*OVARC*1000681//EST//9.2e-21;179.80/Hs.132635:A1032875
R-*OVARC*1000689//Homo sapiens ataxin-7 (SCAT7) mRNA, complete cds//0.053;160.64/Hs.108447:AJ000517
R-*OVARC*1000700//Homo sapiens KIAA0441 mRNA, complete cds//7.1e-09;141.73/Hs.32511:AB007901
40 R-*OVARC*1000703//ESTs//1.7e-46;298.87/Hs.138856:H47461
R-*OVARC*1000730//ESTs, Weakly similar to C2F2F.2 gene product [C.elegans]//1.7e-17;137.86/Hs.7049:
A1141736
R-*OVARC*1000746//ESTs//0.16;366.60/Hs.136969:AA830918
R-*OVARC*1000769//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D.melanogaster]//4.6e-
45 28;430.69/Hs.42457:AA523306
R-*OVARC*1000771//ESTs//1.3e-87;461.94/Hs.22399:AA531016
R-*OVARC*1000781//ESTs//8.3e-119;572.97/Hs.41972:AA626793
R-*OVARC*1000787//EST//7.4e-18;115.93/Hs.164036:AA845659
R-*OVARC*1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR//4.9e-19;119.95/Hs.3069:L11066
40 R-*OVARC*1000802//ESTs//2.2e-41;383.78/Hs.161228:A1419764
R-*OVARC*1000834//Homo sapiens mRNA for atopy related autoantigen CALC//1.2e-106;536.95/Hs.61628:
Y17711
50 R-*OVARC*1000846//Clathrin, light polypeptide (Lcb)/1.6e-66;282.87/Hs.73919:X81637
R-*OVARC*1000850//Homo sapiens PB39 mRNA, complete cds//1.2e-115;579.96/Hs.18910:AF045584
R-*OVARC*1000862//EST//4.3e-14;129.81/Hs.150663:AA923096
R-*OVARC*1000876//ESTs//1.0e-115;573.96/Hs.87287:A1150674
R-*OVARC*1000883//ESTs//3.5e-109;523.98/Hs.28423:AA1336292
R-*OVARC*1000885//ESTs, Highly similar to HYPOTHETICAL OXIDOREDUCTASE IN ROCC-PTA INTERGENE
55

REGION [Bacillus subtilis]/7.9e-98:525:93//Hs.10366:W21953
 R-OVARC1000886//ESTs/8.2e-79:417:94//Hs.7729:AA830777
 R-OVARC1000891//ESTs/6.8e-75:401:94//Hs.5833:H15401
 R-OVARC1000897//ESTs/3.5e-91:440:98//Hs.125264:AA873350
 5 R-OVARC1000912
 R-OVARC1000915//ESTs/1.0e-45:328:82//Hs.163980:AA715814
 R-OVARC1000924//ESTs/1.0e-100:501:96//Hs.30204:AA497127
 R-OVARC1000936//EST/3.0e-74:367:98//Hs.145098:AA421696
 R-OVARC1000937//EST/1.1e-53:290:95//Hs.162846:AA631215
 10 R-OVARC1000945//ESTs/4.9e-51:301:89//Hs.20100:W25794
 R-OVARC1000948//ESTs/3.7e-67:332:98//Hs.112570:AA621971
 R-OVARC1000959//Small inducible cytokine A5 (RANTES)/7.2e-44:283:86//Hs.155464:AF088219
 R-OVARC1000960//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-41:348:80//Hs.43681:AL022394
 R-OVARC1000971//EST/6.2e-05:126:70//Hs.160491:AI254909
 15 R-OVARC1000984//ESTs, Weakly similar to No definition line found [C.elegans]/3.5e-68:346:96//Hs.25544:AA532784
 R-OVARC1000996//EST/0.12:92:71//Hs.117141:AA678811
 R-OVARC1000999//Homo sapiens KIAA0414 mRNA, partial cds//1.5e-44:513:73//Hs.127649:AB007874
 R-OVARC1001000//ESTs/1.8e-22:198:80//Hs.140608:N53448
 20 R-OVARC1001004//Human kpnI repeat mna (cdna clone pcd-kpnI-4), 3' end//1.7e-28:181:77//Hs.139107:K00629
 R-OVARC1001010//EST/2.1e-09:92:85//Hs.147893:AI223270
 R-OVARC1001011//EST/2.4e-14:200:75//Hs.149290:AI248117
 R-OVARC1001032//EST/2.7e-29:304:73//Hs.141733:W80630
 R-OVARC1001034//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//2.1e-09:
 25 137:74//Hs.77579:AF013263
 R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//4.1e-101:501:96//Hs.9899:AF099149
 R-OVARC1001040//ESTs/2.9e-87:415:99//Hs.132812:AI032046
 R-OVARC1001044//ESTs/1.1e-83:432:96//Hs.55043:N94384
 R-OVARC1001051//60S RIBOSOMAL PROTEIN L41//1.2e-16:124:88//Hs.108124:Z12962
 30 R-OVARC1001055//ESTs/2.4e-23:238:76//Hs.141421:H99231
 R-OVARC1001062//ESTs/3.4e-92:469:96//Hs.34658:N98652
 R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds//7.3e-97:463:98//Hs.3426:
 AF082657
 R-OVARC1001072//ESTs/1.3e-34:227:89//Hs.126704:W95844
 35 R-OVARC1001074
 R-OVARC1001085//Human T-cell leukemia virus enhancer factor//1.0:94:69//Hs.103126:U50729
 R-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337,
 LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))//1.4e-96:325:98//Hs.21753:AJ005897
 R-OVARC1001113//Homo sapiens diaphanous 1 (HDI1) mRNA, complete cds//3.3e-75:386:95//Hs.26584:
 40 AF051782
 R-OVARC1001117//Human G protein-coupled receptor (STRL22) mRNA, complete cds//3.9e-37:283:84//Hs.
 46468:U45984
 R-OVARC1001118//ESTs/5.3e-99:485:97//Hs.130815:AA936548
 R-OVARC1001129//ESTs/9.8e-66:351:95//Hs.18616:T99312
 45 R-OVARC1001161//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]/2.2e-
 66:346:95//Hs.53263:AA173226
 R-OVARC1001162//EST/1.5e-44:376:80//Hs.161917:AA483223
 R-OVARC1001167//ESTs/4.7e-110:548:96//Hs.35254:AI133727
 R-OVARC1001169//ESTs/0.22:152:68//Hs.149424:AI274200
 50 R-OVARC1001170//Small inducible cytokine A5 (RANTES)//1.8e-42:305:84//Hs.155464:AF088219
 R-OVARC1001173//EST/2.5e-35:182:84//Hs.161917:AA483223
 R-OVARC1001180//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//6.6e-64:247:
 80//Hs.97203:U83171
 R-OVARC1001188//ESTs/4.1e-18:296:69//Hs.139197:AA228343
 55 R-OVARC1001200//ESTs/2.0e-28:207:85//Hs.35121:AA877826
 R-OVARC1001232//ESTs/3.2e-61:358:91//Hs.6449:W95025
 R-OVARC1001240//ESTs/6.7e-45:316:85//Hs.121675:AA629668
 R-OVARC1001243//ESTs/2.3e-86:409:99//Hs.163091:AA742361

- R-OVARC1001261//ESTs//0.63:125.64//Hs.155743:AI344166
 R-OVARC1001268//ESTs//8.1e-20:113.98//Hs.109477:AA477929
 R-OVARC1001270//ESTs//1.5e-107:530.97//Hs.62905:AA460708
 R-OVARC1001271//ESTs//4.5e-36:401.72//Hs.20190:AA525532
 5 R-OVARC1001282//EST//4.0e-91:428.99//Hs.145599:AI263113
 R-OVARC1001296//ESTs//2.6e-63:301.100//Hs.125753:AA740885
 R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0518 protein, partial cds//3.8e-70:334.100//Hs.23763:AB011090
 R-OVARC1001329//Clathrin, light polypeptide (Lcb)//1.3e-68:304.83//Hs.73919:X81637
 10 R-OVARC1001330//Proline arginine-rich end leucine-rich repeat protein//1.0:147.53//Hs.76494:U41344
 R-OVARC1001339//Small inducible cytokine A5 (RANTES)//5.0e-48:452.76//Hs.155464:AF088219
 R-OVARC1001341//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//6.9e-85:464.93//Hs.23651:AA650356
 R-OVARC1001342//40S RIBOSOMAL PROTEIN S8//4.9e-110:568.95//Hs.118690:X67247
 15 R-OVARC1001344//EST//3.6e-44:341.81//Hs.162197:AA535216
 R-OVARC1001357//TUMOR-ASSOCIATED ANTIGEN L6//9.8e-44:250.93//Hs.3337:M90657
 R-OVARC1001360//ESTs//5.2e-110:534.98//Hs.24743:AA843844
 R-OVARC1001369//ESTs//1.7e-98:478.97//Hs.7729:AA830777
 R-OVARC1001372//ESTs//2.6e-97:456.99//Hs.153648:AI341415
 20 R-OVARC1001376//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.1e-53:344.72//Hs.153468:AB011147
 R-OVARC1001381//ESTs//5.1e-19:200.66//Hs.114031:AA700958
 R-OVARC1001391
 R-nnnnnnnnnnnn//ESTs//0.003 9:48.95//Hs.117964:N20913
 25 R-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//3.2e-111:561.95//Hs.21586:AB006651
 R-OVARC1001419
 R-OVARC1001425//EST//5.7e-20:395.66//Hs.159707:AI393136
 R-OVARC1001436//ESTs//9.6e-90:427.99//Hs.6982:AA622427
 R-OVARC1001442//ESTs//1.1e-66:317.100//Hs.18437:AI206345
 30 R-OVARC1001453//ESTs//2.0e-20:163.84//Hs.133503:AA628592
 R-OVARC1001476//EST//0.23:125.66//Hs.71444:AA131700
 R-OVARC1001480//ESTs//3.1e-56:181.97//Hs.40109:AA928694
 R-OVARC1001489//ESTs//1.0:297.58//Hs.86723:AA393089
 R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds//3.0e-117:585.96//Hs.6534:AF016507
 35 R-OVARC1001506//Small inducible cytokine A5 (RANTES)//1.8e-48:283.90//Hs.155464:AF088219
 R-OVARC1001525//EST//0.80:170.60//Hs.157398:AI364539
 R-OVARC1001542//Homo sapiens hJTB mRNA, complete cds//1.6e-111:566.95//Hs.6396:AB016492
 R-OVARC1001547//ESTs//5.7e-105:564.93//Hs.68835:AA088388
 40 R-OVARC1001577//Homo sapiens SRP46 splicing factor retrospseudogene mRNA//4.4e-20:150.89//Hs.155160:AF031166
 R-OVARC1001600//Human mRNA for KIAA0118 gene, partial cds//8.6e-21:282.72//Hs.154326:D42087
 R-OVARC1001610//ESTs//4.6e-108:555.95//Hs.44295:N32019
 R-OVARC1001611//ESTs//0.0021:117.71//Hs.135568:AA972965
 45 R-OVARC1001615//Homo sapiens KIAA0409 mRNA, partial cds//9.2e-19:114.78//Hs.5158:AB007869
 R-OVARC1001668//ESTs//1.0:127.69//Hs.153290:AI022659
 R-OVARC1001702//ESTs//4.8e-44:225.97//Hs.96855:AA346854
 R-OVARC1001703//ESTs//2.3e-89:426.99//Hs.27099:W60080
 R-OVARC1001711//ESTs//1.9e-57:251.99//Hs.9732:AA527784
 50 R-OVARC1001726//ESTs, Highly similar to APICAL PROTEIN [Xenopus laevis]//1.2e-27:236.81//Hs.15485:AA046954
 R-OVARC1001731//Tropomyosin4 (fibroblast)//7.9e-74:422.90//Hs.102824:X05276
 R-OVARC1001745//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//1.7e-62:300.83//Hs.144563:AF057280
 55 R-nnnnnnnnnnnn//ESTs, Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [S.cerevisiae]//6.8e-100:540.92//Hs.117741:AA903456
 R-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//1.1e-109:567.94//Hs.155377:U97670

- R-nnnnnnnnnnn/Homo sapiens mRNA for KIAA0675 protein, complete cds//2.0e-109:529:97//Hs.15869:AB014575
- R-OVARC1001768//ESTs//3.5e-59:327:94//Hs.107923:H66127
- R-OVARC1001791//ESTs//1.3e-111:565:96//Hs.6107:AA160604
- 5 R-OVARC1001795//ESTs//2.8e-97:526:93//Hs.72158:AA156978
- R-OVARC1001802//Homo sapiens DEC-205 mRNA, complete cds//4.8e-36:276:81//Hs.153563:AF011333
- R-OVARC1001805//ESTs//4.1e-78:375:98//Hs.126902:AI374688
- R-OVARC1001812//EST//4.8e-45:349:80//Hs.162677:AA604831
- 10 R-OVARC1001813//Homo sapiens mRNA for KIAA0538 protein, partial cds//2.1e-15:519:63//Hs.25639:AB011110
- R-OVARC1001820//ESTs//9.5e-50:314:80//Hs.140491:W52705
- R-OVARC1001828//ESTs//0.11:186:63//Hs.29055:AI374621
- R-OVARC1001846//ESTs//0.34:134:66//Hs.152992:AJ242160
- R-OVARC1001861//ESTs//2.3e-19:120:92//Hs.42225:N31809
- 15 R-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence//1.9e-105:571:91//Hs.25300:AF070611
- R-OVARC1001879//EST//1.3e-24:185:85//Hs.136617:AA630476
- R-OVARC1001880//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.2e-49:302:90//Hs.153468:AB011147
- R-OVARC1001883//ESTs//1.0e-51:295:93//Hs.164059:AA447310
- 20 R-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//1.6e-87:346:90//Hs.6216:AF061749
- R-OVARC1001901//ESTs//6.8e-24:132:98//Hs.130797:AA904435
- R-OVARC1001911//ESTs//1.1e-88:491:92//Hs.32343:W73855
- R-OVARC1001916//ESTs//7.9e-97:491:95//Hs.24989:H97842
- 25 R-OVARC1001928
- R-OVARC1001942//ESTs, Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [S.cerevisiae]//2.5e-39:253:88//Hs.117741:AA903456
- R-OVARC1001943//ESTs//9.3e-13:78:100//Hs.143680:W38637
- R-OVARC1001949//ESTs, Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]//8.3e-96:498:94//Hs.22744:AI379892
- 30 R-OVARC1001950//EST//1.3e-35:236:81//Hs.132635:AI032875
- R-OVARC1001987//ESTs//5.6e-94:514:92//Hs.21148:AI183729
- R-OVARC1001989//ESTs//9.7e-46:228:99//Hs.127046:AA935887
- R-OVARC1002044//ESTs//3.4e-45:303:85//Hs.132722:AA618531
- 35 R-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.4e-109:542:96//Hs.108258:AB007934
- R-OVARC1002066//ESTs//8.5e-97:455:99//Hs.135477:AI088556
- R-OVARC1002082//Homo sapiens mRNA for KIAA0772 protein, complete cds//8.1e-47:340:82//Hs.15519:AB018315
- 40 R-OVARC1002107//ESTs//5.9e-103:498:98//Hs.157207:AA629860
- R-OVARC1002127//ESTs//3.0e-87:419:98//Hs.127833:AI347130
- R-OVARC1002138//ESTs, Weakly similar to HYPOTHETICAL 54.7 KD PROTEIN C07A9.1 IN CHROMOSOME III [Caenorhabditis elegans]//1.7e-102:485:98//Hs.137516:AA805691
- R-OVARC1002143//ESTs//1.3e-79:428:92//Hs.158126:W26825
- 45 R-OVARC1002156//ESTs//1.6e-38:198:98//Hs.22957:AA478923
- R-OVARC1002158//ESTs//7.3e-81:412:96//Hs.12211:AA908631
- R-OVARC1002165//ESTs//1.8e-09:154:72//Hs.49354:AA424160
- R-OVARC1002182//ESTs//4.3e-80:465:91//Hs.77067:AA040478
- 50 R-PLACE1000004//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//7.5e-32:164:99//Hs.144194:AA706337
- R-PLACE1000005//EST//0.37:212:60//Hs.127020:AA934920
- R-PLACE1000007//Homo sapiens clone 24422 mRNA sequence//3.8e-16:100:97//Hs.109268:AF070557
- R-PLACE1000014//EST//9.6e-44:344:77//Hs.161917:AA483223
- R-PLACE1000031//ESTs//2.2e-32:374:70//Hs.117969:H94870
- 55 R-PLACE1000040//ESTs//0.00017:316:59//Hs.23342:AI310440
- R-PLACE1000048//Human Line-1 repeat mRNA with 2 open reading frames//4.8e-79:519:86//Hs.23094:M19503
- R-PLACE10000501//ESTs//9.7e-90:453:96//Hs.27410:N25612
- R-PLACE1000061//Ribosomal protein L37a//5.5e-22:126:97//Hs.1946:L06499

R-PLACE1000066/ESTs, Weakly similar to C. elegans cDNA yk10c10.3 [C.elegans]/1.4e-61.33:1
94/Hs.30026:A1356771

R-PLACE1000078/ESTs/2.6e-30:212:85/Hs.89312:AA167659

R-PLACE1000081

R-PLACE1000094

R-PLACE1000133/ESTs//4.4e-87:448:94/Hs.93748:AA884505

R-PLACE1000142/ESTs, Weakly similar to enoyl-CoA hydratase [H.sapiens]/5.5e-103:538:94/Hs.9670:
AA632135

R-PLACE1000184/Homo sapiens estrogen-related receptor gamma mRNA, complete cds//4.1e-114:594:94/Hs.
151017:AF058291

R-PLACE1000185/ESTs, Weakly similar to No definition line found [C.elegans]/2.0e-119:114:95/Hs.7036:
W22072

R-PLACE1000213/ESTs//9.4e-99:944:96/Hs.24398:A162946

R-PLACE1000214/ESTs//5.3e-98:466:98/Hs.28661:AA805916

R-PLACE1000236/Homo BENE mRNA, partial cds//1.7e-119:162:84/Hs.85889:U17077

R-PLACE1000246/EST//0.026:134:66/Hs.135611:Z21545

R-PLACE1000292/ESTs//2.5e-80:418:96/Hs.138233:N57912

R-PLACE1000332/EST//1.7e-82:422:96/Hs.118637:T61940

R-PLACE1000347/ESTs//8.5e-36:180:100/Hs.6377:AA632424

R-PLACE1000374/ESTs//2.8e-90:434:98/Hs.161765:AI423126

R-PLACE1000380/ESTs//1.0e-81:399:97/Hs.47105:AI334994

R-PLACE1000383/ESTs//3.7e-75:405:94/Hs.23200:AA203708

R-PLACE1000401/ESTs//1.4e-16:212:72/Hs.151665:AA020959

R-PLACE1000406/ESTs//2.1e-51:259:97/Hs.129651:N53089

R-PLACE1000420/ESTs//7.7e-92:471:95/Hs.144407:AA737799

R-PLACE1000421/ESTs//2.9e-14:282:67/Hs.142068:AA176125

R-PLACE1000424/EST//2.9e-35:453:70/Hs.162404:AA573131

R-PLACE1000435/Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete
cds//1.6e-47:472:77/Hs.113259:AF023456

R-PLACE1000444/ESTs, Moderately similar to platelet glycoprotein IIb precursor [H.sapiens]/2.0e-58:410:81/
Hs.97579:AA398118

R-PLACE1000453/ESTs//2.3e-85:442:95/Hs.9725:AA039793

R-PLACE1000481/ESTS, Weakly similar to Ndr protein kinase [H.sapiens]/3.2e-109:549:95/Hs.19074:U69566

R-PLACE1000492/ESTs, Highly similar to vacuolar protein sorting homolog v-rps33b [R.norvegicus]/3.5e-83:
435:94/Hs.26510:AA700425

R-PLACE1000540/ESTs//3.2e-58:281:99/Hs.118270:AA844729

R-PLACE1000547/Homo sapiens mRNA for KIAA0640 protein, partial cds//2.2e-32:208:88/Hs.153026:
AB014540

R-PLACE1000562/ESTs, Weakly similar to HYPOTHETICAL 23.0 KD PROTEIN IN IXR1-TFA1 INTERGENIC
REGION [Saccharomyces cerevisiae]/1.9e-26:220:81/Hs.163791:W25348

R-PLACE1000564/ESTs//1.1e-54:302:92/Hs.158520:AI380485

R-PLACE1000583/Human mRNA for KIAA0355 gene, complete cds//5.5e-43:404:75/Hs.153014:AB002353

R-nnnnnnnnnnnn/Guanylate binding protein 1, interferon-inducible, 67kD//6.1e-79:542:82/Hs.62661:M55442

R-PLACE1000596/ESTs//0.0028:364:59/Hs.106900:AA457030

R-PLACE1000599/Human mRNA for KIAA0118 gene, partial cds//4.3e-49:295:90/Hs.154326:D42087

R-PLACE1000610/ESTs//0.0010:104:74/Hs.17413:N45301

R-PLACE1000636/ESTs//1.8e-64:340:95/Hs.100895:AA479308

R-PLACE1000653/Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//5.3e-101:506:
96/Hs.5819:AF102265

R-PLACE1000656/Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and
LLNL110F1857Q7 (RPZD Berlin))//1.4e-102:559:92/Hs.29595:AJ005896

R-PLACE1000706/Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds//2.8e-10:281:
64/Hs.128763:AF009353

R-PLACE1000712/ESTs//7.8e-60:317:95/Hs.8245:AA115485

R-PLACE1000716

R-PLACE1000748/ESTs//8.9e-87:466:93/Hs.25245:AA176701

R-PLACE1000749/EST//0.019:186:61/Hs.135443:AI077396

R-PLACE1000755/ESTs, Weakly similar to HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III [C.ele-

- egans]/[3.9e-40:224.94//Hs.87889:AA262008
 R-PLACE1000769//Homo sapiens clone 24566 mRNA sequence/[6.5e-27:531.66//Hs.133342:AF070536
 R-PLACE1000785//Homo sapiens mRNA for KIA0648 protein, partial cds/[8.5e-103:513.96//Hs.31921:AB014548
- 5 R-PLACE1000786//ESTs/[5.2e-93:449.97//Hs.58389:W74482
 R-nnnnnnnnnnn/Hs.sapiens mRNA for chemokine HCC-1/10.88:201.60//Hs.20144:AF088219
 R-PLACE1000798//ESTs/[1.1e-97:508.94//Hs.139119:N32189
 R-PLACE1000841//ESTs, Highly similar to guanine nucleotide regulatory protein [H.sapiens]/[7.7e-31:220.86//Hs.117576:R33135
- 10 R-nnnnnnnnnnn/ESTs/[1.8e-87:459.94//Hs.43100:AA186588
 R-PLACE1000856//ESTs/[0.0084:224.59//Hs.145906:AI275039
 R-PLACE1000863//ESTs, Highly similar to PUTATIVE 40S RIBOSOMAL PROTEIN YHR148W [Saccharomyces cerevisiae]/[2.2e-92:467.95//Hs.6118-.AI141558
 R-PLACE1000909//ESTs/[4.7e-89:435.97//Hs.95744:AI392846
- 15 R-PLACE1000931//EST/[1.9e-28:261.73//Hs.135545:AI097091
 R-PLACE1000948//ESTs/[0.034:329.58//Hs.114851:AA608697
 R-PLACE1000972//EST/[3.3e-24:264.74//Hs.130321:AI002941
 R-PLACE1000977//EST/[0.085:153.65//Hs.131646:AI025689
 R-PLACE1000979
- 20 R-PLACE1001000//ESTs/[4.7e-56:284.96//Hs.117978:AA810725
 R-PLACE1001007//ESTs, Moderately similar to MNK1 [H.sapiens]/[5.2e-63:343.93//Hs.5662:AA868361
 R-PLACE1001010//EST/[0.96:53.71//Hs.96973:AA351146
 R-PLACE1001015//Oxytocin receptor/[2.8e-25:308.71//Hs.2820:X64878
 R-PLACE1001024//ESTs/[5.0e-12:79.96//Hs.97910:AA404736
- 25 R-PLACE1001036//ESTs/[4.0e-15:301.65//Hs.137947:AI025762
 R-PLACE1001062//ESTs/[5.2e-15:199.73//Hs.138982:AA056120
 R-PLACE1001076//ESTs/[3.9e-84:406.98//Hs.115455:AA678124
 R-PLACE1001088//ESTs/[3.0e-106:518.97//Hs.158964:AA639580
 R-PLACE1001092//Homo sapiens SEC63 (SEC63) mRNA, complete cds/[0.035:259.59//Hs.31575:AF100141
- 30 R-PLACE1001104//ESTs/[6.1e-115:582.95//Hs.10972:AA164268
 R-PLACE1001118//ESTs/[6.9e-81:440.93//Hs.5383:AA913610
 R-PLACE1001136//ESTs/[7.4e-41:168.83//Hs.95115:AA206594
 R-PLACE1001168//ESTs/[3.9e-21:116.99//Hs.5897:AA148834
 R-PLACE1001171//ESTs, Highly similar to CYTOCHROME B-245 LIGHT CHAIN [H.sapiens]/[0.91:77.71//Hs.115211:AA287527
- 35 R-PLACE1001185//ESTs/[1.5e-65:330.96//Hs.26368:AA789297
 R-PLACE1001238//ESTs, Moderately similar to RNA polymerase I associated factor [M.musculus]/[1.9e-99:512.94//Hs.24884:AA176812
 R-PLACE1001241//ESTs/[1.1e-81:446.93//Hs.42278:AI073464
- 40 R-PLACE1001257//EST/[6.4e-46:298.87//Hs.162404:AA573131
 R-PLACE1001272//ESTs/[0.31:158.61//Hs.42960:N95371
 R-PLACE1001279//ESTs/[1.8e-77:376.97//Hs.29276:AA427780
 R-PLACE1001280//ESTs/[1.1e-30:134.89//Hs.163492:AI334460
 R-PLACE1001294//ESTs, Moderately similar to GAMETOGENESIS EXPRESSED PROTEIN GEG-154 [M.musculus]/[2.7e-22:181.84//Hs.48320:AA149548
- 45 R-PLACE1001304//ESTs, Weakly similar to ZINC FINGER PROTEIN 135 [H.sapiens]/[4.2e-34:195.92//Hs.86276:W27601
 R-PLACE1001311//ESTs/[9.1e-91:438.97//Hs.41055:AI339056
 R-PLACE1001323//Human transmembrane 4 superfamily protein (SAS) mRNA, complete cds/[5.5e-44:215.86//Hs.50984:U01160
- 50 R-PLACE1001351//ESTs/[2.4e-101:494.97//Hs.23944:AI097077
 R-PLACE1001366//Small inducible cytokine A5 (RANTES)/[8.7e-43:284.85//Hs.155464:AF088219
 R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds/[2.3e-81:431.93//Hs.152005:AF009615
- 55 R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence/[1.0e-36:192.97//Hs.12342:AF055030
 R-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds/[1.0e-86:456.94//Hs.21301:AF093419
 R-PLACE1001387//ESTs/[6.0e-74:383.94//Hs.55016:AI298280

- R-PLACE1001395//ESTs//2.3e-94:473:95//Hs.22394:N32555
 R-PLACE1001399//ESTs//2.6e-41:204:100//Hs.24462:N36348
 R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//2.6e-45:242:95//Hs.110404:AF091087
- 5 R-PLACE1001414//ESTs//0.0013:77:75//Hs.144614:AA291800
 R-PLACE1001440
 R-PLACE1001456//EST//0.76:120:62//Hs.34011:H48115.
 R-PLACE1001468//ESTs//4.0e-80:403:96//Hs.131832:AJ017547
 R-PLACE1001484//ESTs//3.0e-16:201:72//Hs.153413:AJ248625
- 10 R-PLACE1001502//ESTs//8.1e-31:161:99//Hs.126264:AA455617
 R-PLACE1001503//ESTs//2.4e-37:176:81//Hs.141581:AA315361
 R-PLACE1001517//Homo sapiens hGAAI mRNA, complete cds//2.1e-57:339:90//Hs.4742:AB006969
 R-PLACE1001534//ESTs//3.6e-61:304:97//Hs.45207:AI042153
 R-PLACE1001545//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.6e-22:170:85//Hs.155456:AA070265
- 15 R-PLACE1001551//ESTs//1.5e-39:202:98//Hs.139269:AA894431
 R-PLACE1001570//EST//1.1e-70:495:82//Hs.144234:W52249
 R-PLACE1001602//EST//0.33:297:57//Hs.149839:AI287601
 R-PLACE1001603//ESTs//2.0e-17:181:76//Hs.155334:AA827904
- 20 R-PLACE1001610//EST//1.1e-86:442:95//Hs.112580:AA608683
 R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds//1.1e-42:217:97//Hs.75258:AF054174
 R-PLACE1001632//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//1.5e-78:458:91//Hs.114547:AA167095
- 25 R-PLACE1001634//ESTs//0.0035:40:97//Hs.101577:AI168526
 R-PLACE1001640//ESTs//0.0028:377:57//Hs.131044:D61640
 R-PLACE10016727//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.98:141:62//Hs.153060:AA195804
 R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//4.7e-113:545:97//Hs.3688:AF069250
- 30 R-PLACE1001692//EST//3.0e-43:430:75//Hs.162975:AA679124
 R-PLACE1001705//ESTs//3.0e-81:418:94//Hs.22646:AI374903
 R-PLACE1001716//EST//0.76:150:62//Hs.128906:AA983667
 R-PLACE1001720//ESTs//2.4e-64:385:90//Hs.60455:AA010993
- 35 R-PLACE1001729//ESTs//2.9e-84:418:96//Hs.134740:AA282171
 R-PLACE1001739//ESTs, Weakly similar to P68 PROTEIN [H.sapiens]//9.1e-32:206:89//Hs.6366:AA614113
 R-PLACE1001740//EST//6.5e-05:113:68//Hs.139949:AA644266
 R-PLACE1001745//ESTs//3.3e-92:473:95//Hs.104270:AA236479
 R-PLACE1001746//ESTs//8.8e-93:443:98//Hs.112198:AI423937
- 40 R-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//4.1e-93:540:89//Hs.4812:AF061243
 R-PLACE1001756//ESTs//0.17:157:66//Hs.141565:N64662
 R-PLACE1001761
 R-PLACE1001771//ESTs//0.92:165:62//Hs.473 87:N51980
- 45 R-PLACE1001781//ESTs//5.7e-84:437:95//Hs.23363:AA081236
 R-PLACE1001799//EST//0.00039:126:65//Hs.123267:AA807352
 R-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA; partial cds//1.3e-93:463:95//Hs.40820:AF058953
- 50 R-PLACE1001821//Small inducible cytokine A5 (RANTES)//2.7e-35:328:75//Hs.155464:AF088219
 R-PLACE1001845
 R-PLACE1001869//EST//1.0:207:62//Hs.137298:W32868
 R-PLACE1001897//ESTs//2.4e-23:219:80//Hs.7503:H50009
 R-PLACE1001912//ESTs//1.5e-32:162:78//Hs.136810:AA789098
 R-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//3.9e-74:363:97//Hs.17839:AF099936
- 55 R-PLACE1001928//Homo sapiens mRNA for KIAA0623 protein, complete cds//0.85:130:66//Hs.151406:AB014523
 R-PLACE1001983//ESTs//2.8e-66:334:96//Hs.110155:AA007313

- R-PLACE1001989//ESTs//1.3e-88.453.95//Hs.132717:AA171941
R-PLACE1002046
R-PLACE1002052//ESTs//1.7e-79.428.94//Hs.6737:N32595
R-PLACE1002066//ESTs//2.8e-82.427.94//Hs.132972:AA543094
5 R-PLACE1002072//ESTs//0.27:108.66//Hs.123163:AA809619
R-PLACE1002073//EST//5.5e-70:369.95//Hs.132339:AI028552
R-PLACE1002090//ESTs//6.3e-73.361.96//Hs.134469:AA731632
R-PLACE1002115//ESTs//4.6e-34:233.88//Hs.163443:R23311
10 R-PLACE1002119//ESTs//1.2e-88.444.96//Hs.15725:AA521293
R-PLACE1002140//ESTs//6.6e-22:118:100//Hs.22793:W91937
R-PLACE1002150//ESTs//4.0e-96.465.98//Hs.7312:AI167614
R-PLACE1002157//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG[H.sapiens]//3.6e-39:400:76//Hs.162172:AA534189
15 R-PLACE1002163//ESTs//3.2e-83.428.95//Hs.137011:AI185965
R-PLACE1002171//ESTs//5.3e-68.392.90//Hs.62273:AA143745
R-PLACE1002205//ESTs//1.5e-39:211.95//Hs.28338:N48793
R-PLACE1002213//ESTs//5.1e-38:290.83//Hs.146811:AA410788
R-PLACE1002227//EST//1.3e-14:214:72//Hs.46979:N49892
R-PLACE1002256//ESTs//2.4e-100.484.98//Hs.9343:AI004257
20 R-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//5.8e-67:501:81//Hs.23094:M19503
R-PLACE1002319//ESTs//1.4e-28:17.8:92//Hs.7353:AA209308
R-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds//1.6e-95:501:93//Hs.18277:AB018271
R-PLACE1002395//ESTs//3.6e-25:248.77//Hs.3853:AA034291
R-PLACE1002399//ESTs//1.5e-27:238.78//Hs.13014:W26381
25 R-PLACE1002433//ESTs//4.3e-108:511.98//Hs.98324:AA621959
R-PLACE1002437//EST//1.2e-06:158.61//Hs.159833:T24110
R-PLACE1002439//Sjogren syndrome antigen B (autoantigen La)//0.93:176:60//Hs.83715:X69804
R-PLACE1002450//ESTs//1.5e-89:432.98//Hs.47371:AA136333
R-PLACE1002465//ESTs//1.6e-92:488.93//Hs.78110:AA741320
30 R-PLACE1002474//Human matrilin-2 precursor mRNA, partial cds//4.9e-23:166.85//Hs.19368:U69263
R-PLACE1002477//ESTs//2.5e-62:305.98//Hs.88605:AA421132
R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds//3.6e-55:307:91//Hs.17200:AF042273
R-PLACE1002499//ESTs//7.4e-72:373.96//Hs.128221:AA972429
35 R-PLACE1002500//Homo sapiens KIAA0409 mRNA, partial cds//1.2e-40:296.83//Hs.5158:AB007869
R-PLACE1002514//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.sapiens]//6.4e-14:217.69//Hs.152230:AI140609
R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//5.1e-88:582.85//Hs.88756:AB018256
40 R-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//2.7e-19:116.93//Hs.99348:AC004774
R-PLACE1002537//ESTs//4.8e-93:440.99//Hs.164005:AA766491
R-PLACE1002571//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]//1.3e-108:555:95//Hs.23259:AA532437
R-PLACE1002578//EST//1.9e-40:337.81//Hs.162404:AA573131
45 R-PLACE1002583//EST//1.2e-07:264.65//Hs.156414:AI339738
R-PLACE1002591//ESTs//2.3e-67:372.94//Hs.143046:N73778
R-PLACE1002598//ESTs, Highly similar to PROTEIN HI1715 [Haemophilus influenzae]//1.2e-44:228.97//Hs.7527:AA843208
R-PLACE1002604//ESTs//3.3e-106:532.96//Hs.86828:AA632147
R-PLACE1002625//EST//3.8e-13:173.74//Hs.138597:H77749
50 R-PLACE1002665//Small inducible cytokine A4 (homologous to mouse Mip-1b)//1.0:189:58//Hs.75703:J04130
R-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//3.8e-79:390:97//Hs.124903:AF068180
R-PLACE1002714//ESTs//8.2e-63:340.93//Hs.7973:H19830
60 R-PLACE1002722//ESTs, Weakly similar to putative G-protein-coupled receptor [H.sapiens]//6.8e-75:445.90//Hs.29202:R71586
75 R-PLACE1002768//ESTs//1.2e-70:359.95//Hs.132600:HI12865
R-PLACE1002772//ESTs//8.1e-49:362.82//Hs.141254:AI334099
R-PLACE1002782//ESTs//2.4e-58:284.98//Hs.143545:AI149014

- R-PLACE1002794//ESTs//5.4e-21:114:100//Hs.77365:W93593
 R-PLACE1002811//ESTs//6.7e-68:329:98//Hs.78026:AA456955
 R-PLACE1002815//ESTs//6.8e-103:537:93//Hs.5459:AI304392
 R-PLACE1002816//ESTs//3.9e-05:118:68//Hs.98641:AA429916
 5 R-PLACE1002834//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//2.1e-42:233:94//Hs.61518:AA167094
 R-PLACE1002839//ESTs//1.7e-10:292:64//Hs.93012:R96142
 R-PLACE1002851//ESTs//1.7e-73:381:95//Hs.135021:AI096756
 R-PLACE1002853//ESTs//1.2e-89:453:96//Hs.23630:N57539
 10 R-PLACE1002881//ESTs//1.1e-71:360:96//Hs.34392:AI066762
 R-PLACE1002908//EST//2.7e-31:177:94//Hs.147925:AI249332
 R-PLACE1002941//ESTs//4.0e-96:519:92//Hs.125139:AA523995
 R-PLACE1002962
 R-PLACE1002968//ESTs//4.7e-31:420:69//Hs.116518:AA653202
 15 R-PLACE1002991//ESTs//9.0e-81:418:95//Hs.132717:AA171941
 R-PLACE1002993//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H. sapiens]//1.3e-86:502:89//Hs.32232:AA604268
 R-PLACE1002996//ESTs//1.9e-44:218:100//Hs.63657:AI144268
 R-PLACE1003025//ESTs//8.4e-104:517:96//Hs.10711:AI151499
 20 R-PLACE1003027//Human mRNA for KIAA0238 gene, partial cds//0.97:156:60//Hs.82042:D87075
 R-PLACE1003044//Human onconeural ventral antigen-1 (Nova-1) mRNA, complete cds//1.0:200:63//Hs.214:U04840
 R-PLACE1003092//ESTs//0.0046:267:60//Hs.133095:AA927777
 R-PLACE1003100//ESTs, Highly similar to NODULATION PROTEIN G [Rhizobium meliloti]//9.5e-94:941:93//Hs.6318:AI131178
 25 R-PLACE1003108//ESTs//0.00065:184:66//Hs.154366:AA527359
 R-PLACE1003136//Signal recognition particle 54 kD protein//0.057:317:59//Hs.49346:U51920
 R-PLACE1003145//ESTs//1.9e-98:534:92//Hs.61929:AA044757
 R-PLACE1003153//ESTs//5.8e-76:367:98//Hs.105196:AA483467
 30 R-PLACE1003174//ESTs//1.7e-44:226:98//Hs.59688:AA453924
 R-PLACE1003176
 R-PLACE1003190//ESTs//1.6e-74:356:99//Hs.121282:AI091453
 R-PLACE1003200//ESTs//4.6e-93:461:96//Hs.24321:AA971017
 R-PLACE1003205//ESTs//0.037:171:61//Hs.157077:H44802
 35 R-PLACE100323 8//ESTs, Weakly similar to KIAA0001 [H. sapiens]//2.5e-82:436:94//Hs.58561:W79123
 R-PLACE1003249//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//7.9e-44:313:84//Hs.73614:U83460
 R-PLACE1003256//EST//9.6e-46:284:88//Hs.162404:AA573131
 R-PLACE1003258//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H. sapiens]//8.3e-102:551:92//Hs.52431:AA625326
 40 R-PLACE1003296//ESTs//1.9e-88:451:96//Hs.57749:W92986
 R-PLACE1003302//ESTs, Highly similar to ZINC FINGER PROTEIN 43 [Homo sapiens]//8.2e-93:458:96//Hs.29147:AA883993
 R-PLACE1003334//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H. sapiens]//3.3e-94:463:97//Hs.155050:AA908765
 45 R-PLACE1003342//ESTs//6.0e-88:447:96//Hs.107527:R66438
 R-PLACE1003343//EST//0.0087:412:58//Hs.159963:AA977701
 R-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds//1.1e-99:469:98//Hs.6564:U92715
 50 R-PLACE1003361//ESTs//3.5e-64:332:95//Hs.163861:AI199636
 R-PLACE1003366//ESTs//1.0e-87:492:92//Hs.72222:AA158234
 R-PLACE1003369//ESTs, Weakly similar to ZK1058.4 [C. elegans]//3.5e-18:109:95//Hs.27670:AI051591
 R-PLACE1003373//Homo sapiens mRNA for KIAA0472 protein, partial cds//2.6e-54:279:80//Hs.6874:AB007941
 R-PLACE1003375//ESTs//1.7e-88:431:97//Hs.41327:AI039909
 55 R-PLACE1003383//ESTs//0.00084:177:64//Hs.120695:AI377755
 R-PLACE1003401//ESTs//1.1e-16:147:80//Hs.132187:AI039020
 R-PLACE1003420//ESTs//1.4e-93:481:94//Hs.122565:AI126840
 R-PLACE1003454//ESTs//4.0e-57:310:93//Hs.121688:AA743697

R-PLACE1003478//EST//1.0:162:63//Hs.147003:AI184671
 R-PLACE1003493//ESTs//1.2e-73:383.95//Hs.28852:R64270
 R-PLACE1003516//ESTs//3.2e-23:206.80//Hs.138632:H97952
 R-PLACE1003519//H.sapiens hnRNP-E1 mRNA//1.7e-22:236.79//Hs.2853:Z29505
 5 R-PLACE1003521//ESTs//5.8e-74:371.96//Hs.30818:AA194980
 R-PLACE1003528//ESTs//1.1e-40:219.82//Hs.138856:H47461
 R-PLACE1003537//ESTs, Weakly similar to multispanning membrane protein [H.sapiens]//7.4e-69:338.98//Hs.110439:N93209
 R-PLACE1003553//ESTs//2.2e-87:438.97//Hs.132022:AI040321
 10 R-PLACE1003566//ESTs//1.2e-62:298.92//Hs.30799:AI052591
 R-PLACE1003575//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.4e-22:145.80//Hs.92381:AB007956
 R-PLACE1003583//ESTs, Weakly similar to hypothetical L1 protein [H.sapiens]//1.5e-14:264.65//Hs.158253:R86178
 15 R-PLACE1003584
 R-PLACE1003592//ESTs//1.3e-15:213.69//Hs.139507:T77542
 R-PLACE1003593//ESTs, Highly similar to FRG1 gene product [H.sapiens]//5.8e-75:459.89//Hs.23884:AD77106
 R-PLACE1003596//ESTs//0.011:273.61//Hs.71719:AA142875
 R-PLACE1003602//Homo sapiens mRNA expressed in placenta//7.8e-97:576.88//Hs.56851:D83200
 20 R-PLACE1003605//ESTs//3.7e-86:407.99//Hs.136057:AA988299
 R-nnnnnnnnnnn//ESTs//1.0:78:71//Hs.101248:T26446
 R-PLACE1003618//ESTs//6.8e-30:281.79//Hs.114455:AA411943
 R-PLACE1003625//ESTs//7.2e-78:377.98//Hs.102708:AA292285
 R-PLACE1003638//ESTs//6.7e-38:274.82//Hs.138852:AA284247
 25 R-PLACE1003669//ESTs//9.7e-83:418.95//Hs.4842:AI342607
 R-PLACE1003704//ESTs//3.0e-13:99.89//Hs.81648:W26521
 R-PLACE1003709//ESTs//0.019:178.60//Hs.32100:N59866
 R-PLACE1003711//ESTs//0.99:126.63//Hs.47005:N98639
 R-PLACE1003723//ESTs//1.7e-89:448.96//Hs.157222:AA766987
 30 R-PLACE1003738//ESTs//2.5e-36:182.100//Hs.122162:AI057087
 R-PLACE1003760//Human globin gene//L9e-98:538.91//Hs.100090:M69023
 R-PLACE1003762//EST//2.9e-15:125.85//Hs.162083:AA487512
 R-PLACE1003768//Human P042 gene, complete cds//3.1e-18:300.69//Hs.158302:U88965
 R-PLACE1003771//ESTs//1.2e-09:64.100//Hs.23799:AI003798
 35 R-PLACE1003783//ESTs, Weakly similar to D2085.5 [C.elegans]//3.8e-38:199.97//Hs.115197:AA215757
 R-PLACE1003784//ESTs//3.7e-87:428.97//Hs.157985:AI366909
 R-PLACE1003795//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.2e-36:236.88//Hs.153468:AB011147
 R-PLACE1003833//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//8.5e-62:313.96//Hs.121020:AA526092
 40 R-PLACE1003850//ESTs//4.0e-67:351.96//Hs.159303:T91059
 R-PLACE1003858//ESTs//0.96:87.66//Hs.107112:AA679058
 R-nnnnnnnnnnn
 R-PLACE1003870//EST//2.9e-34:281.79//Hs.160895:AI365871
 R-nnnnnnnnnnn
 45 R-PLACE1003886//ESTs//6.7e-85:410.97//Hs.25129:W93595
 R-PLACE1003888//ESTs//0.0085:165.64//Hs.96739:AA441915
 R-PLACE1003900//EST//2.4e-05:129.69//Hs.127931:AA969259
 R-PLACE1003903//ESTs, Highly similar to CTP SYNTHASE [Homo sapiens]//1.5e-54:282.96//Hs.58553:AA100804
 50 R-PLACE1003915//EST//0.87:55.76//Hs.145930:AI275760
 R-PLACE1003923//ESTs//1.7e-89:456.95//Hs.14125:AA156236
 R-PLACE1003932//ESTs//3.0e-50:340.84//Hs.151208:AI126110
 R-PLACE1003936//EST//1.8e-08:208.65//Hs.162656:AA603567
 55 R-PLACE1003968//ESTs//7.4e-49:301.90//Hs.93850:AA115330
 R-PLACE1004104//ESTs//1.9e-46:254.94//Hs.96802:AA443231
 R-PLACE1004114//ESTs//1.2e-64:322.97//Hs.28928:AI052052
 R-PLACE1004118//ESTs//1.0e-83:404.98//Hs.112764:AA609770

- R-PLACE1004128//ESTs//5.3e-80.415.95//Hs.11835:AA040244
 R-PLACE1004149//ESTs//7.2e-25.331.72//Hs.141084:H11714
 R-PLACE1004156//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.0e-56.491.76//Hs.113283:AF018080
 R-PLACE1004161//ESTs//2.0e-59.355.88//Hs.13830:AA918601
 5 R-PLACE1004183//Homo sapiens cytochrome c oxidase assembly protein COX11(COX11) mRNA, complete cds//
 4.7e-78.434.91//Hs.153504:AF044321
 R-PLACE1004197
 R-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds//
 1.5e-105.501.98//Hs.24640:AF069493
 10 R-PLACE1004242//ESTs//1.0e-71.364.87//Hs.138632:H97952
 R-PLACE1004256//EST//0.0011:347.61//Hs.131385:AI022630
 R-PLACE1004257//EST//0.027.99.71//Hs.97587:AA398209
 R-PLACE1004258//KERATIN, TYPE I CYTOSKELETAL, 14//0.72:180.63//Hs.117729:100124
 R-PLACE1004270//ESTs//0.011.264.59//Hs.110044:AA181800
 15 R-PLACE1004274//Human retinoic acid receptor-beta associated open reading frame, complete sequence//0.28:
 121.66//Hs.1938:S82362
 R-PLACE1004277//Homo sapiens two pore domain K⁺ channel (TASK-2) mRNA, complete cds//1.4e-107.581:
 91//Hs.127007:AF084830
 R-PLACE1004284//ESTs//5.0e-22.187.82//Hs.23141:W92114
 20 R-PLACE1004289//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.9e-28:
 279.77//Hs.38687:AA744496
 R-PLACE1004302//ESTs, Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]//8.2e-61:313.95//Hs.
 71435:AI253099
 R-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//6.0e-115.590.94//Hs.11171:Y11588
 25 R-PLACE1004336//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//6.7e-69:572:
 77//Hs.1361:M55053
 R-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//7.7e-72:
 379.93//Hs.16232:AF100153
 R-PLACE1004376//ESTs//0.49:362.59//Hs.138086:AI056309
 30 R-PLACE1004384//EST//1.0:47.76//Hs.128546:AA905556
 R-PLACE1004388//ESTs, Weakly similar to contains similarity to ATP/GTP-binding site motif [C.elegans]//1.3e-
 98:572:90//Hs.14202:N46000
 R-PLACE1004405//ESTs//3.4e-99:507.95//Hs.28792:AI343467
 R-PLACE1004425//ESTs//2.7e-85:442.95//Hs.12544:N53665
 35 R-PLACE1004428//ESTs//1.0e-07:114.78//Hs.140225:AA704101
 R-PLACE1004437//Human NAD⁺-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene
 encoding mitochondrial protein, complete cds//9.4e-90:516.88//Hs.155410:U49283
 R-PLACE1004451
 R-PLACE1004460//ESTs//5.4e-14:338.64//Hs.97464:AA662980
 40 R-PLACE1004467//ESTs//3.3e-85:467.92//Hs.9527:W52721
 R-PLACE1004471//ESTs//3.0e-73:389.94//Hs.23240:R46578
 R-PLACE1004473//ESTs, Weakly similar to F20D1.2 [C.elegans]//3.8e-101:510.95//Hs.16986:W89194
 R-PLACE1004491//Human mitochondrial 1,25-dihydroxyvitamin D3 24-hydroxylase mRNA, complete cds//0.23:
 278.61//Hs.89663:L13286
 45 R-PLACE1004506//ESTs//2.5e-98:559.90//Hs.19447:AI057117
 R-PLACE1004510//ESTs//1.5e-91:436.98//Hs.24846:AI420493
 R-PLACE1004516//EST//1.7e-66:344.96//Hs.99303:AA453164
 R-PLACE1004518//ESTs//5.2e-79:410.94//Hs.27091:AA436553
 R-PLACE1004548//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.8e-40:332.72//Hs.
 50 115325:084488
 R-PLACE1004550
 R-PLACE1004564//ESTs//5.5e-76:367.98//Hs.49683:AA564742
 R-PLACE1004629//ESTs, Weakly similar to OS-9 precursor [H.sapiens]//8.1e-40:272.87//Hs.7100:W07181
 R-PLACE1004645//ESTs//6.3e-14:83.100//Hs.17270:AA701903
 55 R-PLACE1004646//ESTs//3.7e-22:231.76//Hs.141250:N29734
 R-PLACE1004658//ESTs//2.0e-12:109.84//Hs.23508:AA101113
 R-nnnnnnnnnnn/Homo sapiens mRNA for KIAA0714 protein, partial cds//7.8e-23:129.99//Hs.123129:AB018257
 R-PLACE1004672//ESTs//2.0e-50:256.98//Hs.136367:AI144254

R-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//L8-90:50:10:91:1/

80019:AF035606

R-PLACE1004681//EST//2.1e-08:283.62//Hs.99543:AA461482

R-PLACE1004686

R-PLACE1004691//EST//7.3e-42:305.82//Hs.141833:AA021552

R-PLACE1004693//ESTs//0.014:135.64//Hs.145333:AA0215374

R-PLACE1004716//ESTs, Weakly similar to No definition line found [C.elegans]/3.4e-80:413.94//Hs.23528: A1279571

R-PLACE1004722//EST//0.14:165.63//Hs.18213:T97997

R-PLACE1004736//ESTs//1.0e-72:385.94//Hs.10657:N6391

R-PLACE1004740//ESTs//1.0:267.58//Hs.101661:AA146619

R-nnnnnnnnnnnnn//EST//0.45:94.69//Hs.147174:AI192195

R-PLACE1004751//EST//9.8e-32:174.83//Hs.147901:AI223374

R-PLACE1004773//Homo sapiens invasin protein mRNA, complete cds//2.7e-89:437.96//Hs.104715:AF084367

R-PLACE1004777//ESTs//1.4e-68:351.94//Hs.23395:AA398548

R-PLACE1004793//ESTs//7.3e-53:290.78//Hs.142375:AA398619

R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0606 protein, partial cds//1.9e-99:580.88//Hs.38176:AB011178

R-PLACE1004813//ESTs//7.6e-86:433.96//Hs.85640:AA535856

R-PLACE1004814//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//1.1e-108:358.99//Hs.3688:AF069250

R-PLACE1004815//EST//4.7e-50:333.84//Hs.142196:AA258356

R-PLACE1004824//Protein kinase, interferon-inducible double stranded RNA dependent//4.8e-46:450.76//Hs. 73821:M35663

R-PLACE1004827//ESTs//2.3e-48:250.96//Hs.138766:AA342185

R-PLACE1004836//ESTs//2.7e-39:222.94//Hs.78661:AA195299

R-PLACE1004838//EST//0.056:198.60//Hs.129589:AA99501

R-PLACE1004840//ESTs, Highly similar to TRANSCRIPTIONAL ACTIVATOR GCN5 [Saccharomyces cerevisiae] //6.5e-71:381.93//Hs.8383:AA013272

R-PLACE1004868//ESTs//4.9e-70:367.94//Hs.100895:AA479308

R-PLACE1004885//Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete cds//1.8e-37:330.78//Hs.113259:AF023456

R-PLACE1004900//EST//1.2e-46:306.86//Hs.149580:AI211881

R-PLACE1004902//Sucrase-isomaltase//0.87:254.61//Hs.2996:X63597

R-nnnnnnnnnnnnn//ESTs//4.5e-75:375.96//Hs.91115:AI221563

R-PLACE1004918//ESTs//2.6e-103:519.95//Hs.143607:AI424948

R-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//6.6e-102:532.93//Hs. 17839:AF098936

R-PLACE1004934//EST//0.035:156.67//Hs.162071:AA478980

R-PLACE1004937//ESTs, Weakly similar to F55B12.3 [C.elegans]/6.4e-80:409.95//Hs.31945:AA702166

R-PLACE1004969//ESTs//9.8e-18:101.99//Hs.112837:T8013

R-PLACE1004972//ESTs//1.3e-65:337.95//Hs.75798:H29106

R-PLACE1004979//EST//1.2e-96:475.96//Hs.120158:AA708789

R-PLACE1004982//ESTs//1.0e-98:471.98//Hs.106496:AI291776

R-PLACE1004985//ESTs//2.1e-88:456.93//Hs.135050:AI420335

R-PLACE1005026

R-PLACE1005027//ESTs, Weakly similar to N-methyl-D-aspartate receptor glutamate-binding chain [R.norvegicus]/0.72:145.66//Hs.11215:N56719

R-PLACE1005046//Homo sapiens mRNA for KIAA0575 protein, complete cds//5.3e-66:297.88//Hs.153468: AB011147

R-PLACE1005052//ESTs, Weakly similar to weak similarity to rat cytosolic acyl coenzyme A thioester hydrolase [C.elegans]/1.2e-106:543.95//Hs.18625:AI074605

R-PLACE1005066//ESTs//3.9e-92:459.96//Hs.62684:AA806103

R-PLACE1005077//Human triadin mRNA, complete cds//1.8e-05:121:69//Hs.68731:U18985

R-PLACE1005085//Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.6e-49:314.74//Hs.113283:AF018080

R-PLACE1005086//ESTs//1.2e-73:379.94//Hs.110128:AA584364

R-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds//8.0e-99:531.92//Hs.75437:L40401

R-PLACE1005102//ESTs//7.2e-68:493.84//Hs.10593:AI201336

R-PLACE1005108//Human DNA fragmentation factor-45 mRNA, complete cds//9.2e-40:232.82//Hs.155344:

U91985

R-PLACE1005111//EST//8.1e-10:189.68//Hs.136356:AA493225
 R-PLACE1005128//ESTs//1.4e-78:501.87//Hs.15093:AA203423
 R-PLACE1005146//ESTs//4.8e-93:460.97//Hs.37896:AA777349
 5 R-PLACE1005162//ESTs//7.5e-51:277.95//Hs.28838:AI089013
 R-nnnnnnnnnnn//ESTs//5.4e-75:366.97//Hs.48119:AA454227
 R-PLACE1005181//EST//0.012:172.66//Hs.147107:AI190589
 R-PLACE1005187//ESTs//5.6e-72:363.95//Hs.16577:AI022830
 R-PLACE1005206//ESTs//5.3e-48:203.88//Hs.31792:H45211
 10 R-PLACE1005232//ESTs//5.1e-41:287.84//Hs.138552:R99532
 R-PLACE1005243//ESTs//1.1e-48:348.83//Hs.113310:R16767
 R-PLACE1005261//ESTs//0.19:175.62//Hs.124337:AA829524
 R-PLACE1005266//ESTs//1.9e-22:388.66//Hs.124146:AA699633
 R-PLACE1005277//ESTs//1.5e-29:314.72//Hs.163710:AA024516
 15 R-PLACE1005287//ESTs//3.6e-95:456.98//Hs.49282:AA970322
 R-PLACE1005305//ESTs//9.9e-71:428.88//Hs.144855:AI197937
 R-PLACE1005308//ESTs//3.8e-32:173.96//Hs.58239:AA215797
 R-PLACE1005313//ESTs//5.2e-74:409.93//Hs.33368:AA206614
 R-PLACE1005327//Chromosome 1 specific transcript KIAA0491//1.7e-104:537.94//Hs.136309:AB007960
 20 R-PLACE1005331//ESTs//2.1e-91:487.93//Hs.9291:AI189343
 R-PLACE1005335//ESTs, Weakly similar to F23B2.4 [C. elegans]//3.8e-90:442.97//Hs.70202:AA732975
 R-PLACE1005373//ESTs//8.0e-93:526.91//Hs.98541:N38901
 R-PLACE1005374//Homo sapiens KIAA0395 mRNA, partial cds//3.3e-44:344.80//Hs.43681:AL022394
 R-PLACE1005409//EST//0.43:174.59//Hs.162077:AA479978
 25 R-PLACE1005453//EST//7.9e-57:330.90//Hs.162306:AA555304
 R-PLACE1005467//ESTs//2.2e-42:294.84//Hs.142257:AA188423
 R-PLACE1005471//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-88:561.86//Hs.23094:M19503
 R-PLACE1005477//Human methionine aminopeptidase mRNA, complete cds//6.9e-80:549.83//Hs.78935:U29607
 30 R-PLACE1005480//EST//0.99:39.82//Hs.157275:AI364046
 R-PLACE1005481//EST//1.5e-31:281.79//Hs.132635:AI032875
 R-PLACE1005494//Homo sapiens mRNA for semaphorin E, complete cds//0.036:319.59//Hs.62705:AB000220
 R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cds//5.4e-57:277.98//Hs.28307:AF071185
 R-PLACE1005526//ESTs//2.5e-30:233.83//Hs.119304:AA443325
 35 R-PLACE1005528//Homo sapiens mRNA for cartilage-associated protein (CASP)//8.9e-20:321.69//Hs.155481:AJ006470
 R-PLACE1005530//ESTs//3.7e-81:438.92//Hs.103380:AI291325
 R-PLACE1005550//ESTs, Highly similar to HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III [Caenorhabditis elegans]//5.2e-95:458.98//Hs.38114:N62927
 40 R-PLACE1005554//ESTs//8.8e-36:267.86//Hs.98288:AA203555
 R-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR [Saccharomyces cerevisiae]//2.2e-64:345.94//Hs.7738:W81261
 R-PLACE1005574//ESTs//2.3e-27:231.83//Hs.117771:R99835
 R-PLACE1005584//ESTs//1.6e-36:188.98//Hs.152050:AA724612
 45 R-PLACE1005595//ESTs//1.6e-91:453.96//Hs.85079:AI276023
 R-PLACE1005603//ESTs//8.2e-99:533.93//Hs.96357:AI026927
 R-PLACE1005611//ESTs//5.2e-28:183.89//Hs.24941:AA261857
 R-PLACE1005623//ESTs//1.4e-102:505.96//Hs.58382:AA808964
 R-PLACE1005630
 50 R-PLACE1005639//ESTs//1.4e-51:256.98//Hs.1975:W72452
 R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.0e-111:585.93//Hs.8765:AF083255
 R-PLACE1005656//ESTs//2.7e-88:469.92//Hs.164054:AA528169
 R-PLACE1005666//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//3.3e-24:401.66//Hs.129727:AF035587
 55 R-PLACE1005698//ESTs//0.00013:82.79//Hs.116331:AA629355
 R-PLACE1005727//EST//0.15:206.63//Hs.105002:AA449332
 R-PLACE1005730//EST//0.0014:129.70//Hs.127931:AA969259

R-PLACE1005739//ESTs, Moderately similar to unknown intracellular protein [M.musculus]/J.1.3e-42:236.94//Hs.23889;AI341137

R-PLACE1005755//ESTs/J.2.8e-32:308.80//Hs.159821;AA524070

R-PLACE1005763//Human mRNA for KIAA0118 gene, partial cds/J.3.3e-47:268.87//Hs.154326:D42087

R-PLACE1005799//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]/J.7.7e-15:88.98//Hs.108957;AA088385

R-PLACE1005802//ESTs/J.2.8e-19:208.76//Hs.109271;W30941

R-PLACE1005803//ESTs/J.2.6e-75:417.92//Hs.7414;AA131327

R-PLACE1005804//EST/J.6.5e-20:182.70//Hs.149844;IA287963

R-PLACE1005828//ESTs/J.3.0e-15:194.77//Hs.106236:N50058

R-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)/J.0.040:435.58//Hs.75770:LA1870

R-PLACE1005845//EST/J.5.0e-61:294.99//Hs.133202:AI050965

R-PLACE1005850//ESTs/J.3.4e-82:425.96//Hs.7966:AI203471

R-PLACE1005851//ESTs/J.2.9e-21:165.84//Hs.23607:N98305

R-PLACE1005874//ESTs/J.0.48:296.57//Hs.39140:AI041842

R-PLACE1005884//ESTs/J.0.0027:177.66//Hs.150295:AA570558

R-PLACE1005898//ESTs/J.1.7e-98:467.98//Hs.159475:AI339981

R-PLACE1005921//ESTs/J.5.8e-96:480.95//Hs.30822:AA885501

R-PLACE1005923//ESTs/J.1.4e-66:333.96//Hs.150890:AI341793

R-PLACE1005925//Human Line-1 repeat mRNA with 2 open reading frames/J.2.8e-27:382.70//Hs.20394:M19503

R-PLACE1005932//ESTs, Moderately similar to MNK1 [H.sapiens]/J.1.1e-70:377.93//Hs.5662:AA868361

R-PLACE1005934//ESTs/J.1.0e-42:251.91//Hs.25092:AA922142

R-PLACE1005936//ESTs/J.1.2e-88:461.94//Hs.94125:N62913

R-PLACE1005951//ESTs/J.1.4e-83:533.86//Hs.21148:AI183729

R-PLACE1005953

R-PLACE1005955//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROTEIN-IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]/J.2.2e-83:494.88//Hs.108117:AI097079

R-PLACE1005966//ESTs/J.1.1e-95:465.97//Hs.98510:AI016239

R-PLACE1005968//EST/J.0.26:103.66//Hs.161300:AI0420897

R-PLACE1005990

R-PLACE1006002//Human mRNA for KIAA0355 gene, complete cds/J.2.0e-45:481.74//Hs.153014:AB002353

R-PLACE1006003//ESTs, Highly similar to HYPOTHETICAL 30.3 KD PROTEIN IN API/LAP4-CWP1 INTERGENIC REGION [Saccharomyces cerevisiae]/J.3.1e-112:93.93//Hs.111449:AI192946

R-PLACE1006011//ESTs, Moderately similar to NAD(+) ADP-RIBOSYLTRANSFERASE [D.melanogaster]/J.5.7e-100:596.88//Hs.24284:AA595596

R-PLACE1006017//ESTs/J.1.2e-18:296.68//Hs.133350:AI056276

R-PLACE1006037//ESTs, Weakly similar to T23D8.3 [C.elegans]/J.4.1e-102:491.98//Hs.61164:AI096332

R-PLACE1006040//ESTs/J.1.2e-92:443.98//Hs.111680:N93765

R-PLACE1006076//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]/J.2.0e-26:213.77//Hs.139007:H74314

R-PLACE1006119//ESTs/J.0.14:257.61//Hs.113149:AA908904

R-PLACE1006129//ESTs/J.3.8e-54:285.97//Hs.18827:W68002

R-PLACE1006139//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP15-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]/J.2.6e-99:560.91//Hs.5249:U55977

R-PLACE1006143//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)/J.0.038:463.59//Hs.904:U84010

R-PLACE1006157//ESTs/J.0.014:341.58//Hs.121773:AI357886

R-PLACE1006159//EST/J.0.00036:247.61//Hs.140054:AA668925

R-PLACE1006164//ESTs/J.2.6e-31:362.73//Hs.141024:H07128

R-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149/J.5.8e-54:286.94//Hs.152894:AC005239

R-nnnnnnnnnn//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicus]/J.2.7e-79:393.96//Hs.19121:AI125280

R-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds/J.5.1e-118:597.95//Hs.30464:AF091433

R-PLACE1006195//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/J.6.8e-94:532.91//Hs.105216:AI361807

R-PLACE1006196//ESTs/J.3.2e-66:382.90//Hs.18665:T99507

R-PLACE1006205//ESTs/J.7.7e-89:448.96//Hs.116665:AA669114

R-PLACE1006223//Human RNase P protein p38 (RPP38) mRNA, complete cds/J.0.90:304.58//Hs.94986:U77666

- R-PLACE1006225//ESTs//7.2e-96:474.97//Hs.91165:AI079555
 R-PLACE1006236//ESTs//8.8e-105:535.95//Hs.7919:AI341472
 R-nnnnnnnnnnn//Homo sapiens BAC clone RG118D07 from 7q31//3.2e-99:497.95//Hs.3781:AC004142
 5 R-PLACE1006246//ESTs. Weakly similar to CMP-sialic acid transporter [M.musculus]/1.3e-104:532.95//Hs.41151:AI301961
 R-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//3.0e-97:499.95//Hs.31921:AB014548
 R-PLACE1006262//ESTs. Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]/11.6e-07:321.62//Hs.53057:W67839
 10 R-PLACE1006288//Voltage-dependent anion channel 1//3.8e-100:605.88//Hs.2060:L06132
 R-PLACE1006318//ESTs//2.4e-102:536.94//Hs.8109:AA005265
 R-PLACE1006325//ESTs//5.2e-105:518.96//Hs.102319:AI246503
 R-PLACE1006335//ESTs//5.1e-45:254.93//Hs.153585:R70900
 R-PLACE1006357//EST//6.5e-09:309.62//Hs.132493:AA923168
 R-PLACE1006360//Human mRNA for KIAA0090 gene, partial cds//0.0097:381.58//Hs.154797:D42044
 15 R-PLACE1006368//ESTs//7.9e-85:412.97//Hs.150587:AI079284
 R-PLACE1006371//ESTs//7.7e-74:442.88//Hs.143671:W61053
 R-PLACE1006382
 R-PLACE1006385//ESTs//5.3e-06:346.61//Hs.163706:AA515748
 R-PLACE1006412//EST//7.7e-46:306.86//Hs.149580:AI281881
 20 R-PLACE1006414//Homo sapiens UM protein mRNA, complete cds//4.1e-43:551.69//Hs.154103:AF061258
 R-PLACE1006438//ESTs//1.1e-77:284.86//Hs.24545:AI278629
 R-PLACE1006445//ESTs//4.4e-53:259.99//Hs.24481:AA573139
 R-PLACE1006469//ESTs//9.4e-102:482.98//Hs.7218:AA936961
 R-PLACE1006470//ESTs//1.0:271.57//Hs.144517:AA938297
 25 R-PLACE1006482//ESTs//4.0e-61:354.92//Hs.51305:T47418
 R-PLACE1006492//EST//11.8e-09:48.91//Hs.144451:AA827722
 R-PLACE1006506//ESTs//0.012:161.61//Hs.145333:AI251374
 R-PLACE1006521//Human mRNA for KIAA0013 gene, complete cds//2.1e-15:415.63//Hs.48824:D87717
 R-PLACE1006531//ESTs//5.6e-31:213.87//Hs.125153:AA453723
 30 R-PLACE1006534//ESTs//6.5e-101:512.95//Hs.27763:W46368
 R-PLACE1006540//ESTs//7.3e-40:320.79//Hs.121659:H02532
 R-PLACE1006552//EST//0.38:418.56//Hs.140470:AA765214
 R-PLACE1006598//ESTs//4.0e-80:409.95//Hs.142868:AI128443
 35 R-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//9.3e-118:590.95//Hs.155377:U97670
 R-PLACE1006617//ESTs//8.1e-31:246.83//Hs.139128:AA205322
 R-PLACE1006626//ESTs//0.90:98.68//Hs.96322:AA541615
 R-PLACE1006629//Human mRNA for KIAA0386 gene, complete cds//5.3e-33:315.78//Hs.101359:AB002384
 40 R-PLACE1006640//ESTs//3.7e-26:137.100//Hs.32672:W16522
 R-PLACE1006673//Interleukin 10//8.4e-47:330.83//Hs.2180:M57627
 R-PLACE1006678//ESTs//1.1e-13:87.98//Hs.34035:D87736
 R-PLACE1006704//ESTs//2.6e-65:394.89//Hs.30582:D12214
 R-PLACE1006731//Homo sapiens clone 23923 mRNA sequence//1.9e-102:486.98//Hs.12472:AF038172
 R-PLACE1006754//EST//11.0e-61:381.89//Hs.14727:T83861
 45 R-PLACE1006760//Homo sapiens clone 24800 mRNA sequence//3.8e-73:394.93//Hs.7252:AF070622
 R-PLACE1006779//ESTs//1.4e-69:405.90//Hs.136235:AA262658
 R-PLACE1006782//EST//1.8e-25:197.86//Hs.137257:N33234
 R-PLACE1006792//ESTs//1.8e-43:317.84//Hs.139190:N55515
 R-PLACE1006795//ESTs//6.4e-68:350.95//Hs.11092:AA916335
 50 R-PLACE1006800//ESTs//1.9e-55:268.100//Hs.126695:AA917989
 R-PLACE1006805//ESTs//6.6e-91:484.93//Hs.94262:AA768847
 R-PLACE1006815//ESTs//2.1e-49:364.83//Hs.142031:AA809159
 R-PLACE1006819//ESTs. Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]/1.0e-87:481.92//Hs.141263:H64113
 55 R-PLACE1006829//ESTs//5.7e-43:332.83//Hs.19906:AA456933
 R-PLACE1006860//ESTs//0.96:138.63//Hs.136649:AA-828359
 R-PLACE1006867//ESTs//1.4e-98:478.97//Hs.10299:N35008
 R-PLACE1006878//EST//8.4e-48:243.97//Hs.54970:N93536

- R-PLACE1006883//ESTs/3.1e-46:300.88//Hs.162404:AA573131
 R-nnnnnnnnnnnnn//ESTs/3.0e-95:496.94//Hs.47546:AA181348
 R-PLACE1006904//ESTs/5.8e-18:304.68//Hs.125816:AA806089
 R-PLACE1006917//Endothelin receptor type B//0.00012:451.60//Hs.82002:D13168
 5 R-PLACE1006932//ESTs/4.6e-56:285.96//Hs.114727:AI379514
 R-PLACE1006935//ESTs/3.6e-12:157.73//Hs.161714:AA229078
 R-nnnnnnnnnnnnn//Human mRNA for KIAA0201 gene, complete cds//3.2e-25:494.63//Hs.36927:D86956
 R-PLACE1006961//Tyrosine aminotransferase//2.5e-46:471.74//Hs.2999:X52520
 10 R-PLACE1006962//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//9.0e-29:324.68//Hs.154257:AI275982
 R-PLACE1006966//ESTs/4.5e-99:470.99//Hs.46913:AI017636
 R-PLACE1006989//ESTs/2.2e-68:353.97//Hs.14394:R61257
 R-PLACE1007014//ESTs/3.4e-86:457.94//Hs.129819:AA838366
 R-PLACE1007021//ESTs/1.6e-93:539.90//Hs.7111:U55971
 15 R-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//6.6e-83:584.82//Hs.23094:M19503
 R-PLACE1007053//ESTs/4.2e-85:550.88//Hs.7984:AI202575
 R-PLACE1007097//ESTs/6.4e-78:493.86//Hs.56406:N91027
 R-PLACE1007105//ESTs/5.3e-70:381.91//Hs.22605:N74202
 R-PLACE1007111//ESTs/8.6e-75:358.99//Hs.145629:AA398646
 R-PLACE1007112//ESTs/6.9e-69:371.94//Hs.71922:AA148417
 20 R-PLACE1007132//ESTs/1.2e-36:373.69//Hs.10762:W28948
 R-PLACE1007140//ESTs/1.7e-70:360.96//Hs.56179:W56794
 R-PLACE1007178//EST/0.68:85.65//Hs.147010:AI184765
 R-PLACE1007226//ESTs/3.1e-78:452.90//Hs.8033:N94998
 R-PLACE1007238//ESTs/5.2e-70:362.95//Hs.85636:AA740619
 25 R-PLACE1007239//Human mRNA for transcription elongation factor S-II, hS-II-T1, complete cds//6.3e-93:534.89//Hs.80598:D50495
 R-PLACE1007242//ESTs/1.2e-80:390.98//Hs.117325:AA699450
 R-PLACE1007243//ESTs, Weakly similar to transporter protein [H. sapiens]//3.7e-73:357.98//Hs.18272:N78499
 R-PLACE1007257//Homo sapiens mRNA for dia-156 protein//4.3e-85:487.91//Hs.121556:Y15909
 30 R-PLACE1007274//ESTs/4.3e-79:430.93//Hs.146023:AI275071
 R-PLACE1007276//ESTs/1.5e-33:338.74//Hs.142850:R38419
 R-PLACE1007282//ESTs/4.8e-98:532.93//Hs.10071:AA100812
 R-PLACE1007286//Human mRNA for KIAA0118 gene, partial cds//2.9e-50:518.74//Hs.154326:D42087
 35 R-PLACE1007301
 R-PLACE1007317
 R-PLACE1007342
 R-PLACE1007346//Human sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds//1.2e-66:367.91//Hs.76596:AF096870
 40 R-PLACE1007367//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-98:488.96//Hs.24359:AA699594
 R-PLACE1007375//ESTs/2.3e-67:375.92//Hs.33368:AA206614
 R-PLACE1007386//ESTs/0.020:242.62//Hs.42768:AI129945
 R-PLACE1007402//ESTs/1.6e-91:441.97//Hs.26243:AA455877
 45 R-PLACE1007409//Human sapiens mitoxantrone resistance protein 1 mRNA, partial sequence//2.4e-113:590.94//Hs.14387:AF093771
 R-PLACE1007416//ESTs, Weakly similar to DIPEPTIDYL PEPTIDASE IV [H.sapiens]//3.8e-115:579.95//Hs.72165:AI243857
 R-PLACE1007450//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.7e-38:311.80//Hs.97203:U83171
 50 R-PLACE1007452//EST//2.5e-42:386.77//Hs.140562:AA826514
 R-PLACE1007460//ESTs/4.9e-87:434.95//Hs.28472:AI028230
 R-PLACE1007478
 R-PLACE1007484//ESTs/6.8e-08:64.92//Hs.100251:AA535975
 55 R-PLACE1007488//Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272//0.26:411.60//Hs.79012:M18533
 R-PLACE1007507//ESTs/2.2e-11:136.76//Hs.128815:AA678072
 R-PLACE1007511//ESTs, Highly similar to KERATIN, TYPE I CYTOSKELETAL 14 [Homo sapiens]//1.5e-41:261.89//Hs.9029:W57657

- R-PLACE1007524//ESTs//5.8e-45:297.87//Hs.154923:AA491377
 R-PLACE1007525//Human mRNA for KIAA0118 gene, partial cds//1.9e-44:422.75//Hs.154326:D42087
 R-PLACE1007544//ESTs//8.4e-59:327.93//Hs.27410:N25612
 R-PLACE1007547//EST//0.00010:107.71//Hs.146867:AI161404
 5 R-PLACE1007557//ESTs//1.6e-43:356.79//Hs.44702:AI148840
 R-PLACE1007583//ESTs//1.7e-41:214.97//Hs.155071:AA584257
 R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence//4.8e-104:554.93//Hs.21838:AF038179
 R-PLACE1007618//Lymphocyte cytosolic protein 1 (L-plastin)//0.54:161.65//Hs.76506:J02923
 10 R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence//4.8e-105:537.94//Hs.151046:AF038176
 R-PLACE1007632
 R-PLACE1007645//ESTs//0.99:187.62//Hs.163453:AI344106
 R-PLACE1007649//ESTs//2.2e-108:561.94//Hs.24398:AJ262946
 R-PLACE1007677//ESTs. Moderately similar to !!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!! [H.sapiens]//
 15 9.0e-37:190.97//Hs.23437:AA707331
 R-PLACE1007688//ESTs//7.5e-79:409.95//Hs.6166:AI376944
 R-PLACE1007690//ESTs. Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Ascaris suum]
 //3.4e-61:384.89//Hs.92918:AA133274
 R-PLACE1007697//ESTs. Highly similar to GCN20 PROTEIN [Saccharomyces cerevisiae]//1.8e-84:501.88//Hs.
 91251:U66685
 20 R-PLACE1007705//Human mRNA for apolipoprotein E receptor 2, complete cds//0.43:307.59//Hs.54481:D86407
 R-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//5.7e-75:374.96//Hs.4812:
 AF061243
 R-PLACE1007725//ESTs. Weakly similar to No definition line found [C.elegans]//3.1e-39:253.88//Hs.108797:
 AA476815
 25 R-PLACE1007729//ESTs//2.7e-44:392.79//Hs.142375:AA398619
 R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//6.7e-94:556.89//Hs.153121:
 AB014585
 R-PLACE1007737//ESTs//1.1e-41:345.80//Hs.114671:N39322
 R-PLACE1007743//ESTs//2.8e-17:98.100//Hs.124258:AA976778
 30 R-PLACE1007746//ESTs//5.3e-69:413.90//Hs.5297:AA156903
 R-PLACE1007791//ESTs. Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//
 8.6e-27:143.98//Hs.144194:AA706337
 R-PLACE1007807//Human Line-1 repeat mRNA with 2 open reading frames//9.9e-45:428.76//Hs.23094:M 9503
 35 R-PLACE1007810//ESTs//5.9e-15:143.82//Hs.126257:AJ279044
 R-PLACE1007829//ESTs//2.2e-22:190.84//Hs.142707:V24050
 R-PLACE1007843//ESTs//5.3e-110:556.95//Hs.107287:AI308839
 R-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-95:525.91//Hs.23094:M19503
 R-PLACE1007852//ESTs//4.5e-14:174.75//Hs.153419:N52017
 40 R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//2.1e-111:574.94//Hs.28020:
 AB018309
 R-PLACE1007866//EST//1.8e-48:262.96//Hs.141009:H01178
 R-PLACE1007877//ESTs//1.2e-94:478.96//Hs.5999:AI207832
 R-PLACE1007897//ESTs//2.3e-92:437.99//Hs.122843:AI189060
 45 R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.8e-89:460.95//Hs.
 92381:AB007956
 R-PLACE1007946//ESTs//2.8e-28:172.78//Hs.126784:AA521510
 R-PLACE1007954//ESTs//6.1e-72:366.95//Hs.27842:AI217966
 R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//3.9e-103:509.96//Hs.
 5671:AF084530
 50 R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//7.2e-89:
 465.93//Hs.78106:AF079529
 R-PLACE1007969//ESTs. Weakly similar to F35C12.2 [C.elegans]//1.4e-113:534.99//Hs.44268:AA455900
 R-PLACE1007990//ESTs. Highly similar to DOSAGE COMPENSATION REGULATOR [Drosophila melanogaster]
 //3.8e-97:493.95//Hs.6141:U69564
 55 R-PLACE1008000//ESTs//0.00013:241.65//Hs.44369:AI206835
 R-PLACE1008002//ESTs//2.2e-83:397.98//Hs.28780:AI263612
 R-PLACE1008044//ESTs. Moderately similar to NUCLEAR PORE COMPLEX PROTEIN NUP107 [R.norvegicus]
 //2.0e-115:575.95//Hs.92395:AA779854

R-PLACE1008045//EST//2.6e-89:465:94//Hs.47374:N51935
 R-PLACE1008080//EST//0.27:118:65//Hs.144110:AI054269
 R-PLACE1008095//ESTs//5.5e-23:268:73//Hs.152525:AA516469
 R-PLACE1008111//ESTs, Weakly similar to oxidoreductase [H.sapiens]//4.4e-108:537:96//Hs.28877:AI309334
 5 R-PLACE1008122//ESTs//6.5e-103:531:94//Hs.34737:AI028617
 R-PLACE1008129//ESTs//0.76:96:66//Hs.65373:AA883511
 R-PLACE1008132//ESTs//5.9e-05:113:72//Hs.13014:W26381
 R-PLACE1008177//ESTs//7.2e-107:557:93//Hs.132851:AI028266
 R-PLACE1008181//ESTs//5.3e-97:473:97//Hs.57483:AA776267
 10 R-PLACE1008198//ESTs//3.9e-16:120:85//Hs.9142:AA662107
 R-nnnnnnnnnnnnn/Homo sapiens mRNA for KIAA0530 protein, partial cds//1.6e-104:551:93//Hs.10801:AB011102
 R-PLACE1008209//ESTs//L2.6e-72:366:96//Hs.92308:AI052701
 R-PLACE1008231//ESTs//1.2e-70:363:94//Hs.25084:R80871
 R-PLACE1008244//ESTs//1.3e-98:543:92//Hs.25130:AA218990
 15 R-PLACE1008273//ESTs//6.1e-16:153:79//Hs.115987:AA483808
 R-nnnnnnnnnnnnn
 R-PLACE1008280//ESTs//1.3e-66:353:94//Hs.156376:AJ338705
 R-PLACE1008309//ESTs//2.8e-100:511:95//Hs.45080:N49852
 R-PLACE1008329//V-myc avian myelocytomatosis viral oncogene homolog//0.53:206:62//Hs.79070:K02276
 20 R-PLACE1008330//ESTs, Weakly similar to EOSINOPHIL LYOPHOSPHOLIPASE [H.sapiens]//8.6e-79:297:91//
 Hs.146477:AI128445
 R-PLACE1008331//ESTs//0.98:156:62//Hs.108548:AA081656
 R-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.1e-99:556:90//Hs.5734:AB014579
 R-PLACE1008368//EST//0.0027:198:63//Hs.160868:AI359052
 25 R-PLACE1008369//ESTs//5.4e-28:167:92//Hs.19530:AA480009
 R-PLACE1008392//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//2.0e-
 41:448:72//Hs.139007:H74314
 R-PLACE1008398//ESTs, Highly similar to Mig-6//1.4e-103:529:94//Hs.11169:AA156242
 R-PLACE1008401//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-81:
 30 536:87//Hs.7570:W31010
 R-nnnnnnnnnnnnn/Homo sapiens mRNA for p115, complete cds//5.1e-103:521:95//Hs.7763:D86326
 R-PLACE1008405//ESTs//1.2e-89:485:92//Hs.138241:AA767440
 R-PLACE1008424//ESTs//6.7e-97:508:93//Hs.6709:AI379778
 R-PLACE1008426//ESTs//5.5e-30:174:92//Hs.7946:AA651757
 35 R-PLACE1008429//ESTs//2.1e-12:188:71//Hs.140769:AA931562
 R-PLACE1008437//ESTs//7.1e-54:266:98//Hs.13068:AA001928
 R-PLACE1008455//ESTs//4.7e-69:471:85//Hs.28337:AA210761
 R-PLACE1008457//EST//8.6e-14:202:71//Hs.149887:AI289387
 R-PLACE1008465//ESTs//3.8e-80:426:93//Hs.153146:AI299636
 40 R-PLACE1008488//ESTs//7.9e-73:388:94//Hs.97268:AA292180
 R-PLACE1008524//ESTs//7.4e-107:545:95//Hs.10441:N62816
 R-PLACE1008531//ESTs//3.8e-68:427:87//Hs.56607:H23560
 R-PLACE1008532
 R-PLACE1008533//ESTs//2.5e-52:318:88//Hs.7274:AA476850
 45 R-PLACE1008568//ESTs//3.2e-99:486:97//Hs.84414:AI423223
 R-PLACE1008584//EST//2.2e-18:154:68//Hs.141498:N50064
 R-PLACE1008621//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//8.6e-67:483:82//Hs.140416:
 AA778649
 R-nnnnnnnnnnnnn
 50 R-PLACE1008626//ESTs//4.7e-73:372:95//Hs.23491:AA642454
 R-PLACE1008627//ESTs//1.6e-90:475:93//Hs.102401:AI004972
 R-PLACE1008629//ESTs//8.0e-93:492:93//Hs.20843:AA699512
 R-PLACE1008630//ESTs//1.0e-94:453:98//Hs.34840:AI279612
 R-PLACE1008643//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:422:79//Hs.153014:AB002353
 55 R-PLACE10086507/Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//7.9e-90:434:97//Hs.
 147967:AF044333
 R-PLACE1008693//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.8e-41:505:71//Hs.51048:X68830
 R-PLACE1008696//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.7e-51:316:

- 76//Hs.1361:M55053
 R-PLACE1008715//EST//0.63:114.64//Hs.121353:AA758600
 R-PLACE1008748//ESTs, Weakly similar to !!! ALU CLASS B WARNING ENTRY !!! [H.sapiens]//2.3e-40:281:83//Hs.142209:AA873303
- 5 R-PLACE1008757//ESTs//1.4e-45:226.99//Hs.22822:H06408
 R-PLACE1008790//ESTs//0.035:67.76//Hs.153554:AI286313
 R-PLACE1008798//ESTs//4.9e-59:285.99//Hs.49018:N79930
 R-PLACE1008807//ESTs//1.7e-82:413.96//Hs.130745:AA573217
 R-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 mRNA, complete cds//1.1e-98:499:95//Hs.7179:AF011905
- 10 R-PLACE1008813//ESTs, Weakly similar to coded for by C. elegans cDNA cm10e3 [C.elegans]//4.2e-92:490.93//Hs.110454:H11810
 R-PLACE1008851//ESTs//2.4e-84:421.95//Hs.158893:AI378428
 R-nnnnnnnnnnnnn
- 15 R-PLACE1008867//ESTs//1.1e-77:400.95//Hs.44198:AI093502
 R-PLACE1008887//Oxytocin receptor//1.1e-43:601.67//Hs.2820:X64878
 R-PLACE1008902//ESTs//0.023:208.61//Hs.154164:AI246893
 R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.6e-56:344.89//Hs.62318:AB018308
 R-PLACE1008925//ESTs//0.17:294.57//Hs.105113:AA457018
- 20 R-PLACE1008934//ESTs//2.0e-61:339.92//Hs.100448:AA622653
 R-PLACE1008941//ESTs, Moderately similar to ATP-BINDING CASSETTE TRANSPORTER 2 [Mus musculus]//1.3e-19:488.63//Hs.15780:U66680
 R-PLACE1008947//ESTs//1.3e-81:385.99//Hs.71574:AI376573
 R-PLACE1009020//ESTs//2.9e-79:419.94//Hs.121816:AA775419
- 25 R-PLACE1009027//Homo sapiens mRNA for doublecortin//3.1e-82:434.94//Hs.34780:AJ003112
 R-PLACE1009039//ESTs//2.8e-83:448.92//Hs.129179:AA988520
 R-PLACE1009045//ESTs//1.6e-64:318.97//Hs.103423:AA814195
 R-PLACE1009048//ESTs//2.7e-17:403.63//Hs.149343:AI249139
 R-PLACE1009050//ESTs//2.0e-88:475.92//Hs.122925:AA909008
- 30 R-PLACE1009060//ESTs, Highly similar to HYPOTHETICAL 98.3 KD PROTEIN R10E12.1 IN CHROMOSOME III [Caenorhabditis elegans]//1.2e-112:555.96//Hs.9663:AA527142
 R-PLACE1009090//ESTs//5.0e-13:175.75//Hs.140608:N53448
 R-PLACE1009094//Human splicing factor SRp30c mRNA, complete cds//0.98:161.63//Hs.77608:AL021546
 R-PLACE1009099//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//0.037:63.84//Hs.39943:AA203136
- 35 R-PLACE1009110//EST//5.8e-17:307.65//Hs.117264:AA682549
 R-PLACE1009111//ESTs//1.9e-57:349.90//Hs.11260:N98983
 R-PLACE1009130//ESTs, Weakly similar to hypothetical protein 2 [H.sapiens]//6.5e-97:501.94//Hs.11123:AA703945
- 40 R-PLACE1009150//LAMIN B1//0.064:393.60//Hs.89497:L37747
 R-PLACE1009155//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//2.5e-36:163.82//Hs.93332:AA811920
 R-PLACE1009158//ESTs//0.30:149.65//Hs.155796:R80005
 R-PLACE1009166//ESTs//3.3e-34:292.77//Hs.140255:AA708322
- 45 R-PLACE1009172//EST//8.9e-21:364.67//Hs.142557:AA64948
 R-PLACE1009174//ESTs//2.9e-18:274.70//Hs.139241:AA283707
 R-PLACE1009183//ESTs//2.3e-44:297.87//Hs.136839:H93717
 R-PLACE10091867//ESTs, Weakly similar to No definition line found [C.elegans]//1.5e-109:572.94//Hs.54943:Z78396
- 50 R-PLACE1009190//ESTs//2.6e-53:318.90//Hs.25245:AA176701
 R-PLACE1009200//H.sapiens mRNA for sortilin//3.2e-33:195.92//Hs.104247:X98248
 R-PLACE1009230//ESTs//3.0e-31:153.92//Hs.124116:AA772680
 R-PLACE1009246//ESTs//2.7e-90:488.92//Hs.10706:AA909018
 R-PLACE1009308//ESTs//0.022:46.97//Hs.36545:AA075423
 R-PLACE1009319//ESTs//7.7e-99:533.92//Hs.109654:N91279
- 55 R-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//7.3e-82:578.82//Hs.23094:M19503
 R-PLACE1009335//EST//1.3e-64:311.99//Hs.130558:AI004397
 R-PLACE1009338//ESTs//6.0e-70:386.93//Hs.3542:AI015782
 R-PLACE1009368//ESTs//1.4e-18:107.98//Hs.133303:W04760

R-PLACE1009375//ESTs//8.9e-36:313.76//Hs.24608:AA161260
 R-PLACE1009388//EST//4.4e-11:101.83//Hs.147074:AI188883
 R-PLACE1009398//ESTs//5.7e-63:335.93//Hs.149003:AJ243186
 R-nnnnnnnnnnnnn//ESTs//3.6e-94:452.98//Hs.103177:W72798
 5 R-PLACE1009410//ESTs//2.2e-112:553.96//Hs.61779:AA195255
 R-PLACE1009434//EST//3.4e-15:109.74//Hs.103742:U48632
 R-PLACE1009443//EST//7.5e-61:302.98//Hs.157787:AI361269
 R-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA/6.6e-85:479.90//Hs.76987:AF012872
 R-PLACE1009459//ESTs//9.3e-86:437.95//Hs.104871:AI161427
 10 R-PLACE1009476//Homo sapiens Chromosome 16 BAC clone C1987SK-A-67A1//1.3e-42:266.89//Hs.155049:AC004531
 R-PLACE1009477//ESTs//2.0e-50:367.82//Hs.152788:AA630925
 R-PLACE1009493//ESTs//4.5e-14:150.78//Hs.143918:AA699596
 R-PLACE1009524//ESTs//2.9e-97:454.99//Hs.7189:AA767698
 15 R-PLACE1009539//ESTs//9.1e-94:454.97//Hs.154706:AI262131
 R-PLACE1009542//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.4e-10:289.63//Hs.77579:AF013263
 R-PLACE1009571//ESTs//2.1e-23:125.100//Hs.41767:AA732326
 R-PLACE1009581//ESTs, Weakly similar to FIBRINOGEN ALPHA AND ALPHA-E CHAIN PRECURSORS [H. sapiens]//0.0012:56.91//Hs.12151:AA001818
 20 R-PLACE1009595//Homo sapiens mRNA for KIAA0635 protein, complete cds//6.0e-42:547.70//Hs.69157:AB014535
 R-PLACE1009596//ESTs//1.9e-102:588.90//Hs.142395:AI374735
 R-PLACE1009607//ESTs//0.0093:107.70//Hs.70932:AA126482
 25 R-PLACE1009613//ESTs//7.5e-101:488.97//Hs.5905:AA946680
 R-PLACE1009621//EST//0.99:261.60//Hs.149030:AI243338
 R-PLACE1009622//ESTs//8.0e-93:508.92//Hs.20967:AI422858
 R-PLACE1009637//EST//8.7e-90:442.97//Hs.121372:AA758701
 R-PLACE1009639//EST//8.5e-49:279.93//Hs.117447:R27213
 30 R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.3e-109:589.92//Hs.21862:AB011159
 R-PLACE1009665//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//9.9e-62:483.79//Hs.140416:AA778649
 R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//6.6e-63:310.97//Hs.109590:AF062534
 35 R-PLACE1009708//ESTs//3.0e-94:471.96//Hs.40091:N48582
 R-PLACE1009721//ESTs, Weakly similar to MSF1 PROTEIN [S.cerevisiae]//4.2e-98:529.92//Hs.3945:AA004210
 R-PLACE1009731//ESTs, Weakly similar to immune associated protein 38 [M.musculus]//6.8e-85:489.89//Hs.26194:AA033989
 R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//2.0e-117:598.95//Hs.154320:AF046024
 40 R-PLACE1009794//ESTs//7.9e-102:529.95//Hs.42927:N20989
 R-nnnnnnnnnnnnn//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubi-quinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, Cl-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs//1.1e-113:549.97//Hs.16411:AL030996
 45 R-PLACE1009845//ESTs//9.5e-106:560.93//Hs.117751:AI056868
 R-PLACE1009879//ESTs//1.8e-61:399.86//Hs.141012:R68748
 R-PLACE1009886//EST//0.54:153.64//Hs.144281:AA081328
 R-PLACE1009888//ESTs//2.7e-105:520.97//Hs.108646:AA613031
 50 R-nnnnnnnnnnnnn//ESTs, Weakly similar to similar to mouse MMR1 [C.elegans]//1.6e-114:594.94//Hs.67466:AI219740
 R-PLACE1009921//ESTs//7.6e-05:291.60//Hs.124786:AA825563
 R-PLACE1009924//EST//1.2e-42:216.98//Hs.31742:H20276
 R-PLACE1009925//ESTs//5.4e-30:154.100//Hs.114605:AI04317
 55 R-PLACE1009935//ESTs//1.4e-83:417.97//Hs.131755:AA496543
 R-PLACE1009947//Keratin 9//1.0:273.61//Hs.2783:Z29074
 R-PLACE1009971//ESTs//1.5e-87:424.98//Hs.13781:AI160540
 R-PLACE1009992//ESTs//1.3e-87:531.87//Hs.55044:AA460698

R-PLACE1009995//ESTs//1.3e-103:575.91//Hs.71218:C75347
 R-PLACE1009997//Small inducible cytokine A5 (RANTES)//1.1e-42:286.86//Hs.155464:AF088219
 R-PLACE1010023//ESTs, Weakly similar to C27F.2 gene product [C.elegans]//1.7e-17:137.86//Hs.7049:
 AI141736
 5 R-PLACE1010031//ESTs//0.22:191:62//Hs.127787:AA832204
 R-PLACE1010053//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spur [M.musculus]//
 7.6e-104:546.94//Hs.8215:AA521150
 R-PLACE1010069//ESTs//0.99:173:59//Hs.21415:AI150905
 10 R-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.5e-88:543.88//Hs.
 11183AF065482
 R-PLACE1010076//ESTs//3.4e-106:530:95//Hs.28005:AA604375
 R-PLACE1010083//ESTs//4.1e-65:395.88//Hs.6103:AA496424
 R-PLACE1010089//ESTs//1.6e-70:348.97//Hs.9011:AA418615
 R-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.norvegicus]//2.8e-104:565.92//Hs.11469:
 15 U69567
 R-PLACE1010102//ESTs//7.7e-50:311:89//Hs.5518:AI052015
 R-PLACE1010105//ESTs//6.0e-94:483.94//Hs.62684:AA806103
 R-PLACE1010106//ESTs, Weakly similar to putative p150 [H.sapiens]//1.6e-107:575.93//Hs.48301:AA122270
 R-PLACE1010134//EST//8.5e-59:314.94//Hs.135005:AI095130
 20 R-PLACE1010148//A-KINASE ANCHOR PROTEIN 79//0.52:351.56//Hs.48714:M90359
 R-PLACE1010152//ESTs//1.9e-40:240:90//Hs.17054:AI139897
 R-PLACE1010181//ESTs//3.6e-64:307.99//Hs.154163:AJ003313
 R-PLACE1010194//ESTs//2.7e-70:366.96//Hs.5301:T58466
 R-PLACE1010202//ESTs//0.57:120:67//Hs.58873:W95037
 25 R-PLACE1010231
 R-PLACE1010261//EST//6.9e-50:251:98//Hs.148208:AA897478
 R-PLACE1010270//ESTs//1.9e-87:430.96//Hs.25252:AI079545
 R-PLACE1010274//ESTs//1.9e-57:439.81//Hs.30078:H04535
 R-PLACE1010293//ESTs//8.1e-41:310.81//Hs.146811:AA410788
 30 R-PLACE1010321//ESTs//5.7e-50:246.99//Hs.151445:AA351081
 R-PLACE1010324//ESTs//0.00025:377.60//Hs.97430:AA398568
 R-PLACE1010329//Small inducible cytokine A5 (RANTES)//2.4e-40:300.82//Hs.155464:AF088219
 R-PLACE1010341//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//9.9e-
 32:190:77//Hs.152369:AA504818
 35 R-PLACE1010362//ESTs//8.2e-86:404:99//Hs.25625:AA669327
 R-PLACE1010364//ESTs//1.5e-105:556.93//Hs.12229:AA149594
 R-PLACE1010383//Homo sapiens mRNA for putative lipolic acid synthetase, partial//4.9e-35:166.86//Hs.53531:
 AJ224162
 R-PLACE1010401//ESTs//2.3e-85:450.93//Hs.23193:AA418152
 40 R-PLACE1010481//ESTs//0.012:280.59//Hs.5579:AI392816
 R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds//2.4e-89:438.96//Hs.13313:
 AF039081
 R-PLACE1010492
 R-PLACE1010522//EST//0.43:82:68//Hs.89303:AA284031
 45 R-nnnnnnnnnnnnn//ESTs//3.4e-36:228.89//Hs.128724:AA215455
 R-PLACE1010562//ESTs//4.8e-68:408.90//Hs.17244:W86306
 R-PLACE1010579//EST//0.015:193.63//Hs.67093:C14033
 R-PLACE1010580//ESTs//2.4e-93:445.98//Hs.127325:AA234116
 R-PLACE1010599
 50 R-PLACE1010616//ESTs//2.9e-101:497.97//Hs.142197:AA573418
 R-PLACE1010622//ESTs//7.1e-23:157.91//Hs.159877:N57895
 R-PLACE1010624//ESTs//1.4e-89:428.98//Hs.116561:AA658475
 R-PLACE1010628//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.4e-74:
 391.95//Hs.163495:W57637
 55 R-PLACE1010629//ESTs//5.8e-75:359.99//Hs.123630:AI250805
 R-PLACE1010630//ESTs//9.5e-101:519.94//Hs.77873:AA731719
 R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//8.3e-94:497.93//Hs.10801:AB011102
 R-PLACE1010661//ESTs, Highly similar to TESTIS-SPECIFIC PROTEIN PBS13 [Mus musculus]//4.8e-83:467:

- 91//Hs.22383;R51067
 R-PLACE1010662//ESTs. Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE
 PRECURSOR [D.melanogaster]/8.3e-103:538:94//Hs.105794:AA701659
 R-PLACE1010702//Homo sapiens DNA from chromosome 19, BAC 33152/4,8e-46:531:71//Hs.55452:AC003973
 5 R-PLACE1010714//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.0074:351:60//
 Hs.46440:U21943
 R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//1.2e-56:300:
 95//Hs.50758:AF092564
 R-PLACE1010739//Homo sapiens mRNA for oligophrenin 1//2.6e-84:501:88//Hs.158122:AJ001189
 10 R-PLACE1010743
 R-PLACE1010761//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//5.2e-
 94:442:96//Hs.3688:AF069250
 R-PLACE1010771//ESTs//3.8e-54:264:99//Hs.27299:AI074024
 R-PLACE1010786//ESTs. Highly similar to MYOSIN HEAVY CHAIN IB [Acanthamoeba castellanii]/7.6e-111:575:
 15 94//Hs.10260:AI126627
 R-PLACE1010800//ESTs//1.9e-109:557:95//Hs.11460:AA057558
 R-PLACE1010802//ESTs//0.00021:428:58//Hs.70258:AI091203
 R-PLACE1010811//ESTs//7.4e-73:394:93//Hs.48499:AA428896
 R-PLACE1010833//ESTs//9.0e-33:274:78//Hs.24391:W27472
 20 R-PLACE1010856//ESTs//5.8e-41:351:81//Hs.17401:W81048
 R-PLACE1010857//ESTs. Weakly similar to T14B4.2 gene product [C.elegans]/1.4e-71:326:92//Hs.3385:N25917
 R-PLACE1010870//ESTs//5.8e-57:303:96//Hs.30503:H05090
 R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//2.3e-101:501:96//Hs.118087:
 AB011182
 25 R-PLACE1010891
 R-PLACE1010896//EST//0.0039:249:57//Hs.126090:AA867983
 R-PLACE1010900//Human Xq28 mRNA, complete cds//3.3e-07:106:76//Hs.20136:U46023
 R-PLACE1010916//Plasminogen activator inhibitor, type II (arginine-serpin)/0.25:190:61//Hs.75716:Y00630
 R-PLACE1010917//ESTs//1.3e-82:452:92//Hs.68055:AA081093
 30 R-PLACE1010925//ESTs//1.1e-92:471:95//Hs.17448:AI125479
 R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//1.3e-66:402:89//Hs.74750:AB011126
 R-nnnnnnnnnnn/Homo sapiens intersectin short form mRNA, complete cds//8.9e-82:441:93//Hs.66392:
 AF064244
 R-PLACE1010944
 35 R-PLACE1010947//ESTs//6.7e-15:102:91//Hs.116908:AA211519
 R-PLACE1010954//Small inducible cytokine A5 (RANTES)/8.8e-51:278:93//Hs.155464:AF088219
 R-PLACE1010960//ESTs. Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]/1.0e-103:565:
 92//Hs.23259:AA532437
 R-PLACE1010965//EST//6.3e-80:447:91//Hs.139529:AA219580
 40 R-PLACE1011026//ESTs//4.6e-99:463:99//Hs.149732:AI199846
 R-PLACE1011032//ESTs//6.3e-56:295:94//Hs.143576:AI147867
 R-PLACE1011041//ESTs//5.3e-27:168:91//Hs.7936:AA923249
 R-nnnnnnnnnnn/Homo sapiens mRNA for KIAA0581 protein, partial cds//9.4e-102:563:91//Hs.41143:AB011153
 R-PLACE1011054//EST//1.1e-15:245:69//Hs.112648:AA609135
 45 R-PLACE1011056//Small inducible cytokine A5 (RANTES)/3.5e-38:285:82//Hs.155464:AF088219
 R-PLACE1011057//ESTs//3.5e-81:410:96//Hs.96499:AA252537
 R-PLACE1011090//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/1.6e-54:
 398:84//Hs.108740:W20094
 R-PLACE1011109//EST//1.3e-48:321:85//Hs.146794:AI149478
 50 R-PLACE1011114//ESTs//5.4e-90:475:94//Hs.69331:AA099587
 R-PLACE1011133//ESTs. Highly similar to 40 KD PROTEIN [Borna disease virus]/3.0e-105:552:93//Hs.31257:
 AA875998
 R-PLACE1011143//ESTs//0.40:127:65//Hs.118701:AA420795
 R-PLACE1011160//Homa sapiens mRNA for HRIHFB2038, partial cds//7.7e-97:534:91//Hs.28719:AB015333
 55 R-PLACE1011165//ESTs//1.0:135:69//Hs.32163:AI374673
 R-PLACE1011185//ESTs. Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]/3.4e-85:442:
 95//Hs.136910:AA810782
 R-PLACE1011203//EST//0.0047:268:60//Hs.68832:AA088438

- R-PLACE1011995//ESTs//4.5e-39:304.81//Hs.138852:AA284247
 R-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//8.0e-106:540.95//Hs.88756:AB018256
- 5 R-PLACE2000003//ESTs//2.0e-103:488.98//Hs.8341:AA490069
 R-PLACE2000007//ESTs//2.4e-110:564.95//Hs.65135:W89120
 R-PLACE2000011//Homo sapiens clone 614 unknown mRNA, complete sequence//4.8e-105:524.95//Hs.21811:AF091080
- 10 R-PLACE2000015//ESTs//7.1e-111:543.96//Hs.32178:AA083211
 R-PLACE2000017//EST//8.2e-46:404.79//Hs.133006:AI049504
 R-PLACE2000021//ESTs//4.5e-99:221.71//Hs.150830:AI302868
 R-PLACE2000033//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.6e-43:355.79//Hs.154069:U06452
- 15 R-PLACE2000034//ESTs//2.2e-21:314.70//Hs.107697:W29013
 R-PLACE2000039//H.sapiens mRNA for translin associated protein X//2.9e-45:514.72//Hs.96247:X95073
 R-PLACE2000047//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//4.1e-45:358.81//Hs.159523:AF001622
- 20 R-PLACE2000050//ESTs//4.5e-65:322.98//Hs.155820:N67652
 R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.2e-41:429.72//Hs.153468:AB011147
 R-PLACE2000062//Human mRNA for KIAA0392 gene, partial cds//2.0e-43:296.86//Hs.40100:AB002390
- 25 R-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//6.2e-111:550.95//Hs.9443:AF027219
 R-PLACE2000097//Calcium modulating ligand//6.2e-47:372.80//Hs.13572:AF068179
 R-PLACE2000100//ESTs//8.8e-42:281.86//Hs.150727:AI292236
 R-PLACE2000103//ESTs//4.7e-97:518.93//Hs.118727:W26941
- 30 R-PLACE2000111//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//0.00043:127.71//Hs.42400:AF022789
 R-PLACE2000115//ESTs//7.8e-93:458.96//Hs.104520:AA481662
 R-PLACE2000132//ESTs//3.8e-69:409.91//Hs.98502:AA433988
- 35 R-PLACE2000136//ESTs//6.2e-05:274.61//Hs.114067:AA701558
 R-PLACE2000140//Homo sapiens mRNA for KIAA0562 protein, complete cds//4.7e-44:302.85//Hs.118401:AB011134
 R-PLACE2000164//ESTs//6.3e-106:506.98//Hs.16390:AI052357
- 40 R-PLACE2000170//Small inducible cytokine A5 (RANTES)//3.7e-42:326.79//Hs.155464:AF088219
 R-PLACE2000172//ESTs//9.6e-43:232.94//Hs.6709:AI379778
 R-PLACE2000176//EST//1.6e-24:154.91//Hs.157734:AI360292
 R-PLACE2000187//Human mRNA for KIAA0033 gene, partial cds//2.0e-49:292.90//Hs.22271:D26067
- 45 R-PLACE2000216//ESTs//0.0041:166.64//Hs.159476:AI382378
 R-PLACE2000223//ESTs//0.49:171.60//Hs.86154:AA207191
 R-PLACE2000235//ESTs//2.9e-39:264.85//Hs.136839:H93717
 R-PLACE2000246//NAD(P)H:menadiolone oxidoreductase//4.0e-44:331.82//Hs.80706:M81600
- 50 R-PLACE2000264//Human mRNA for KIAA0365 gene, partial cds//4.0e-38:311.81//Hs.84123:AB002363
 R-PLACE2000274//ESTs, Weakly similar to dynein-related protein [H.sapiens]//1.9e-87:422.98//Hs.9740:AI004779
- 55 R-PLACE2000302//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [Homo sapiens]//4.8e-68:380.92//Hs.107365:AA720664
 R-PLACE2000305//ESTs//2.6e-43:413.75//Hs.118732:AI344055
 R-PLACE2000317//ESTs//2.8e-92:501.92//Hs.28432:R83380
 R-PLACE2000335//ESTs//4.3e-32:300.77//Hs.163035:AA748058
- 60 R-PLACE2000342//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//0.00071:117.73//Hs.42400:AF022789
 R-PLACE2000347//ESTs//1.6e-30:214.86//Hs.135272:AI347618
 R-PLACE2000359//Zinc finger protein 139 (clone pHZ-37)//5.5e-42:288.86//Hs.140090:U09848
- 65 R-PLACE2000366//Thromboxane A2 receptor//6.7e-53:392.82//Hs.89887:D38081
 R-PLACE2000371//ESTs//3.6e-81:409.97//Hs.155138:AA158731
 R-PLACE2000373//Homo sapiens mRNA for KIAA0734 protein, partial cds//0.89:186.62//Hs.101516:AB018277
- 70 R-PLACE2000379//ESTs//3.4e-10:228.64//Hs.57842:W63781
 R-PLACE2000394//ESTs//6.7e-41:462.74//Hs.107657:AA126814

- R-PLACE2000398//ESTs//4.2e-33:373.74//Hs.155184:AA573189
R-PLACE2000399
- 5 R-PLACE2000404//ESTs, Highly similar to LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC [*Saccharomyces cerevisiae*]//4.2e-109:540:96//Hs.6762:AA088424
R-PLACE2000411//ESTs//1.6e-89:459:95//Hs.117589:N25941
R-PLACE2000419//ESTs, Weakly similar to F25H9.6 [*C. elegans*]//1.6e-97:436:95//Hs.24647:W19739
R-PLACE2000425//Homo sapiens PEC-205 mRNA, complete cds//2.2e-44:287.88//Hs.153563:AF011333
R-PLACE2000427//ESTs, Weakly similar to coded for by *C. elegans* cDNA CEES142F [*C. elegans*]//3.0e-113:543:97//Hs.16933:AA976002
- 10 R-PLACE2000433//ESTs//1.8e-46:311:85//Hs.145032:AA343523
R-PLACE2000435//ESTs//2.9e-33:243:87//Hs.90964:AA393986
R-PLACE2000438//ESTs//2.8e-09:66:96//Hs.59548:AI279887
R-PLACE2000450//Human mRNA for KIAA0392 gene, partial cds//3.3e-39:394:74//Hs.40100:AB002390
R-PLACE2000455//ESTs//1.2e-62:301:99//Hs.151708:AA554714
- 15 R-PLACE2000458//ESTs//6.8e-92:473:96//Hs.115897:AA156638
R-PLACE2000465//ESTs//1.3e-45:435:76//Hs.141635:N79228
R-PLACE2000477//ESTs//2.6e-100:536:94//Hs.77822:AA532642
R-PLACE3000004//ESTs//9.1e-114:558:97//Hs.13035:AA151838
R-PLACE3000029//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.3e-64:350:86//Hs.153468:
- 20 AB011147
R-PLACE3000059//EST//0.028:175:61//Hs.159873:R92763
R-PLACE3000070//ESTs//3.8e-16:200:74//Hs.138771:N70979
R-PLACE3000103//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.7e-48:468:75//Hs.51048:X68830
R-PLACE3000119//ESTs//1.2e-45:330:83//Hs.35254:AI133727
- 25 R-PLACE3000124//EST//3.1e-75:391:96//Hs.161515:N71739
R-PLACE3000136//ESTs//8.3e-18:152:84//Hs.10043:D81792
R-PLACE3000142//ESTs//0.047:183:62//Hs.43102:AA131369
R-PLACE3000147//ESTs//6.6e-53:310:90//Hs.8230:W07142
R-PLACE3000148//EST//1.9e-16:184:76//Hs.146570:AI139815
- 30 R-PLACE3000155//ESTs//1.2e-19:192:79//Hs.131350:AA805223
R-PLACE3000156//ESTs, Highly similar to ENV POLYPROTEIN [Avian spleen necrosis virus]//4.8e-36:262:88//Hs.31532:H18272
R-PLACE3000157
R-PLACE3000158//Small inducible cytokine A5 (RANTES)//8.2e-39:296:81//Hs.155464:AF088219
- 35 R-PLACE3000160
R-PLACE3000169//ESTs//1.5e-64:329:97//Hs.129864:R20798
R-PLACE3000194
R-PLACE3000197//ESTs//1.4e-38:197:98//Hs.146341:AI269930
R-PLACE3000199//ESTs, Highly similar to APOLIPOPROTEIN E PRECURSOR [Sus scrofa]//0.018:261:61//Hs.131370:AA927516
- 40 R-PLACE3000207//EST//1.3e-15:154:78//Hs.136617:AA630476
R-PLACE3000208//ESTs//1.6e-18:151:82//Hs.155498:W27084
R-PLACE3000218//ESTs//1.8e-85:463:93//Hs.7849:AI129964
R-PLACE3000220//ESTs//6.4e-44:308:84//Hs.136839:H93717
- 45 R-PLACE3000226//ESTs//L3e-49:269:95//Hs.9059:AI359014
R-PLACE3000230//EST//2.3e-34:258:83//Hs.4382:T02878
R-PLACE3000242//Human troponin mRNA, complete cds//1.1e-63:546:78//Hs.76313:U04811
R-PLACE3000244//ESTs, Highly similar to NEGATIVE REGULATOR OF MITOSIS [*Emmericella nidulans*]//7.5e-110:549:95//Hs.13692:AA632002
- 50 R-PLACE3000254//Human mRNA for KIAA0309 gene, partial cds//2.4e-29:174:94//Hs.87908:AB002307
R-PLACE3000271//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.3e-62:287:82//Hs.97203:U83171
R-PLACE3000276//ESTs//7.5e-07:187:64//Hs.80720:AA031782
R-PLACE3000304//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//4.0e-59:456:80//Hs.108966:U48696
- 55 R-PLACE3000310//ISLET AMYLOID POLYPEPTIDE PRECURSOR//6.0e-45:302:86//Hs.51048:X68830
R-PLACE3000320//Interleukin 10//9.6e-42:288:85//Hs.2180:M57627
R-PLACE3000322//ESTs, Highly similar to ARGININOSUCCINATE LYASE [Homo sapiens]//5.8e-34:190:95//Hs.

- 114531:N74103
R-PLACE3000331//Homo sapiens mRNA for KIAA0772 protein, complete cds//3.7e-32:239:84//Hs.15519:AB018315
- 5 R-PLACE3000339//ESTs//1.3e-109:548:96//Hs.7871:AI041837
R-PLACE3000341//EST//1.1e-11:231:68//Hs.131328:AA922688
R-PLACE3000350//Human mRNA for adipogenesis inhibitory factor//8.0e-40:291:76//Hs.1721:X58377
R-PLACE3000352//EST//1.8e-72:343:100//Hs.144871:AI202380
R-PLACE3000353//ESTs//2.0e-75:395:95//Hs.107260:W52683
R-PLACE3000362//EST//2.8e-80:381:99//Hs.136233:AA261888
- 10 R-PLACE3000363
R-PLACE3000365//EST//4.8e-50:307:88//Hs.149580:AI281881
R-PLACE3000373//ESTs//5.8e-60:422:83//Hs.142826:W87430
R-PLACE3000388//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-35:427:73//Hs.138795:R98534
- 15 R-PLACE3000399//ESTs//6.5e-05:162:66//Hs.149440:AI274570
R-PLACE3000400//ESTs//8.3e-05:310:63//Hs.17697:AA287528
R-PLACE3000401//ESTs//4.6e-60:326:80//Hs.139555:N48230
R-PLACE3000402//Homo sapiens clone 24629 mRNA sequence//0.50:227:62//Hs.142570:AF052160
R-PLACE3000405//Human HsLIM15 mRNA for HsLim15, complete cds//5.3e-43:315:82//Hs.37181:D64108
- 20 R-PLACE3000406//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.4e-47:302:87//Hs.73614:U83460
R-PLACE3000413//ESTs//1.6e-116:571:97//Hs.10235:H93077
R-PLACE3000416//Small inducible cytokine A5 (RANTES)//1.8e-41:300:85//Hs.155464:AF088219
R-PLACE3000425//Human sapiens 4F5S mRNA, complete cds//1.6e-46:307:85//Hs.32567:AF073519
- 25 R-PLACE3000455//ESTs//1.0:160:64//Hs.156045:AA884461
R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA, complete cds//6.1e-84:440:92//Hs.153487:U43899
R-PLACE3000477//ESTs//2.4e-113:568:96//Hs.24557:AA142980
R-PLACE4000009//ESTs//1.5e-72:361:96//Hs.10119:AA700227
- 30 R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//8.8e-85:433:95//Hs.105399:AB018352
R-PLACE4000034//ESTs//7.0e-110:550:96//Hs.76607:AA156240
R-PLACE4000049//EST//0.028:87:75//Hs.89303:AA284031
R-PLACE4000052//ESTs//5.6e-116:553:98//Hs.19067:AA521292
- 35 R-PLACE4000063//ESTs//5.0e-80:388:98//Hs.135028:AI096444
R-PLACE4000089//ESTs//2.3e-97:479:97//Hs.102425:AA807547
R-PLACE4000093//ESTs//1.5e-82:391:99//Hs.160730:AI142739
R-PLACE4000100
R-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.7e-98:419:91//Hs.129937:AB007931
- 40 R-PLACE4000128//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.8e-11:184:71//Hs.154278:N45985
R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//5.2e-21:118:100//Hs.118164:AB007969
- 45 R-PLACE4000147//EST//1.6e-23:175:79//Hs.162236:AA551582
R-PLACE4000156//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.0e-47:306:88//Hs.153468:AB011147
R-PLACE4000192//ESTs, Weakly similar to similar to Human zinc finger protein(ZNF142) [H.sapiens]//6.7e-31:232:82//Hs.16493:T92186
- 50 R-PLACE4000222//ESTs//2.2e-53:195:85//Hs.141575:AA211734
R-PLACE4000233//ESTs//2.9e-81:456:93//Hs.124964:R81949
R-PLACE4000247//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.5e-72:307:85//Hs.113283:AF018080
R-PLACE4000250//Small inducible cytokine A5 (RANTES)//7.1e-43:301:83//Hs.155464:AF088219
R-PLACE4000252//EST//1.6e-40:275:85//Hs.162197:AA535216
- 55 R-PLACE4000261//EST//0.0063:384:58//Hs.136284:AA400442
R-PLACE4000269//ESTs//7.3e-67:345:97//Hs.5000:R44586
R-PLACE4000270//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//2.1e-37:352:77//Hs.77579:AF013263

R-PLACE4000300//EST//0.26:103.68//Hs.144438:AA780782
 R-PLACE4000320//EST//2.7e-44:298.85//Hs.162404:AA573131
 R-PLACE4000323//ESTs//8.8e-38:178.79//Hs.155475:AA761454
 R-PLACE4000326//ESTs//7.4e-103:516.96//Hs.55042:AA150460
 5 R-PLACE4000344//ESTs//9.9e-94:463.96//Hs.100057:AA001414
 R-PLACE4000367//ESTs//0.81:102.73//Hs.107692:H38478
 R-PLACE4000369//ESTs//1.5e-69:390.92//Hs.13733:AA418656
 R-PLACE4000379//ESTs//1.3e-67:373.91//Hs.48569:AA905425
 R-PLACE4000387//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.9e-44:379.78//Hs.152369:AA504818
 10 R-PLACE4000392//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//2.3e-70:482.83//Hs.140416:AA778649
 R-PLACE4000401//ESTs//1.3e-18:151.84//Hs.150355:AI273502
 R-PLACE4000411//ESTs//1.1e-108:543.96//Hs.23901:AA169780
 15 R-PLACE4000445//ESTs, Weakly similar to C05D9.6 gene product [C.elegans]//2.6e-111:530.98//Hs.12003:AA643063
 R-PLACE4000465//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//8.5e-58:409.72//Hs.1361:M55053
 R-PLACE4000489//ESTs//5.0e-70:342.98//Hs.72865:AI380932
 20 R-PLACE4000494//EST&I//1.4e-109:525.98//Hs.22539:AI334210
 R-PLACE4000522//ESTs//6.3e-88:471.93//Hs.8121:AA521290
 R-PLACE4000548//ESTs//3.3e-86:441.96//Hs.5070:AA149527
 R-PLACE4000558//Human putative monocarboxylate transporter (MCT) mRNA, complete cds//5.7e-46:425.76//Hs.23590:U9185
 25 R-THYRO1000026//ESTs//2.6e-42:331.82//Hs.137875:AA993532
 R-THYRO1000034//ESTs//2.1e-43:214.100//Hs.153018:AI243524
 R-THYRO1000035//ESTs//7.6e-52:325.90//Hs.49817:AA001249
 R-THYRO1000040//ESTs//1.7e-94:459.98//Hs.48712:AI027889
 R-THYRO1000070//ESTs//6.7e-43:283.86//Hs.37573:H59651
 30 R-THYRO1000072//ESTs//1.3e-57:313.96//Hs.127827:H13438
 R-THYRO1000085//ESTs//1.1e-90:439.98//Hs.150539:AA908435
 R-THYRO1000092//Human mRNA for KIAA0355 gene, complete cds//1.3e-41:344.79//Hs.153014:AB002353
 R-THYRO1000107//Interleukin 10//2.8e-43:292.84//Hs.2180:M57627
 R-THYRO1000111//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//1.0e-52:413.80//Hs.140385:AA773359
 35 R-THYRO1000121//EST//0.24:78.74//Hs.156632:AI345108
 R-THYRO1000124//ESTs//2.8e-86:428.96//Hs.141634:AI122764
 R-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds//6.8e-90:449.96//Hs.87619:AF087142
 40 R-THYRO1000132//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//5.2e-49:486.77//Hs.24164:N95217
 R-THYRO1000156//ESTs//6.1e-36:344.75//Hs.70279:AA757426
 R-THYRO1000163//Homo sapiens LIM protein mRNA, complete cds//4.8e-38:278.84//Hs.154103:AF061258
 R-THYRO1000173//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [Mus musculus]//1.1e-111:554.96//Hs.18894:AA910946
 45 R-THYRO1000186//ESTs//1.0e-44:339.83//Hs.155184:AA573189
 R-THYRO1000187//Small inducible cytokine A5 (RANTES)//1.1e-41:305.81//Hs.155464:AF088219
 R-THYRO1000190//Small inducible cytokine A5 (RANTES)//2.3e-44:301.85//Hs.155464:AF088219
 R-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//3.6e-110:535.97//Hs.43445:AJ005698
 50 R-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.3e-115:559.97//Hs.79672:AB014552
 R-THYRO1000206//ESTs//3.1e-90:507.90//Hs.32456:W29063
 R-THYRO1000221//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.1e-72:357.98//Hs.140002:AA635349
 55 R-THYRO1000241//Homo sapiens mRNA for KIAA0688 protein, complete cds//7.8e-69:524.82//Hs.141874:AB014589
 R-THYRO1000242//ESTs//4.2e-27:222.85//Hs.77554:W87927

R-THYRO1000253//Siolaphorin (gpL115, leukosialin, CD343)/7.3e-40:318.80//Hs. 80738;X52075
R-THYRO1000270//ESTs//1.9e-99:531.94//Hs. 17677;A162925
R-THYRO1000270//ESTs//2.7e-54:266.99//Hs. 149527;A1280674
R-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds//3.5e-100:566.91//Hs. 25846;AB016068
R-THYRO1000320//POLYPOSIS LOCUS PROTEIN 1//1.0:321.58//Hs. 74648;M73547
R-THYRO1000327//Autocrine motility factor receptor//9.2e-54:289.93//Hs. 80731;M63175
R-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//3.4e-113:559.96//Hs. 12002;AB018333
R-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds//1.5e-48:317.87//Hs. 7833;U29091
R-THYRO1000368//ESTs//4.7e-88:430.98//Hs. 146085;AA021064
R-nnnnnnnnnnnnn//ESTs//1.0:253.57//Hs. 128783;AA436250
R-THYRO1000387//Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds//4.6e-69:294.84//Hs. 151614;AF032456
R-THYRO1000394//Thromboxane A2 receptor//4.1e-40:232.87//Hs. 89887;D38081
R-THYRO1000395//ESTs//3.3e-20:160.83//Hs. 101570;AA0505429
R-THYRO1000401//ESTs//1.3e-109:516.99//Hs. 78524;A140601
R-THYRO1000438//ESTs//2.1e-48:360.83//Hs. 141203;H52638
R-THYRO1000452//ESTs, Weakly similar to No definition line found [C.elegans]//8.5e-40:239.90//Hs. 84009;A1309761
R-THYRO1000471//ESTs//3.3e-36:302.80//Hs. 70279;AA757426
R-THYRO1000484//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.2e-49:479.75//Hs. 17630;AB018280
R-THYRO1000488//Homo sapiens mRNA for HRIHF2038, partial cds//4.1e-89:471.94//Hs. 28719;AB015333
R-THYRO1000501//ESTs//L5e-46:287.89//Hs. 125300;R62360
R-THYRO1000502//ESTs//1.7e-08:63.96//Hs. 116319;A1208005
R-THYRO1000505//ESTs, Weakly similar to KIAA0281 [H. sapiens]//3.9e-57:286.96//Hs. 105861;A1206965
R-THYRO1000558//ESTs//1.7e-95:454.99//Hs. 120563;AA648511
R-THYRO1000569//ESTs//3.2e-89:463.94//Hs. 20555;W22193
R-THYRO1000570//ESTs//2.8e-97:471.97//Hs. 8245;AA115485
R-nnnnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds//2.6e-108:533.97//Hs. 151411;AF075587
R-THYRO1000596//ESTs//3.1e-99:527.94//Hs. 6084;AA045247
R-THYRO1000602//EST//6.9e-50:381.83//Hs. 161917;AA483223
R-THYRO1000605//ESTs, Weakly similar to monocytic leukaemia zinc finger protein [H.sapiens]//1.2e-96:483.96//Hs. 21907;N24415
R-THYRO1000625//ESTs//5.6e-36:257.84//Hs. 139657;AA191742
R-THYRO1000637
R-THYRO1000641//ESTs, Weakly similar to ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN [H.sapiens]//4.9e-46:245.95//Hs. 97398;AA398634
R-THYRO1000658//ESTs//5.8e-48:281.90//Hs. 142259;AA828840
R-nnnnnnnnnnnnn//ESTs//1.5e-82:389.99//Hs. 155573;AA487384
R-THYRO1000666//ESTs//1.4e-26:179.88//Hs. 98382;A4779866
R-THYRO1000676//EST//6.4e-05:88.77//Hs. 133424;A1061063
R-THYRO1000684//ESTs//1.9e-69:374.94//Hs. 144617;R77109
R-THYRO1000699//ESTs//1.7e-58:394.86//Hs. 26373;AA700713
R-THYRO1000712
R-THYRO1000734//EST//2.0e-06:95.73//Hs. 156201;AA724287
R-THYRO1000748//EST//4.1e-12:155.74//Hs. 118694;AA148713
R-THYRO1000756//ESTs, Weakly similar to CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE [H.sapiens]//8.1e-82:497.87//Hs. 109672;V22624
R-THYRO1000777
R-THYRO1000783//EST//5.6e-100:470.99//Hs. 123515;AA812932
R-THYRO1000787//EST//8.0e-34:175.99//Hs. 99607;AA463897
R-THYRO1000793//ESTs//2.2e-106:505.99//Hs. 50929;AA443144
R-THYRO1000796//ESTs//4.3e-44:445.75//Hs. 55855;AA621381
R-THYRO1000805//EST//2.6e-32:407.67//Hs. 123424;AA813594
R-THYRO1000815//Human mRNA for KIAA0033 gene, partial cds//2.0e-56:307.87//Hs. 22271;D26067

- R-THYRO1000829
 R-THYRO1000843//Interleukin 10//1.1e-44:285:87//Hs.2180:M57627
 R-THYRO1000852//EST//2.3e-20:157:85//Hs.149580:AI281881
 R-THYRO1000855//ESTs//2.6e-44:359:81//Hs.140329:AA714011
 5 R-THYRO1000865//Protein kinase, interferon-inducible double stranded RNA dependent//2.8e-44:374:79//Hs.73821:M35663
 R-THYRO1000895//ESTs//1.0e-32:196:85//Hs.138630:H97871
 R-THYRO1000916//ESTs//4.6e-99:492:96//Hs.152442:AA528234
 10 R-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//3.1e-110:566:94//Hs.78106:AF079529
 R-THYRO1000934//ESTs//7.4e-102:535:95//Hs.58194:W72182
 R-THYRO1000951//ESTs//4.2e-11:91:89//Hs.6278:T15859
 R-THYRO1000952//ESTs//3.9e-93:489:94//Hs.48928:AA211761
 15 R-THYRO1000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds//1.1e-60:321:95//Hs.14454:AF047440
 R-THYRO1000975//EST//9.8e-49:303:89//Hs.149580:AI281881
 R-THYRO1000983//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 [Arabidopsis thaliana]//1.6e-90:474:93//Hs.106616:AI027524
 R-THYRO1000984//ESTs//5.9e-97:481:96//Hs.142457:AI202777
 20 R-THYRO1000988//EST//3.5e-42:241:83//Hs.162404:AA573131
 R-THYRO1001003//ESTs, Weakly similar to ubiquitin-conjugating enzyme [H.sapiens]//3.0e-57:341:91//Hs.44049:AA521489
 R-THYRO1001031//ESTs//5.5e-47:322:85//Hs.136839:H93717
 R-THYRO1001033//ESTs//5.7e-89:427:98//Hs.71508:AA809070
 25 R-THYRO1001062//EST//1.5e-46:291:89//Hs.161917:AA483223
 R-THYRO1001093//ESTs//2.7e-80:468:90//Hs.124601:AA203497
 R-THYRO1001100
 R-THYRO1001120//ESTs, Moderately similar to fractionated X-irradiation-induced 29 thymoma [M.musculus]//6.6e-86:491:89//Hs.89135:AI138834
 30 R-THYRO1001121//Homo sapiens mRNA for beta-tubulin folding cofactor D//2.6e-82:429:94//Hs.12570:AJ006417
 R-THYRO1001133//ESTs//2.9e-39:242:90//Hs.152340:AA521399
 R-THYRO1001134//ESTs//1.8e-102:521:95//Hs.108408:N31922
 R-THYRO1001142//ESTs//0.26:84:69//Hs.153434:AI287853
 35 R-THYRO1001173//Human mRNA for KIAA0238 gene, partial cds//0.0012:305:62//Hs.82042:D87075
 R-THYRO1001177
 R-THYRO1001189//H.sapiens F11 mRNA//1.5e-59:260:83//Hs.159639:X77744
 R-THYRO1001204//ESTs, Weakly similar to TH1 protein [D.melanogaster]//1.0e-75:431:91//Hs.5184:AA709151
 R-THYRO1001213//ESTs//1.3e-75:409:92//Hs.140213:AA828932
 40 R-THYRO1001262//Human kpn1 repeat mna (cdna clone pcd-kpn1-4), 3' end//1.3e-48:349:83//Hs.139107:K00629
 R-THYRO1001271//PUTATIVE PROTEIN PHOSPHATASE 2C//1.0:128:64//Hs.118728:D13640
 R-THYRO1001290//ESTs//2.1e-89:424:99//Hs.118152:AA702561
 R-THYRO1001313//ESTs//3.5e-17:139:87//Hs.15827:H16269
 R-THYRO1001320//ESTs//1.4e-61:403:79//Hs.139555:N48230
 45 R-THYRO1001321//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)//8.5e-05:326:60//Hs.82314:M31642
 R-NNNNNNNNNNNN//ESTs//0.16:422:5.9//Hs.23876:AA082935
 R-THYRO1001347//ESTs, Weakly similar to C35A5.8 [C.elegans]//1.1e-106:562:94//Hs.15032:AA774250
 R-THYRO1001363//ESTs//1.4e-99:508:95//Hs.5028:D51033
 50 R-THYRO1001365
 R-THYRO1001374
 R-THYRO001401//Human HsLIM15 mRNA for HsLIM15, complete cds//2.5e-48:467:75//Hs.37181:D64108
 R-THYRO1001403//Interleukin 10//2.1e-46:305:85//Hs.2180:M57627
 R-THYRO1001405//ESTs//4.8e-25:197:84//Hs.6907:W72733
 55 R-THYRO1001406//EST//0.0023:117:66//Hs.162931:AA633197
 R-THYRO1001411//ESTs//6.1e-77:421:93//Hs.22973:R40979
 R-THYRO1001426//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//9.1e-49:305:86//Hs.159187:AB007977

R-THYRO10010434//ESTs//0.40.161:61//Hs. 161993:AA503172
R-THYRO10010458//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//1.7e-05:159:66//Hs. 104239:AA488082
R-THYRO10010480//Small inducible cytokineA5 (KANTES)//1.3e-40:331:79//Hs. 155464:AF088219
R-THYRO10010487//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.1e-17:134:76//Hs. 15731:AB011135
R-THYRO10010534//ESTs//4.6e-96:447:100//Hs. 135204:AI093110
R-THYRO10010537//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.0e-33:304:80//Hs. 108740:W20094
R-THYRO10010541//Human peptide transporter (HPEPT1) mRNA, complete cds//9.0e-49:427:76//Hs. 2217:U21936
R-THYRO10010559//ESTs//0.99:210:62//Hs. 33619:AA021594
R-THYRO10010570//ESTs//4.9e-48:287:91//Hs. 27131:AA442413
R-THYRO10010573//ESTs//2.1e-87:446:95//Hs. 143669:AA621958
R-THYRO10010584//ESTs//1.5e-64:354:95//Hs. 146222-AA397741
R-THYRO10010595//ESTs//5.7e-39:366:78//Hs. 22562:E54247
R-THYRO1001602//Insulin-like growth factor 1 (somatomedia C)/I//7.4e-12:288:67//Hs. 85112:X57025
R-THYRO1001605//Human GS2 mRNA, complete cds//6.9e-49:359:83//Hs. 264:U03886
R-THYRO1001617//Homo sapiens peroxisomal acyl-CoA:dihydroxyacetonephosphate acyltransferase (DHAPAT) mRNA, complete cds//1.3e-82:434:93//Hs. 12482-AJ002190
R-THYRO1001637//Homo sapiens KIAA0414 mRNA, partial cds//7.1e-58:331:83//Hs. 127649:AB007874
R-THYRO1001656//ESTs//3.8e-19:209:75//Hs. 92186:AI080282
R-THYRO1001660//ESTs//1.4e-56:323:91//Hs. 24984:AA534446
R-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform//1.6e-111:562:95//Hs. 118633:AJ225089
R-THYRO1001673//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-17:246:73//Hs. 67619:AB007957
R-THYRO1001703//ESTs//1.1e-39:142:97//Hs. 110748:AI341726
R-THYRO1001706//ESTs//2.2e-42:214:99//Hs. 112536:AI147691
R-THYRO1001721
R-nnnnnnnnnnnn//ESTs, Weakly similar to ZK1128.6 [C.elegans]//1.7e-10:147:77//Hs. 158196:R53184
R-THYRO1001745//ELK1, member of ETS oncogene family//1.8e-12:282:65//Hs. 116549:AL009172
R-THYRO1001766//EST//0.0073:226:61//Hs. 146544:AI125323
R-THYRO1001772//ESTs//8.2e-100:495:97//Hs. 144993-AA243474
R-THYRO1001793//ESTs//2.5e-89:430:97//Hs. 58127-AA534224
R-THYRO1001809//ESTs//1.0e-41:327:80//Hs. 146811:AA410788
R-THYRO1001854//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//5.7e-38:242:83//Hs. 92381:AB007956
R-THYRO1001895//ESTs//1.7e-08:213:64//Hs. 156056:AI352123
R-THYRO1001907//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3.7e-41:362:79//Hs. 139007:H74314
R-VESEN1000122
R-Y79AA1000013//ESTs//0.99:233:57//Hs. 132216:AA923289
R-Y79AA1000033//EST//1.9e-62:324:95//Hs. 157692-AI359321
R-Y79AA1000037//ESTs//6.1e-47:234:98//Hs. 30773:AA557178
R-Y79AA1000059//Homo sapiens mRNA for KIAA0640 protein, partial cds//2.8e-51:330:89//Hs. 153026:AB014540
R-Y79AA1000065//ESTs//2.0e-91:497:94//Hs. 37759:H56929
R-Y79AA1000133//EST//2.3e-16:184:75//Hs. 141501:N50792
R-Y79AA1000181//ESTs, Weakly similar to No definition line found [C.elegans]//2.4e-110:553:95//Hs. 23159:AA113849
R-Y79AA1000202//Human mRNA for KIAA0169 gene, partial cds//0.094:185:62//Hs. 79414:D79991
R-Y79AA1000214//ESTs//1.7e-93:495:94//Hs. 11673:W68103
R-Y79AA1000230//ESTs//3.5e-114:553:98//Hs. 47125:AI421812
R-Y79AA1000231//ESTs//1.1e-106:526:97//Hs. 82856-AI246624
R-Y79AA1000258//ESTs//1.5e-99:490:97//Hs. 6459-AI092936
R-Y79AA1000268//Human mRNA for KIAA0365 gene, partial cds//1.3e-44:320:84//Hs. 84123:AB002363
R-Y79AA1000313//ESTs//1.7e-105:558:93//Hs. 18851-AA857826

R-Y79AA1000328//ESTs/1.9e-76:448.91/Hs.16470:AA6412635
R-Y79AA1000342//ESTs, Weakly similar to MATRN 3 [H.sapiens]/J2.0e-37:239.88/Hs.23476:AA401210
R-Y79AA1000346//ESTs/J7.9e-12:139.76/Hs.115987:AA463808
R-Y79AA1000349//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spnr [M.musculus]/
4.4e-66:339.97/Hs.8215-AA521150
R-Y79AA1000355//ESTs, Moderately similar to !!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]/J3.2e-
44:279.88/Hs.139007:H74314
R-Y79AA1000368//ESTs/J3.8e-97:513.94/Hs.68090:AA641018
R-Y79AA1000405//ESTs/J4.4e-47:267.94/Hs.125304:RS1613
R-Y79AA1000410//ESTs/J7.4e-49:359.82/Hs.158107:AA707758
R-Y79AA1000440//EST/J0.17:99.69/Hs.160859:A1352292
R-Y79AA1000469//ESTs, Highly similar to ancient ubiquitous 46 kDa protein AUP46 precursor [M.musculus]/J3.1e-
60:362.88/Hs.6381:A1188509
R-Y79AA1000480//ESTs/J1.0e-75:433.91/Hs.78110:AA741320
R-Y79AA1000538//EST/J7.9e-48:307.87/Hs.149580:A1281881
R-Y79AA1000539//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds/J0.95:172.62/Hs.
41723:U37426
R-Y79AA1000540//ESTs/J1.5e-97:534.93/Hs.67991:AA147848
R-Y79AA1000560//ESTs, Highly similar to ALPHA-DAPTIN [Rattus norvegicus]/J8.2e-97:482.97/Hs.19121:
A1125280
R-Y79AA1000574//ESTs, Weakly similar to M04B2.4 [C.elegans]/J1.3e-107:564.93/Hs.16361:A1147455
R-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds/J3.4e-99:517.94/Hs.60580:
AF060503
R-Y79AA1000705//ESTs, Weakly similar to HYPOTHETICAL 128.5 KD HELICASE IN AT51-TPD3 INTERGENIC
REGION [Saccharomyces cerevisiae]/J8.1e-27:140.100/Hs.129049:H28818
R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds/J8.7e-114:586:
95/Hs.83023:AF093670
R-Y79AA1000748//ESTs, Weakly similar to HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III
[C.elegans]/J9.8e-111:563.95/Hs.19845:A1005330
R-Y79AA1000752//Homo sapiens (huca) mRNA, complete cds/J0.97:235.59/Hs.1701:L26405
R-Y79AA1000774//ESTs/J5.9e-109:559.95/Hs.17138:N91463
R-Y79AA1000782//Homo mRNA for KIAA0246 gene, partial cds/J1.6e-18:107.100/Hs.84753:D87433
R-Y79AA1000784//EST/J0.80:87.67/Hs.158558:A1368359
R-Y79AA1000794//ESTs/J2.7e-99:498.96/Hs.25441:AA580512
R-Y79AA1000800//ESTs/J1.2e-97:532.93/Hs.77822:AA532642
R-nnnnnnnnnnnn/Carboxypeptidase E/O1.018:354.59/Hs.75360:X51405
R-Y79AA1000805
R-Y79AA1000824//ESTs/J0.99:276.61/Hs.153992:AA280227
R-Y79AA1000827//ESTs/J1.2e-55:326.92/Hs.158127:A1334650
R-Y79AA1000850//Homo sapiens small optic lobes homolog (SOLH) mRNA, complete cds/J0.016:386.59/Hs.
55836:U85647
R-Y79AA1000962//EST/J0.024:177.63/Hs.25214:R37079
R-Y79AA1000968
R-Y79AA1000969//ESTs/J2.9e-70:251.98/Hs.120858:AA417181
R-Y79AA1000976//ESTs/J7.8e-56:299.95/Hs.120125:M86049
R-Y79AA1000985
R-Y79AA1001023//ESTs/J5.7e-66:379.90/Hs.64616:W22851
R-Y79AA1001041//ESTs/J8.6e-06:54.100/Hs.8980:AA629067
R-Y79AA1001048//ESTs/J4.4e-97:461.99/Hs.7010:AA837407
R-Y79AA1001061//ESTs/J3.8e-105:493.99/Hs.128419:A1271325
R-Y79AA1001068//Homo sapiens mRNA for KIAA0563 protein, complete cds/J4.8e-53:279.83/Hs.15731:
AB011135
R-Y79AA1001077//ESTs/J1.9e-51:339.87/Hs.11197:AA309047
R-Y79AA1001078//ESTs/J8.3e-98:528.92/Hs.24608:AA161260
R-Y79AA1001105//ESTs/J6.0e-77:393.96/Hs.30837:H08155
R-Y79AA1001145//ESTs/J1.7e-13:285.64/Hs.128258:AA343015
R-Y79AA1001167
R-Y79AA1001177//EST/J1.2e-05:92.76/Hs.65277:T15884

R-Y79AA1001186//ESTs/1.3e-70:344.97//Hs.49760:AA74A051
R-Y79AA1001211//ESTs/1.3e-70:344.97//Hs.49760:AA74A051
R-Y79AA1001216//ESTs/5.8e-63:416.88//Hs.8595:W60933
R-Y79AA1001231//ESTs/9.3e-101:483.98//Hs.13916:AIO25750
R-Y79AA1001233//EST/0.00027:232.62//Hs.132431:AA909674
R-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110113Q? (RPZD Berlin))//1.e-110:549.95//Hs.23170:AJ005892
R-Y79AA1001281//ESTs/3.6e-98:466.99//Hs.104442:AA481271
R-Y79AA1001299//Human Inr1 mRNA, complete cds//9.6e-25:133.100//Hs.155626:U04847
R-Y79AA1001312//ESTs/3.4e-92:454.97//Hs.127319:AI191149
R-Y79AA1001323//ESTs/1.6e-67:422.89//Hs.118559:AA870084
R-Y79AA1001384//ESTs/3.1e-104:496.98//Hs.153692:AA604143
R-Y79AA1001391//ESTs/2.2e-77:418.94//Hs.118608:AA101819
R-Y79AA1001394//ESTs/2.1e-78:409.95//Hs.23413:AA579854
R-Y79AA1001402//EST/9.3e-08:128.75//Hs.141607:N63891
R-Y79AA1001493//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 [Arabidopsis thaliana]//4.4e-109:553.95//Hs.106616:AIO27524
R-Y79AA1001511//ESTs/4.9e-49:27.192//Hs.109045:AA523704
R-Y79AA1001533//ESTs, Moderately similar to RNA polymerase I associated factor [M.musculus]//6.2e-46:260.94//Hs.24884:AA176812
R-nnnnnnnnnnnn//EST/0.62:126.67//Hs.137020:AA868563
R-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//3.5e-95:517.91//Hs.76987:AF012872
R-Y79AA1001555//Collagen, type XI, alpha 1//1.0:157.64//Hs.82772:J04177
R-Y79AA1001585//ESTs/1.9e-90:430.98//Hs.48333:AA704508
R-Y79AA1001594//ESTs/9.6e-23:122.100//Hs.63795:AI126237
R-Y79AA1001603//ESTs/1.0e-50:193.100//Hs.25635:AI336204
R-Y79AA1001613//ESTs, Weakly similar to zinc finger protein [H.sapiens]//7.2e-81:400.97//Hs.13323:AA897542
R-Y79AA1001647//ESTs, 6.8e-92:479.95//Hs.154270:N26486
R-Y79AA1001665//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//2.5e-19:112.97//Hs.26252:AA643235
R-Y79AA1001679//ESTs, Highly similar to LAMBDA-CRYSTALLIN [Oryctolagus cuniculus]//9.7e-99:553.92//Hs.108896:R54040
R-nnnnnnnnnnnn
R-Y79AA1001696//ESTs/1.4e-84:478.91//Hs.6606:AA211783
R-Y79AA1001705//ESTs/6.7e-107:546.95//Hs.106805:AA481849
R-Y79AA1001711//Human DNA sequence from clone 119D9 on chromosome 20p12. Contains part of a gene for a PAK1 LIKE Serine/Threonine-Protein Kinase and part of the PLCB4 gene for Phospholipase C, beta (1-Phosphatidylinositol -4,5-Bisphosphate Phosphodiesterase Beta 4). Contains ESTs, STSs and GSSs//0.0085:251.63//Hs.21864:AL031652
R-Y79AA1001781//ESTs, Weakly similar to partial CDS [C.elegans]//9.4e-87:427.97//Hs.18645:AIO23798
R-nnnnnnnnnnnn//ESTs/1.1e-112:558.97//Hs.109755:AA180809
R-Y79AA1001827//ESTs, Weakly similar to Similar to S.cerevisiae YD9335.03c protein [H.sapiens]//8.1e-95:530.91//Hs.72444:W23217
R-Y79AA1001846//EST/2.8e-41:312.81//Hs.162236:AA551582
R-Y79AA1001848//Human adhalin (DAC2) mRNA, complete cds//0.54:221.58//Hs.99931:L34355
R-Y79AA1001866//ESTs/2.2e-102:498.97//Hs.130683:AI278630
R-Y79AA1001874//ESTs/1.9e-76:377.98//Hs.79707:AA350494
R-Y79AA1001875//ESTs/0.64:152.63//Hs.156159:AI333652
R-Y79AA1001923//EST/0.19:180.58//Hs.148290:AA908404
R-Y79AA1002027//ESTs/1.6e-104:497.98//Hs.21275:T73275
R-Y79AA1002083//Homo sapiens mRNA for KIAA0563 protein, complete cds//0.69:93.73//Hs.15731:AB011135
R-Y79AA1002089//Homo sapiens PYRJN (MEFV) mRNA, complete cds//1.1e-46:392.80//Hs.113283:AF018080
R-Y79AA1002093//Homo sapiens CT198 mRNA, complete ORF//1.2e-12:80.100//Hs.78185:L38933
R-Y79AA1002103//ESTs/1.3e-52:535.76//Hs.142167:AA147785
R-Y79AA1002115//ESTs/4.2e-101:519.96//Hs.23977:AA115275
R-Y79AA1002125//ESTs/9.8e-68:363.94//Hs.72085:AA193399
R-Y79AA1002139//ESTs/1.2e-100:498.96//Hs.72020:AA149858
R-Y79AA1002204//ESTs/2.1e-83:434.95//Hs.22979:R43725

Homology Search Result Data 6

[0314] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences. In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be compared. Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark. //

2276

C-HEMBA1000460
 C-HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).//3.3E-45//481aa//29%//Q04652
 C-HEMBA1000491//RAS-LIKE PROTEIN 2.//2E-22//188aa//31%//P22279
 C-HEMBA1000501
 5 C-HEMBA1000508
 C-HEMBA1000520
 C-HEMBA1000531//HEAT SHOCK 70 KD PROTEIN COGNATE 1 (HEAT SHOCK 70 KD PROTEIN 70C) (FRAG-
 MENTS).//2.6E-12//73aa//41%//P02826
 C-HEMBA1000534
 10 C-HEMBA1000555
 C-HEMBA1000568
 C-HEMBA1000588
 C-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8E-55//179aa//61%//O43295
 C-HEMBA1000636
 15 C-HEMBA1000682
 C-HEMBA1000686
 C-HEMBA1000719
 C-HEMBA1000727
 C-HEMBA1000752
 20 C-HEMBA1000817
 C-HEMBA1000851
 C-HEMBA1000867
 C-HEMBA1000869
 C-HEMBA1000872
 25 C-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN).//
 1.6E-30//127aa//40%//P43366
 C-HEMBA1000918
 C-HEMBA1000919//HYPOTHETICAL 65.5 KD TRP-ASP REPEATS CONTAINING PROTEIN F02E8.5 IN CHRO-
 MOSOME X.//1E-10//288aa//23%//Q19124
 30 C-HEMBA1000946
 C-HEMBA1000968
 C-HEMBA1000971
 C-HEMBA1000975
 C-HEMBA1001009
 35 C-HEMBA1001022
 C-HEMBA1001043//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)(FRAGMENT).//
 1.4E-12//131aa//38%//Q01485
 C-HEMBA1001052
 C-HEMBA1001080
 40 C-HEMBA1001085
 C-HEMBA1001088//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//3.5E-50//
 176aa//57%//P48059
 C-HEMBA1001109
 C-HEMBA1001122
 45 C-HEMBA1001133
 C-HEMBA1001137//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946)
 (FRAGMENT).//1.5E-116//197aa//58%//Q06730
 C-HEMBA1001140
 C-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//6.8E-79//179aa//80%//P51646
 50 C-HEMBA1001197//Homo sapiens mRNA for KIAA0871 protein, complete cds.//9.5E-257//1307bp//94%//
 AB020678
 C-HEMBA1001235
 C-HEMBA1001257//Homo sapiens mRNA 2-methylacyl-CoA racemase.//0//1672bp//99%//AJ130733
 C-HEMBA1001281
 55 C-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//0.00000002//198aa//
 29%//Q60401
 C-HEMBA1001303
 C-HEMBA1001310

C-HEMBA1001326
 C-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//1.4E-133//614bp//99%//AF057358
 5 C-HEMBA1001387//GTP-BINDING PROTEIN TC10.//2.9E-64//104aa//82%//P17081
 C-HEMBA1001388
 C-HEMBA1001398
 C-HEMBA1001405
 C-HEMBA1001407
 10 C-HEMBA1001413
 C-HEMBA1001415
 C-HEMBA1001446
 C-HEMBA1001450
 C-HEMBA1001455
 C-HEMBA1001510//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).//1.7E-16//63aa//61%//P18850
 15 C-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//4.9E-37//399aa//29%//P29166
 C-HEMBA1001533
 C-HEMBA1001579//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1662bp//99%//AB020657
 C-HEMBA1001581
 20 C-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//4.9E-156//348aa//83%//Q14141
 C-HEMBA1001635//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA).//1.6E-10//155aa//28%//Q63679
 C-HEMBA1001661//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//4.6E-36//365aa//33%//P33450
 25 C-HEMBA1001702
 C-HEMBA1001714//Homo sapiens mRNA; cDNA DKFZp564G0422 (from clone DKFZp564G0422).//0//1845bp//99%//AL050386
 C-HEMBA1001731
 C-HEMBA1001744//SCY1PROTEIN.//9.9E-32//481aa//25%//P53009
 30 C-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//3.8E-11//206aa//36%//P11675
 C-HEMBA1001815
 C-HEMBA1001819//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.9E-135//459aa//52%//Q99676
 C-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//7.6E-64//221aa//55%//Q07230
 C-HEMBA1001864
 35 C-HEMBA1001869//TRITHORAX PROTEIN.//0.000096//166aa//27%//P20659
 C-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (ME2GLYDH).//9.3E-36//395aa//26%//Q63342
 C-HEMBA1001987
 C-HEMBA1002018
 40 C-HEMBA1002049
 C-HEMBA1002084
 C-HEMBA1002125
 C-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.4E-51//180aa//56%//P79293
 45 C-HEMBA1002177//TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).//6E-13//190aa//36%//P43694
 C-HEMBA1002191
 C-HEMBA1002199
 C-HEMBA1002212//TYROSINE-PROTEIN KINASE 2 (EC 2.7.1.112) (FRAGMENT).//3E-17//267aa//29%//P18161
 50 C-HEMBA1002237
 C-HEMBA1002265
 C-HEMBA1002267//Sus scrofa decorin mRNA, complete cds.//1.1E-46//302bp//90%//AF125537
 C-HEMBA1002349
 55 C-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//1847bp//99%//AF092563
 C-HEMBA1002419//TRICHOHYALIN.//1.9E-09//299aa//24%//P22793
 C-HEMBA1002430

- C-HEMBA1002439
C-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.//4.2E-24//109aa//55%//Q00994
C-HEMBA1002460
C-HEMBA1002462
- 5 C-HEMBA1002469//DXS8237E PROTEIN (FRAGMENT).//3.5E-50//199aa//61%//P98175
C-HEMBA1002475//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.1E-12//285aa//31%//P17437
C-HEMBA1002477
C-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1.//6.8E-53//257aa//36%//P48732
- 10 C-HEMBA1002515
C-HEMBA1002542
C-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds.//6.8E-305//951bp//99%//AF075587
C-HEMBA1002583
- 15 C-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds.//1.4E-253//1149bp//99%//AB011169
C-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//0//1539bp//99%//AB018351
C-HEMBA1002688
C-HEMBA1002696
C-HEMBA1002750
- 20 C-HEMBA1002768//Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4).//1E-80//882bp//61%//AJ000414
C-HEMBA1002770//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//1532bp//99%//AB020636
C-HEMBA1002777
C-HEMBA1002794
C-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//8.2E-314//1437bp//99%//AF071185
- 25 C-HEMBA1002818//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819
C-HEMBA1002850
C-HEMBA1002863
C-HEMBA1002876//HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II.//1.5E-44//188aa//52%//Q09297
- 30 C-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//1483bp//100%//AB011148
C-HEMBA1002937
C-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//2E-34//300aa//34%//P16157
- 35 C-HEMBA1002951//Homo sapiens mRNA for KIAA0903 protein, partial cds.//0//1752bp//99%//AB020710
C-HEMBA1002954
C-HEMBA1002971
C-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17) (DPDE4).//1.2E-27//63aa//100%//P14646
- 40 C-HEMBA1002997//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//3.8E-25//534aa//24%//Q02224
C-HEMBA1003033
C-HEMBA1003035
C-HEMBA1003041
C-HEMBA1003046//MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT PRECURSOR (EC 3.4.24.64) (BETA-MPP) (P-52).//2.5E-263//489aa//99%//O75439
- 45 C-HEMBA1003067
C-HEMBA1003096
C-HEMBA1003117
C-HEMBA1003129
- 50 C-HEMBA1003136//MANNOSYL-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSYL-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//8.5E-51//221aa//33%//P41940
C-HEMBA1003148//Homo sapiens mRNA full-length insert cDNA clone EUROIMAGE 381801.//0//1583bp//99%//AL079278
- 55 C-HEMBA1003175
C-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE (EC 2.1.1.61).//5.9E-74//134aa//53%//P44551
C-HEMBA1003199

- C-HEMBA1003222
 C-HEMBA1003235//TROPOMYOSIN./0.0000023//109aa//33%//Q02088
 C-HEMBA1003250//PROTEIN KINASE APK1A (EC 2.7.1.-).//17.2E-41//245aa//42%//Q06548
- 5 C-HEMBA1003257
 C-HEMBA1003281//POLIOVIRUS RECEPTOR PRECURSOR./6E-11//239aa//32%//P32506
 C-HEMBA1003286//Homo sapiens mRNA for beta-1,4-galactosyltransferase IV, complete cds./5.4E-229//1043bp//99%//AB024436
 C-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds./0//791bp//99%//AB011109
- 10 C-HEMBA1003322
 C-HEMBA1003327
 C-HEMBA1003369//CENTROMERIC PROTEIN E (CENP-E PROTEIN)./0.00000002//248aa//23%//Q02224
 C-HEMBA1003370
 C-HEMBA1003380
 C-HEMBA1003395
- 15 C-HEMBA1003402
 C-HEMBA1003408//Homo sapiens mRNA for KIAA0905 protein, complete cds./0//1732bp//98%//AB020712
 C-HEMBA1003417//Homo sapiens mRNA; cDNA DKFZp586C021 (from clone DKFZp586C021)./1.6E-312//1414bp//99%//AL050287
 C-HEMBA1003418//TRICHOHYALIN./8.7E-19//281aa//31%//P37709
- 20 C-HEMBA1003433//Homo sapiens gene for NBS1, complete cds./0//511bp//94%//AB013139
 C-HEMBA1003447
 C-HEMBA1003461
 C-HEMBA1003463
 C-HEMBA1003528
- 25 C-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (ISLET-2)./8.8E-189//360aa//96%//P50480
 C-HEMBA1003555//NUCLEOTIDE-BINDING PROTEIN (NBP)./2.1E-68//251aa//52%//P53384
 C-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAMMA-1)./1.2E-31//171aa//100%//P16874
 C-HEMBA1003568//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))./7.9E-49//279aa//32%//P19474
- 30 C-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1./6.9E-206//445aa//74%//Q13330
 C-HEMBA1003581//TALIN./4.4E-45//52aa//98%//P26039
 C-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP)./4.4E-10//118aa//35%//P19682
- 35 C-HEMBA1003615
 C-HEMBA1003617//Homo sapiens HRIHFB2157 mRNA, partial cds./8.2E-178//501bp//97%//AB015344
 C-HEMBA1003621
 C-HEMBA1003662//TBX2 PROTEIN (T-BOX PROTEIN 2)./1.2E-75//151aa//99%//Q13207
 C-HEMBA1003690//HISTONE DEACETYLASE HDA1./2.1E-59//249aa//47%//P53973
- 40 C-HEMBA1003711
 C-HEMBA1003807
 C-HEMBA1003864
 C-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT)./3.8E-16//89aa//46%//P16372
- 45 C-HEMBA1003959
 C-HEMBA1003989
 C-HEMBA1004074
 C-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds./8.5E-221//1188bp//78%//AF091234
- 50 C-HEMBA1004146
 C-HEMBA1004199//Homo sapiens mRNA for KIAA0928 protein, partial cds./0//1893bp//98%//AB023145
 C-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds./0//1892bp//99%//U50748
 C-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds./5.7E-217//1217bp//88%//AF095927
- 55 C-HEMBA1004246
 C-HEMBA1004276//Homo sapiens AP-4 adaptor complex beta4 subunit mRNA, complete cds./4.8E-257//738bp//99%//AF092094
 C-HEMBA1004289

- C-HEMBA1004509//Homo sapiens CGI-21 protein mRNA, complete cds.//0//1512bp//96%//AF132955
 C-HEMBA1004534//Homo sapiens gamma-filamin (ABPL) mRNA, complete cds.//1.2e-316//1445bp//99%//AF089841
- 5 C-HEMBA1004596
 C-HEMBA1004693
 C-HEMBA1004736
 C-HEMBA1004753
- 10 C-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds.//9.1E-34//515bp//66%//U49082
 C-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds.//2.6E-246//1249bp//94%//L39060
 C-HEMBA1004763
 C-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.4E-111//314aa//58%//P08547
 C-HEMBA1004771
 C-HEMBA1004776
- 15 C-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).//3.8E-69//198aa//66%//P50851
 C-HEMBA1004806
 C-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//8.2E-154//317aa//94%//Q00004
 C-HEMBA1004850
- 20 C-HEMBA1004863//Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp586M2022).//0//1443bp//100%//AL080114
 C-HEMBA1004923
 C-HEMBA1004929
 C-HEMBA1004930//26S PROTEASOME SUBUNIT S5B (KIAA0072) (HA1357).//3.3E-27//65aa//100%//Q16401
 C-HEMBA1004933
- 25 C-HEMBA1004954
 C-HEMBA1004972//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//0.00000096//286aa//23%//P12036
 C-HEMBA1005475
- 30 C-HEMBA1005581//Homo sapiens SLIT2 (SUL2) mRNA, complete cds.//0//1721bp//100%//AF133270
 C-HEMBA1006248//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//8.6E-23//151aa//37%//P16372
 C-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//3.7E-225//1189bp//88%//AF076183
- 35 C-HEMBA1006344//RADIXIN.//1.5E-31//333aa//28%//P26043
 C-HEMBA1006377
 C-HEMBA1006467
 C-HEMBA1006474//40 KD PROTEIN.//1.4E-39//292aa//34%//Q01552
 C-HEMBA1006530
- 40 C-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//0.00000043//111aa//40%//Q01485
 C-HEMBA1006795
 C-HEMBA1006877//OXISTEROL-BINDING PROTEIN.//2E-59//378aa//39%//P16258
 C-HEMBA1006936
- 45 C-HEMBA1007018//Homo sapiens dynein light chain-A mRNA, complete cds.//1.5E-267//1215bp//99%//AP078849
 C-HEMBA1007342
 C-HEMBA1000008
 C-HEMBA1000018
- 50 C-HEMBA1000024
 C-HEMBA1000025
 C-HEMBA1000036
 C-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//2.8E-187//1582bp//80%//AF084928
- 55 C-HEMBA1000083//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//1.9E-22//426aa//25%//P11799
 C-HEMBA1000103
 C-HEMBA1000119//Homo sapiens ASMTL gene.//0//1891bp//99%//Y15521

C-HEMBB1000136
 C-HEMBB1000215
 C-HEMBB1000226//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE EEEED8.5//
 2.7E-12//112aa//47%//Q09530
 5 C-HEMBB1000244
 C-HEMBB1000266//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHRO-
 MOSOME V.//6.1E-09//242aa//26%//Q23256
 C-HEMBB1000338
 C-HEMBB1000339
 10 C-HEMBB1000391
 C-HEMBB1000438
 C-HEMBB1000449
 C-HEMBB1000589
 C-HEMBB1000591
 15 C-HEMBB1000623
 C-HEMBB1000630
 C-HEMBB1000631//LONGEVITY-ASSURANCE PROTEIN 1 (LONGEVITY ASSURANCE FACTOR 1).//4.1E-19//
 232aa//28%//P78970
 C-HEMBB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//2.2E-28//273aa//31%//P27671
 20 C-HEMBB1000671
 C-HEMBB1000673
 C-HEMBB1000705
 C-HEMBB1000706
 C-HEMBB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//6.2E-130//692bp//93%//
 U53475
 25 C-HEMBB1000763//Homo sapiens CGI-89 protein mRNA, complete cds.//0//1676bp//96%//AF151847
 C-HEMBB1000781//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.//
 1.2E-126//613bp//97%//AF111105
 C-HEMBB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//5.1E-
 54//232aa//43%//P39956
 30 C-HEMBB1000807
 C-HEMBB1000810
 C-HEMBB1000848
 C-HEMBB1000852
 35 C-HEMBB1000870
 C-HEMBB1000887
 C-HEMBB1000908
 C-HEMBB1000927//Homo sapiens calsenillin mRNA, complete cds.//1.1E-70//595bp//76%//AF120102
 C-HEMBB1000947//Homo sapiens clone HAW 100 putative ribonuclease III mRNA, complete cds.//0//2292bp//
 99%//AF116910
 40 C-HEMBB1000973//Mus musculus schlafen3 (Sfn3) mRNA, complete cds.//3.4E-120//580bp//67%//AF099974
 C-HEMBB1000975
 C-HEMBB1000985//MEPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//8.6E-
 18//178aa//30%//P28575
 45 C-HEMBB1000991
 C-HEMBB1001011//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.4E-73//230aa//45%//
 P51523
 C-HEMBB1001014
 C-HEMBB1001024
 50 C-HEMBB1001056//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED
 NUCLEOLAR PROTEIN P120).//2.9E-19//264aa//34%//P46087
 C-HEMBB1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds.//3.6E-52//331bp//
 80%//AF010144
 C-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.4E-307//1447bp//97%//AF034803
 55 C-HEMBB1001096
 C-HEMBB1001105
 C-HEMBB1001117
 C-HEMBB1001126

- C-HEMBB1001137//Homo sapiens mRNA for putative phospholipase, complete cds.//0/3069bp//99%//AB019435
 C-HEMBB1001151//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//4.2E-210//1835bp//76%//AF110267
- 5 C-HEMBB1001153
 C-HEMBB1001169
 C-HEMBB1001175//ANKYRIN.//6.9E-11//169aa//31%//Q02357
 C-HEMBB1001182
 C-HEMBB1001199
- 10 C-HEMBB1001210//Homo sapiens mRNA for KIAA0970 protein, complete cds.//0/1816bp//99%//AB023187
 C-HEMBB1001242//Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds.//1.8E-284//713bp//100%//AF089897
 C-HEMBB1001288//Homo sapiens CGI-32 protein mRNA, complete cds.//1.8E-274//642bp//99%//AF132966
 C-HEMBB1001289
- 15 C-HEMBB1001294//GTP-BINDING PROTEIN TC10.//1.2E-79//196aa//80%//P17081
 C-HEMBB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.3E-129//724bp//86%//U92703
 C-HEMBB1001331
 C-HEMBB1001339//DXS8237E PROTEIN (FRAGMENT).//0.0000046//124aa//37%//P98175
 C-HEMBB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.1E-58//292bp//99%//AF097441
- 20 C-HEMBB1001369
 C-HEMBB1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0/1586bp//99%//AF100757
 C-HEMBB1001387
 C-MAMMA1002317
 C-MAMMA1002319
- 25 C-MAMMA1002385//RIBONUCLEOPROTEIN RB97D.//0.00000015//206aa//29%//Q02926
 C-NT2RM1000080//UNC-1 PROTEIN.//5.9E-25//211aa//31%//Q21190
 C-NT2RM1000042
 C-NT2RM1000257//MAGO NASHI PROTEIN.//7.9E-69//143aa//91%//P49028
 C-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V-ATPASE 28 KD ACCESSORY PROTEIN).//1.5E-106//118aa//97%//P39942
- 30 C-NT2RM1000669
 C-NT2RM1000781
 C-NT2RM1000867//Homo sapiens HSPC033 mRNA, complete cds.//6.3E-172//798bp//99%//AF092138
 C-NT2RM1001008
- 35 C-NT2RM1001044//Homo sapiens HSPC031 mRNA, complete cds.//0.000000002//980bp//95%//AF085360
 C-NT2RM1001074
 C-NT2RM1001115//ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14).//0.0000056//239aa//27%//
 C-NT2RM2000006//Human DNA sequence from clone 796F18 on chromosome 1p36.11-36.33 Contains a pseudogene similar to MMS2, ESTs and GSSs, complete sequence.//0/1740bp//99%//AL031291
- 40 C-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//2.2E-144//362aa//71%//P25167
 C-NT2RM2000030//DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DH IC) (CYTOPLASMIC DYNEIN INTERMEDIATE CHAIN).//0.00000043//136aa//31%//P54703
- 45 C-NT2RM2000032
 C-NT2RM2000042
 C-NT2RM2000092//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//1.3E-36//160aa//40%//P50102
- 50 C-NT2RM2000093
 C-NT2RM2000101
 C-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0/1574bp//99%//AF067223
 C-NT2RM2000192
 C-NT2RM2000239
- 55 C-NT2RM2000250//Homo sapiens mRNA; cDNA DKFZp564L232 (from clone DKFZp564L232).//4.2E-314//1416bp//100%//AL080069
 C-NT2RM2000259

- C-NT2RM2000260//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//3.6E-19//181-aa//34%//P14918
- C-NT2RM2000287
- 5 C-NT2RM2000322//Homo sapiens mRNA for KIAA0859 protein, complete cds.//3.4E-294//863bp//99%//AB020666
- C-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds.//0//1637bp//99%//AB011132
- C-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN.//1.8E-14//245aa//29%//P11274
- C-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//0//1506bp//99%//U48251
- 10 C-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLEOTIDE).//1.7E-68//419aa//36%//P50849
- C-NT2RM2000374
- C-NT2RM2000395
- 15 C-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHE-
ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-
NENT).//1.6E-54//344aa//33%//P32802
- C-NT2RM2000407
- C-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//1E-222//237aa//89%//Q08469
- 20 C-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION.//0.0000001//
157aa//28%//P36113
- C-NT2RM2000469//NITROGEN PERMEASE REACTIVATOR PROTEIN (EC 2.7.1.-).//0.0000089//377aa//24%//P22211
- C-NT2RM2000490//SYNAPTOTAGMIN(P65).//1.8E-13//166aa//34%//P41823
- 25 C-NT2RM2000502
- C-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//1673bp//99%//AF061243
- C-NT2RM2000522//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.3E-12//282aa//
32%//P17437
- C-NT2RM2000540
- 30 C-NT2RM2000567
- C-NT2RM2000569
- C-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS).//
1.7E-187//741aa//46%//P73505
- C-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds.//0//3001bp//99%//D68987
- 35 C-NT2RM2000588//HISTONE DEACETYLASE HDA1.//2.8E-60//384aa//40%//P53973
- C-NT2RM2000594//Homo sapiens DNA cytosine-5 methyltransferase 3 beta 3 (DNMT3B) mRNA, complete cds.//
0//2712bp//99%//AF156487
- C-NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.//4.9E-70//838bp//69%//
AF179221
- 40 C-NT2RM2000624//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR
SRP75).//4.4E-32//319aa//35%//Q06170
- C-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds.//0//3791bp//99%//AB018272
- C-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds.//0//2530bp//99%//AB014558
- C-NT2RM2000639
- 45 C-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1543bp//99%//AB014576
- C-NT2RM2000669
- C-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//3.7E-142//285aa//90%//P32391
- C-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP1).//3.8E-23//184aa//
36%//Q15404
- 50 C-NT2RM2000718//Homo sapiens HRIHFB2436 mRNA, partial cds.//4.4E-231//1065bp//99%//AB015342
- C-NT2RM2000740//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//5.7E-53//266aa//43%//
P41877
- C-NT2RM2000795
- C-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETACOP).//9.5E-279//545aa//
98%//P23514
- 55 C-NT2RM2000837
- C-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//1.7E-200//927bp//99%//
AB015046

C-NT2RM2000952
 C-NT2RM2000984
 C-NT2RM2001004
 5 C-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//8.2E-154//285aa//99%/Q60809
 C-NT2RM2001065
 C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//2.4E-15//266aa//
 26%/P46577
 C-NT2RM2001131
 C-NT2RM2001141
 10 C-NT2RM2001152
 C-NT2RM2001177//Homo sapiens mRNA; cDNA DKFZp586G1822 (from clone DKFZp586G1822).//2.1E-293//
 1335bp//99%/AL080109
 C-NT2RM2001194
 C-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.3E-20//267aa//35%/P05143
 15 C-NT2RM2001201//EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF5).//0.00000015//95aa//35%/P48724
 C-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (PCIP10).//3.6E-10//177aa//
 32%/P97924
 C-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS)(L-GLUTAMINE AMI-
 20 DOHYDROLASE).//1.3E-180//328aa//99%/P13264
 C-NT2RM2001243
 C-NT2RM2001247
 C-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.6E-166//312aa//98%/P53995
 25 C-NT2RM2001291
 C-NT2RM2001306//Homo sapiens mRNA; cDNA DKFZp564I052 (from clone DKFZp564I052).//0//1694bp//99%/AL080063
 C-NT2RM2001312
 C-NT2RM2001319
 30 C-NT2RM2001324//ZYXIN.//6.8E-55//200aa//41%/Q04584
 C-NT2RM2001345//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E1.//0.000000029//334aa//22%/000808
 C-NT2RM2001370
 C-NT2RM2001393
 C-NT2RM2001420
 35 C-NT2RM2001424//Homo sapiens mRNA; cDNA DKFZp586D0920 (from clone DKFZp586D0920).//0//1621bp//
 100%/AL050146
 C-NT2RM2001499//LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2).//7.4E-121//
 437aa//57%/P52569
 C-NT2RM2001504
 40 C-NT2RM2001524
 C-NT2RM2001544
 C-NT2RM2001547//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.9E-27//
 90aa//42%/P38660
 C-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SSA)) (RO(SS-A)).//4.3E-
 45 61//312aa//44%/P19474
 C-NT2RM2001582
 C-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds.//0//1000bp//100%/AB014610
 C-NT2RM2001896//CELL DIVISION PROTEIN FTSJ.//5.1E-26//204aa//34%/P28692
 C-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds.//0//2390bp//99%/AB007931
 50 C-NT2RM2001930
 C-NT2RM2001935
 C-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//2.7E-27//216aa//34%/P28320
 C-NT2RM2001950//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION.//0.0000001//
 212aa//23%/P38250
 55 C-NT2RM2001982
 C-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//1.9E-39//253aa//35%/P37838
 C-NT2RM2001997//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//1.3E-10//232aa//

28%//Q12730
 C-NT2RM2001998//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME 1.//3.1E-12//206aa//30%//Q09782
 C-NT2RM2002004//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//0.00000029//83aa//44%//P40796
 5 C-NT2RM2002014//HYPOTHETICAL 81.4 KD PROTEIN IN GREB-FEOA INTERGENIC REGION.//1.1E-89//425aa//41%//P46837
 C-NT2RM2002030//Homo sapiens mRNA for Glutamine-fructose-6-phosphate amidotransferase, complete cds.//0//1959bp//99%//AB016789
 10 C-NT2RM2002049
 C-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.00000099//338aa//24%//Q07878
 C-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//5E-62//104aa//57%//Q61990
 15 C-NT2RM2002091
 C-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//0//1807bp//99%//AJ010840
 C-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//0//1868bp//99%//AF030435
 C-NT2RM2002128//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//4.9E-13//487aa//26%//P49695
 20 C-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//8E-31//105aa//47%//P47805
 C-NT2RM2002178//Homo sapiens mRNA; cDNA DKFZp434E0335 (from clone DKFZp434E0335).//0//1683bp//99%//AL117402
 C-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//7.1E-155//381aa//72%//P25167
 25 C-NT2RM4000061
 C-NT2RM4000104//ZINC FINGER PROTEIN 135.//1.5E-81//251aa//53%//P52742
 C-NT2RM4000139//R. norvegicus trg mRNA.//2.3E-114//1161bp//72%//X68101
 C-NT2RM4000169//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//4.8E-13//686aa//23%//P25386
 30 C-NT2RM4000191//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.//9.2E-75//439aa//41%//P16381
 C-NT2RM4000197
 C-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//0//1926bp//100%//AB018255
 C-NT2RM4000229//Gallus gallus actin filament-associated protein (AFAP-110) mRNA, complete cds.//1.1E-27//633bp//64%//L20303
 35 C-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//2.2E-276//1124bp//97%//M99438
 C-NT2RM4000344//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//0//2030bp//99%//AJ132637
 40 C-NT2RM4000349//Homo sapiens HSPC028 mRNA, complete cds.//0//1827bp//99%//AF083246
 C-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//1.5E-21//208aa//35%//Q24371
 C-NT2RM4000386//Mus musculus mRNA for Ten-m3, complete cds.//0//2156bp//86%//AB025412
 C-NT2RM4000395
 C-NT2RM4000421//Homo sapiens mRNA for nuclear transport receptor.//0//1730bp//99%//AJ133769
 45 C-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME 1.//8E-20//393aa//24%//Q10297
 C-NT2RM4000471//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2092bp//99%//AF097025
 C-NT2RM4000486//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.8E-11//242aa//31%//P04280
 50 C-NT2RM4000496//SAP1 PROTEIN.//8.3E-53//434aa//29%//P39955
 C-NT2RM4000511
 C-NT2RM4000515//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H) (FRAGMENT).//1.1E-11//394aa//24%//P16884
 C-NT2RM4000520
 55 C-NT2RM4000558
 C-NT2RM4000595//Homo sapiens leucine-rich repeats containing F-box protein FBL3 mRNA, complete cds.//1.1E-285//1293bp//99%//AF186273
 C-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds.//0//1940bp//95%//AB014587

C-NT2RP1000035//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657
 C-NT2RP1000040
 C-NT2RP1000063
 C-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsa12.//0//1162bp//99%//X98834
 5 C-NT2RP1000101
 C-NT2RP1000111//COP1 REGULATORY PROTEIN.//4E-116//296aa//51%//P93471
 C-NT2RP1000112
 C-NT2RP1000124
 C-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//4.5E-50//181aa//60%//P51859
 10 C-NT2RP1000163//Homo sapiens mRNA for KIAA0948 protein, complete cds.//0//1889bp//98%//AB023165
 C-NT2RP1000170
 C-NT2RP1000191
 C-NT2RP1000202//ANKYRIN.//1E-25//302aa//34%//Q02357
 C-NT2RP1000243
 15 C-NT2RP1000259
 C-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//5.8E-114//616bp//93%//AF067730
 C-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.3E-275//1249bp//99%//AF053551
 20 C-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//8.7E-47//155aa//58%//P32447
 C-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.7E-15//162aa//30%//P25343
 C-NT2RP1000357
 C-NT2RP1000376//Homo sapiens mRNA: cDNA DKFZp434A102 (from clone DKFZp434A102).//0//12265bp//95%//AL080187
 25 C-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds.//0//1056bp//99%//AB011159
 C-NT2RP1000416
 C-NT2RP1000439//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//1.8E-94//1019bp//63%//AF111423
 C-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN).//2.4E-10//227aa//25%//Q08257
 30 C-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//2.6E-94//254aa//47%//P34580
 C-NT2RP1000478//TUBULIN BETA-5 CHAIN (CLASS-V).//4.5E-240//445aa//97%//P09653
 C-NT2RP1000481
 35 C-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds.//0//2728bp//99%//D87686
 C-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.1E-27//193aa//35%//P49020
 C-NT2RP1000574//HOMEOBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//3.5E-75//151aa//94%//P97367
 40 C-NT2RP1000581
 C-NT2RP1000630//NECDIN.//2.4E-44//227aa//41%//P25233
 C-NT2RP1000688
 C-NT2RP1000695
 C-NT2RP1000733//Human mRNA for GSPT1-TK protein, complete cds.//0//2057bp//99%//E14379
 45 C-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds.//0//2186bp//99%//AF101434
 C-NT2RP1000782//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%//O35566
 C-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//8.2E-83//334aa//50%//Q07960
 50 C-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1494bp//99%//AF067223
 C-NT2RP1000846
 C-NT2RP1000851
 55 C-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%//O35566
 C-NT2RP1000915//AUTOANTIGEN NGP-1.//1.7E-19//343aa//25%//Q13823
 C-NT2RP1000947//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds.//4.6E-

- 105//504bp//99%//UJ39317
 C-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//1.4E-23//370aa//28%//Q04652
 C-NT2RP1000958//AUTOANTIGEN NGP-1.//1.4E-19//343aa//25%//Q13823
 C-NT2RP1000959//Human acidic ribosomal phosphoprotein P0 mRNA, complete cds.//2.5E-236//966bp//99%//
 5 M17885
 C-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//8.9E-299//554aa//99%//P19338
 C-NT2RP1000980
 C-NT2RP1000988
 C-NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds.//2.2E-78//
 10 1529bp//61%//L01790
 C-NT2RP1001014
 C-NT2RP1001395
 C-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//8.9E-141//396aa//67%//P91917
 C-NT2RP1001424
 15 C-NT2RP1001449
 C-NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).//1.2E-137//629bp//
 100%//AJ005257
 C-NT2RP1001466
 C-NT2RP1001475
 20 C-NT2RP1001482
 C-NT2RP1001494//MALE STERILITY PROTEIN 2.//7.2E-40//261aa//27%//Q08891
 C-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.6E-166//506aa//60%//
 P42803
 C-NT2RP1001546//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-
 25 OPROTEIN SFA-1) (CD151 ANTIGEN).//1.6E-30//232aa//30%//Q35566
 C-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//5.8E-121//
 271aa//89%//P47758
 C-NT2RP1001616
 C-NT2RP1001665//CALMODULIN.//0.00000051//83aa//30%//P02594
 30 C-NT2RP2000008//DNAJ PROTEIN (40 KD HEAT SHOCK CHAPERONE PROTEIN) (HSP40).//9.8E-17//79aa//
 55%//O34136
 C-NT2RP2000007
 C-NT2RP2000008//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.4E-177//726aa//47%//
 P51523
 35 C-NT2RP2000032//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP1).//1.8E-22//184aa//
 34%//Q01730
 C-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//
 0//1390bp//98%//AF061749
 C-NT2RP2000054
 40 C-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP-EP-
 SILON).//9.4E-16//45aa//100%//P49446
 C-NT2RP2000067
 C-NT2RP2000070//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//3.4E-51//
 383aa//32%//P33450
 45 C-NT2RP2000079
 C-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//0//2286bp//100%//AB018338
 C-NT2RP2000091
 C-NT2RP2000097
 C-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//0//2244bp//99%//AB018356
 50 C-NT2RP2000120
 C-NT2RP2000126//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//2.5E-117//541aa//42%//
 P41877
 C-NT2RP2000133//Homo sapiens mRNA for KIAA0989 protein, partial cds.//0//2286bp//99%//AB023206
 C-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN
 55 AP47) (GOLGI ADAPTOR AP-1-47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN
 ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//4.4E-226//423aa//99%//P35585
 C-NT2RP2000153//GAR2 PROTEIN.//9.8E-23//311aa//28%//P41891
 C-NT2RP2000157//MLO2 PROTEIN.//2.6E-11//62aa//40%//Q09329

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C-NT2RP2000161//Homo sapiens mRNA for KIAA1008 protein, complete cds.//3.4e-315//1430bp//99%//AB023225

C-NT2RP2000173

C-NT2RP2000175

5 C-NT2RP2000195

C-NT2RP2000205

C-NT2RP2000208//Homo sapiens mRNA for KIAA0892 protein, partial cds.//0//2898bp//99%//AB020699

C-NT2RP2000224//INSULIN RECEPTOR SUBSTRATE-1 (IRS1).//0.000043//103aa//28%//P35568

10 C-NT2RP2000232

C-NT2RP2000233

C-NT2RP2000239

C-NT2RP2000248//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//3.4E-21//210aa//33%//P56558

15 C-NT2RP2000270

C-NT2RP2000274

C-NT2RP2000283

C-NT2RP2000288//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//1.6E-27//576aa//25%//Q10297

20 C-NT2RP2000297//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.3E-186//256aa//60%//Q99676

C-NT2RP2000298

C-NT2RP2000310//Human proline-dehydrogenase/proline oxidase (PRODH) mRNA, complete cds.//4.3E-279//1193bp//99%//U82381

C-NT2RP2000328

C-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//226aa//92%//P08760

25 C-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//6.3E-115//674aa//46%//P17564

C-NT2RP2000369

C-NT2RP2000412

30 C-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F).//4.3E-228//415aa//100%//P52597

C-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//0//1757bp//99%//AF102265

C-NT2RP2000438

35 C-NT2RP2000448//KES1 PROTEIN.//8.7E-54//392aa//38%//P35844

C-NT2RP2000503

C-NT2RP2000510

C-NT2RP2000516

C-NT2RP2000603

40 C-NT2RP2000617

C-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//0//2482bp//99%//AB014514

C-NT2RP2000656

C-NT2RP2000658

C-NT2RP2000668//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E-271//349aa//32%//Q01577

45 C-NT2RP2000704

C-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE)//2.7E-100//488aa//44%//O32038

C-NT2RP2000764//NIFS PROTEIN.//6.6E-36//252aa//42%//P12623

C-NT2RP2000809//Homo sapiens mRNA for KIAA0873 protein, partial cds.//0//3347bp//99%//AB020680

50 C-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//0.000000056//179aa//29%//Q99104

C-NT2RP2000814//GELATION FACTOR (ACTIN BINDING PROTEIN 120) (ABP-120).//0.00000011//96aa//29%//P13466

C-NT2RP2000816//MAGNESIUM-CHELATASE 30 KD SUBUNIT.//0.000000079//172aa//28%//P26174

55 C-NT2RP2000819

C-NT2RP2000841

C-NT2RP2000845

C-NT2RP2000863

- C-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2.//0//694aa//99%/060841
C-NT2RP2000892
C-NT2RP2000931//MATRIN 3.//2.4E-289//467aa//95%/P43244
C-NT2RP2000932//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp5640043).//0//2487bp//99%/AL050390
C-NT2RP2000938
C-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//0//3458bp//99%/AB018298
C-NT2RP2000965//Homo sapiens mRNA for fls353, complete cds.//0//1989bp//96%/AB024704
C-NT2RP2000985
C-NT2RP2001036
C-NT2RP2001044
C-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488.//0//2749bp//99%/AB007957
C-NT2RP2001065
C-NT2RP2001070//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE).//5.8E-46//222aa//45%/IQ20939
C-NT2RP2001081//SYNAPTOTAGMIN IV.//4.2E-118//430aa//54%/P50232
C-NT2RP2001094
C-NT2RP2001119
C-NT2RP2001127//Homo sapiens mRNA for PLU-1 protein.//0//2514bp//99%/AJ132440
C-NT2RP2001218
C-NT2RP2001245//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHAIN) (NMMHC).//2.2E-10//366aa//28%/P14105
C-NT2RP2001381
C-NT2RP2001397//Homo sapiens mRNA; cDNA DKFZp434B174 (from clone DKFZp434B174).//0//1495bp//100%/AL080146
C-NT2RP2001427
C-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds.//0//1748bp//99%/AB018340
C-NT2RP2001675
C-NT2RP2001721
C-NT2RP2001907
C-NT2RP2001969
C-NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA, complete cds.//4.7E-177//1538bp//74%/AF062378
C-NT2RP2002046
C-NT2RP2002154
C-NT2RP2002208
C-NT2RP2002270//AF-9 PROTEIN.//0.0000012//74aa//36%/P42568
C-NT2RP2002312//Homo sapiens mRNA for CDS2 protein.//0//2333bp//99%/Y16521
C-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds.//8.4E-254//1158bp//99%/AB015594
C-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//4.3E-240//1105bp//99%/AF038958
C-NT2RP2002426
C-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//0//2180bp//99%/AB005289
C-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//6.2E-19//288aa//26%/Q11073
C-NT2RP2002595//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//7.5E-35//181aa//42%/P12815
C-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.-).//1.7E-51//326aa//38%/P55345
C-NT2RP2002621
C-NT2RP2002672
C-NT2RP2002701//HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME II.//1.9E-14//210aa//30%/O14345
C-NT2RP2002769
C-NT2RP2002862//60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN).//8.8E-10//203aa//27%/P29764

- C-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//1.9E-136//623bp//100%//AF038392
- C-NT2RP2002954
- 5 C-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//4.6E-80//147aa//100%//P51669
- C-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//0.00000001//98aa//36%//P10129
- C-NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds.//0//2209bp//99%//AB026190
- 10 C-NT2RP2003108
- C-NT2RP2003117
- C-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete eds.//2.3E-82//642bp//68%//AF079765
- C-NT2RP2003125//RING CANAL PROTEIN (KELCH PROTEIN).//2.4E-38//539aa//25%//004652
- C-NT2RP2003177
- 15 C-NT2RP2003194
- C-NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.//0//1580bp//99%//AF151811
- C-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds.//0//1526bp//99%//AB006572
- C-NT2RP2003329//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//3.6E-14//332aa//32%//P26337
- 20 C-NT2RP2003367
- C-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//5E-131//269aa//91%//P38378
- C-NT2RP2003446
- C-NT2RP2003533
- 25 C-NT2RP2003543//HYPOTHETICAL tRNA/tRNA METHYLTRANSFERASE SLR1673 (EC 2.1.1.-).//1.7E-17//148aa//34%//P74261
- C-NT2RP2003596
- C-NT2RP2003629
- C-NT2RP2003687
- 30 C-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//5.4E-29//85aa//72%//Q05481
- C-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//1.7E-75//147aa//93%//P51669
- C-NT2RP2003793
- 35 C-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//1.5E-23//200aa//30%//O09175
- C-NT2RP2003986
- C-NT2RP2004042
- 40 C-NT2RP2004316//Homo sapiens chromosome 1 clone J549L20, WORKING DRAFT SEQUENCE, in unordered pieces.//8.2E-202//926bp//100%//AL096820
- C-NT2RP2004389//PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR.//9.3E-15//126aa//39%//P38120
- C-NT2RP2004392//MNN4 PROTEIN.//1.4E-11//143aa//27%//P36044
- C-NT2RP2004463
- 45 C-NT2RP2004602
- C-NT2RP2004614//Homo sapiens mRNA for KIAA0922 protein, partial cds.//0//2040bp//99%//AB023139
- C-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//8.5E-233//1061bp//99%//AJ006291
- C-NT2RP2004689//HYPOTHETICAL 192.5 KD PROTEIN C6G9.10C IN CHROMOSOME I.//5.6E-64//616aa//33%//Q92355
- 50 C-NT2RP2004791//PUTATIVE LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.4) (LEUCINE-- TRNA LIGASE) (LEURS).//9.5E-73//153aa//59%//Q10490
- C-NT2RP2004799//PROBABLE SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//3.7E-135//414aa//62%//P53588
- C-NT2RP2004802
- 55 C-NT2RP2004841
- C-NT2RP2004936
- C-NT2RP2004959//P54 PROTEIN PRECURSOR.//0.00000095//297aa//20%//P13692
- C-NT2RP2004999

C-NT2RP2005000
 C-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//0//1694bp//99%//AB014515
 C-NT2RP2005012//Homo sapiens mRNA for SEC63 protein.//0//1693bp//99%//AJ011779
 C-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//3.3E-47//155aa//59%//P32447
 5 C-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//0//2388bp//98%//X98743
 C-NT2RP2005140
 C-NT2RP2005147
 C-NT2RP2005159
 10 C-NT2RP2005239//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2087bp//99%//AF097025
 C-NT2RP2005270
 C-NT2RP2005276//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2122bp//99%//D89053
 C-NT2RP2005293
 C-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1515bp//99%//AB014576
 15 C-NT2RP2005358//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds.//0//2199bp//99%//AF072247
 C-NT2RP2005393//AUTOANTIGEN NGP-1.//7.2E-39//224aa//35%//Q13823
 C-NT2RP2005436//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.2E-13//185aa//38%//Q08170
 20 C-NT2RP2005441
 C-NT2RP2005453
 C-NT2RP2005464
 C-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2.//3E-44//252aa//41%//P38127
 C-NT2RP2005472
 25 C-NT2RP2005495
 C-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55).//5.2E-81//166aa//88%//P36876
 C-NT2RP2005509//Homo sapiens CGI-45 protein mRNA, complete cds.//0//1825bp//99%//AF151803
 C-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//3994bp//99%//AF092563
 30 C-NT2RP2005525//Mus musculus kanadaplin mRNA, complete cds.//2.4E-304//1687bp//85%//AF035526
 C-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//0//2856bp//99%//AB007963
 C-NT2RP2005549//PUTATIVE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE).//2E-20//181aa//36%//Q39366
 35 C-NT2RP2005555
 C-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds.//1E-46//576bp//70%//AF062529
 C-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//8.9E-313//1455bp//98%//AF062085
 40 C-NT2RP2005622
 C-NT2RP2005635//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1E-11//128aa//36%//P47623
 C-NT2RP2005637
 C-NT2RP2005640
 45 C-NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).//1.2E-13//74aa//45%//IP56101
 C-NT2RP2005669//Homo sapiens mRNA for DEDD protein.//3.9E-209//957bp//99%//AJ010973
 C-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.4E-200//908bp//99%//AF089814
 C-NT2RP2005683
 50 C-NT2RP2005690
 C-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//0//1684bp//99%//AB018342
 C-NT2RP2005723//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN).//0.00000003//169aa//28%//P38074
 C-NT2RP2005748
 55 C-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//0//1968bp//99%//AF068868
 C-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//1966bp//99%//AF082516

- C-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A (EIF-4A).//1.7E-61//374aa//38%//P47943
 C-NT2RP2005767//G.gallus PB1 gene.//5E-163//1158bp//81%//X90849
 C-NT2RP2005773//Homo sapiens pyrroline 5-carboxylate reductase isoform (P5CR2) mRNA, complete cds.//2.7E-180//656bp//99%//AF151351
- 5 C-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN-BINDING PROTEIN) (SABP).//2.1E-213//249aa//85%//Q02038
 C-NT2RP2005781
 C-NT2RP2005804
- 10 C-NT2RP2005835//SHP1 PROTEIN.//1.8E-28//208aa//32%//P34223
 C-NT2RP2005853
 C-NT2RP2005868
 C-NT2RP2005886
 C-NT2RP2005890
- 15 C-NT2RP2005901//Homo sapiens mRNA for KIAA0971 protein, complete cds.//0//1977bp//99%//AB023188
 C-NT2RP2005933//NUCLEOPORIN NUP57 (NUCLEAR PORE PROTEIN NUP57).//5E-11//155aa//34%//P48837
 C-NT2RP2006038
 C-NT2RP2006043//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.5E-13//185aa//38%//Q08170
- 20 C-NT2RP2006052
 C-NT2RP2006069
 C-NT2RP2006071
 C-NT2RP2006100//Homo sapiens mRNA; cDNA DKFZp564B102 (from clone DKFZp564B102).//0//1759bp//99%//AL049970
- 25 C-NT2RP2006106
 C-NT2RP2006141
 C-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//3.E-189//899bp//97%//AB014554
 C-NT2RP2006196
 C-NT2RP2006200
- 30 C-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.E-214//1026bp//97%//X96484
 C-NT2RP2006237
 C-NT2RP2006238
 C-NT2RP2006275//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//2E-59//388aa//32%//P46821
- 35 C-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.8E-274//1236bp//99%//AF035262
 C-NT2RP2006333
 C-NT2RP2006365
 C-NT2RP2006393
- 40 C-NT2RP2006436//ANTERIOR-RESTRICTED HOMEBOX PROTEIN (RATHKE POUCH HOMEO BOX).//0.00000034//50aa//50%//Q61658
 C-NT2RP2006456
 C-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//0//2181bp//99%//AJ006266
 C-NT2RP2006467
 C-NT2RP2006472
- 45 C-NT2RP2006565//Sus scrofa mRNA for SCAMPI protein.//0//1276bp//84%//Y15710
 C-NT2RP2006571//CYTOCHROME P450 2G1 (EC 1.14.14.1) (CYP11G1) (P450-NMB) (OLFACTIVE).//4.2E-134//486aa//50%//P24461
 C-NT2RP2006573//2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37) (CNP).//0.0000055//169aa//25%//P09543
- 50 C-NT2RP3000031//Homo sapiens mRNA for KIAA0901 protein, complete cds.//0//2547bp//99%//AB020708
 C-NT2RP3000072
 C-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//0//1404bp//97%//AB011164
 C-NT2RP3000220
 C-NT2RP3000251
- 55 C-NT2RP3000252//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2388bp//99%//AF120334
 C-NT2RP3000312
 C-NT2RP3000320//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//100%//AJ242978

- C-NT2RP3000333
C-NT2RP3000348
C-NT2RP3000350//PROBABLE GTP-BINDING PROTEIN
HP0303./0.00000028//185aa//31%//O25074
- 5 C-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3)//2E-111//
226aa//92%//P08760
C-NT2RP3000361//Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1/Zer1
and Prp6./0//2072bp//98%//AB019219
- 10 C-NT2RP3000366//RAS-RELATED PROTEIN RAB-18./2.1E-107//206aa//99%//P35293
C-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)//
1.7E-139//679aa//41%//O43143
- 15 C-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds./0//2364bp//99%//AF071185
C-NT2RP3000484
C-NT2RP3000527//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)/.4.8E-28//536aa//27%//P28160
- C-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN)/.1.9E-12//192aa//30%//
P15151
- C-NT2RP3000596//TRICHOHYALIN./2.5E-17//304aa//28%//Q07283
C-NT2RP3000599
C-NT2RP3000632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)/.3E-140//499aa//46%//P51523
- 20 C-NT2RP3000644
C-NT2RP3000661
C-NT2RP3000665
C-NT2RP3000690
C-NT2RP3000759//ADP-RIBOSYLATION FACTOR./7E-28//176aa//34%//Q94650
- 25 C-NT2RP3000825//NEUROGENIC LOCUS NOTCH 3 PROTEIN./2.5E-36//417aa//31%//Q61982
C-NT2RP3000836
C-NT2RP3000841
C-NT2RP3000850
C-NT2RP3000852
C-NT2RP3000859
- 30 C-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete
cds./6.9E-69//1611bp//61%//U53445
C-NT2RP3000869
C-NT2RP3000901
- 35 C-NT2RP3000917//Homo sapiens Dhm1-like protein mRNA, complete cds./0//3199bp//99%//AF064257
C-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds./1
2.7E-185//585bp//88%//AF015264
C-NT2RP3000980
- 40 C-NT2RP3000994//MATERNAL EFFECT PROTEIN
STAUFEIN./0.00000006//78aa//48%//P25159
C-NT2RP3001004
C-NT2RP3001081
C-NT2RP3001084
- 45 C-NT2RP3001096//Rattus norvegicus leprecan (lepre1) mRNA, complete cds./1.7E-94//787bp//66%//AF087433
C-NT2RP3001107//PEREGRIN (BR140 PROTEIN)/.3E-44//260aa//40%//P55201
C-NT2RP3001109
C-NT2RP3001116
C-NT2RP3001119
C-NT2RP3001133
- 50 C-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds./0//2802bp//99%//AB018305
C-NT2RP3001155//Homo sapiens mRNA for AND-1 protein./0//2732bp//99%//AJ006266
C-NT2RP3001176//HYPOTHETICAL 65.3 KD PROTEIN IN MAD1-SCY1 INTERGENIC REGION./1.7E-10//
196aa//27%//P53154
C-NT2RP3001214
- 55 C-NT2RP3001216//CYCLIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT)/.0.0000023//137aa//33%//
P35663
C-NT2RP3001221//GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-
BUTYROBETAINE HYDROXYLASE)/.1.9E-31//353aa//30%//P80193

C-NT2RP3001236
 C-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CONTAINS: LIGHT CHAIN LC1]//1.2E-166//395aa//51%//P14873
 C-NT2RP3001260//Homo sapiens mRNA for KIAA0911 protein, complete cds.//0//2497bp//99%//AB020718
 5 C-NT2RP3001307
 C-NT2RP3001325
 C-NT2RP3001384//Homo sapiens NAKAP95 mRNA for neighbor of A-kinase anchoring protein 95, complete cds.//0//1213bp//99%//AB025905
 10 C-NT2RP3001392
 C-NT2RP3001396
 C-NT2RP3001398//TRANSCRIPTIONAL REPRESSOR CTCF.//1.3E-61//374aa//36%//P49711
 C-NT2RP3001407//SCY1 PROTEIN.//0.00000033//143aa//25%//P53009
 C-NT2RP3001420
 C-NT2RP3001426//DNAJ PROTEIN (FRAGMENT).//1E-16//77aa//46%//O33529
 15 C-NT2RP3001427//WERNER SYNDROME HELICASE HOMOLOG.//2.7E-10//159aa//33%//O09053
 C-NT2RP3001457
 C-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A.//9.1E-13//87aa//43%//P11632
 C-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//0//1475bp//99%//U13395
 C-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//0//2295bp//99%//AF064801
 20 C-NT2RP3001529//SPOOB-ASSOCIATED GTP-BINDING PROTEIN.//1E-61//345aa//42%//P20964
 C-NT2RP3001621
 C-NT2RP3001629
 C-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210.//6.8E-18//91aa//38%//Q92609
 25 C-NT2RP3001646//WD-40 REPEAT PROTEIN MSI2.//8.8E-09//132aa//31%//O22468
 C-NT2RP3001676
 C-NT2RP3001679
 C-NT2RP3001799//MYOSIN HEAVY CHAIN, STRIATED MUSCLE.//1.6E-11//348aa//27%//P24733
 C-NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN).//7.4E-18//249aa//30%//Q04652
 30 C-NT2RP3001896
 C-NT2RP3001915
 C-NT2RP3001929
 C-NT2RP3003193//ZINC FINGER PROTEIN 135.//7.3E-98//269aa//62%//P52742
 C-NT2RP3004466
 35 C-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//3.3E-113//466aa//42%//P34110
 C-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds.//0//1520bp//99%//AB014532
 C-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds.//0//974bp//95%//AB011126
 C-NT2RP3004569//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).//0.00000038//150aa//28%//Q01484
 40 C-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds.//0//1770bp//99%//AF026445
 C-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//0//1639bp//99%//AB007946
 C-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//0//1807bp//99%//AJ006266
 45 C-NT2RP3004617//ZINC-BINDING PROTEIN A33.//7.2E-75//464aa//35%//Q02084
 C-NT2RP3004618//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//3972bp//98%//AF093097
 C-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN).//1.7E-72//254aa//45%//P54352
 50 C-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64.//2.6E-98//239aa//64%//P35526
 C-NT2RP4000051//SYNAPTONEMAL COMPLEX-PROTEIN SC65.//4.9E-51//335aa//37%//Q64375
 C-NT2RP4000078//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//3013bp//99%//AB020657
 C-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//0//2161bp//99%//AB011538
 C-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//728aa//99%//Q10568
 55 C-NT2RP4000129
 C-NT2RP4000147//Drosophila melanogaster putative ARF1 GTPase activating protein (ARF1-GAP) mRNA, complete cds.//3.8E-28//528bp//67%//AF011427

- C-NT2RP4000150
C-NT2RP4000151
C-NT2RP4000159
C-NT2RP4000185
- 5 C-NT2RP4000212//Homo sapiens mRNA for KIAA0700 protein, partial cds.//0//4149bp//99%//AB014600
C-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//5.9E-15//104aa//40%//P15287
- C-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//0//1932bp//99%//AJ006470
C-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//2.7E-84//208aa//76%//Q03173
- 10 C-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).//5.5E-29//153aa//43%//O23968
C-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//3.5E-297//1024aa//55%//P87115
- C-NT2RP4000312//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE).//1.5E-26//237aa//28%//Q01631
- 15 C-NT2RP4000323//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.0000003//101aa//32%//P26372
- C-NT2RP4000355
C-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//0//4074bp//99%//AB018281
C-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//0//4782bp//99%//AF044195
- 20 C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1).//2.6E-77//262aa//54%//O75570
- C-NT2RP4000376//Homo sapiens mRNA for phospholipase A2 activating protein.//0//2412bp//99%//AJ238243
C-NT2RP4000381
C-NT2RP4000398//ZINC FINGER PROTEIN 140.//2.9E-110//435aa//50%//P52738
- 25 C-NT2RP4000415
C-NT2RP4000417//MANNOSE-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE) (FRAGMENT).//2.6E-51//438aa//33%//P45701
- C-NT2RP4000448//Homo sapiens mRNA; cDNA DKFZp566G0746 (from clone DKFZp566G0746).//0//3991bp//99%//AL050078
- 30 C-NT2RP4000449
C-NT2RP4000455//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//0.0000003//175aa//27%//P09309
C-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15) (DEUBIQUITINATING ENZYME 15).//2.5E-37//291aa//38%//P50101
- 35 C-NT2RP4000480
C-NT2RP4000481//ATP-DEPENDENT RNA HELICASE DOB1 (MRNA TRANSPORT REGULATOR MTR4).//1.9E-67//721aa//29%//Q09475
- C-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//8.8E-50//214aa//50%//P40484
- 40 C-NT2RP4000500
C-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.5E-106//495aa//45%//P45818
C-NT2RP4000524
C-NT2RP4000541
C-NT2RP4000556//SUR4 PROTEIN (SRE1 PROTEIN).//7.4E-14//233aa//31%//P40319
- 45 C-NT2RP4000560
C-NT2RP4000588
C-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//2.9E-188//863bp//99%//AF067730
- C-NT2RP4000638
C-NT2RP4000648//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//0.0000003//175aa//27%//P09309
- 50 C-NT2RP4000657//SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN SPSE.//1.1E-32//350aa//30%//P39625
C-NT2RP4000704
C-NT2RP4000713//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//1.1E-13//295aa//27%//Q11073
- 55 C-NT2RP4000724//RETROVIRUS-RELATED ENV POLYPROTEIN.//3.2E-191//199aa//78%//P10267
C-NT2RP4000728//Homo sapiens mRNA for KIAA0931 protein, partial cds.//0//3392bp//95%//AB023148
C-NT2RP4000737

- C-NT2RP4000739//Homo sapiens mRNA for KIAA1012 protein, complete cds.//0//3574bp//99%//AB023229
 C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.00000032//67aa//31%//P53915
 C-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds.//0//1927bp//99%//AB007939
 5 C-NT2RP4000833
 C-NT2RP4000837//Homo sapiens mRNA for zinc finger protein SALL1.//4.3E-94//810bp//65%//Y18265
 C-NT2RP4000839//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//8.5E-21//271 aa//28%//Q00808
 C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE)(ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV)(AP-B).//5.7E-82//324aa//48%//O09175
 10 C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//4.1E-85//174aa//55%//P16415
 C-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//6.2E-91//173aa//87%//O35682
 C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN).//9.6E-96//513aa//42%//P22314
 C-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//2.6E-26//227aa//36%//Q06828
 15 C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//1.5E-76//346aa//43%//Q61068
 C-NT2RP4000928//Homo sapiens mRNA for CDS2 protein.//0//2487bp//99%//Y16521
 C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HELICASE MJ1505.//0.0000014//185aa//25%//Q58900
 20 C-NT2RP4000955
 C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//1.4E-26//90aa//42%//P3660
 C-NT2RP4000975
 C-NT2RP4000979
 25 C-NT2RP4000984
 C-NT2RP4000989//UNC-47 PROTEIN.//0.0000082//173aa//25%//P34579
 C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//838aa//87%//P70700
 C-NT2RP4001004//VACUOLAR PROTEIN 8.//3.7E-16//401aa//26%//P39968
 30 C-NT2RP4001006
 C-NT2RP4001010//Homo sapiens mRNA for KIAA0964 protein, complete cds.//0//2482bp//99%//AB023181
 C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE)//1.5E-92//443aa//44%//Q09996
 C-NT2RP4001057
 35 C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65.//6.7E-51//335aa//37%//Q64375
 C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2*-ATPASE).//1.3E-123//563aa//46%//P13586
 C-NT2RP4001080//Homo sapiens mRNA for Rodi, complete cds.//0//1439bp//99%//AB023967
 C-NT2RP4001086
 40 C-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-)(DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//2.6E-17//121aa//36%//P51400
 C-NT2RP4001100
 C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.9E-115//224aa//100%//P36378
 45 C-NT2RP4001122//TIPD PROTEIN.//1.4E-65//253aa//41%//O15736
 C-NT2RP4001126//TRICHOHYALIN.//2.9E-18//380aa//26%//Q07283
 C-NT2RP4001138
 C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLYASE (EC 3.5.1.18) (SDAP).//0.00000021//93aa//33%//P44514
 50 C-NT2RP4001148//SOF1 PROTEIN.//1.3E-104//236aa//52%//P33750
 C-NT2RP4001149
 C-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//3.4E-29//385aa//29%//P35331
 C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//4.7E-29//227aa//35%//P52178
 55 C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//4.4E-104//1460bp//65%//U95760
 C-NT2RP4001207

- C-NT2RP4001210
C-NT2RP4001219//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.2E-27//90aa//42%/P38660
- 5 C-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//1.8E-103//508aa//43%/Q04652
C-NT2RP4001235
C-NT2RP4001256
C-NT2RP4001260//Homo sapiens mRNA for KIAA0875 protein, partial cds.//0//2876bp//99%/AB020682
C-NT2RP4001274//Human transporter protein (g17) mRNA, complete cds.//4.4E-58//1196bp//61%/U49082
10 C-NT2RP4001276//TRICHOHYALIN.//7.9E-09//126aa//32%/Q07283
C-NT2RP4001313//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT).//5.9E-17//296aa//29%/P24391
C-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//B.5E-213//1129bp//92%/AJ001119
15 C-NT2RP4001339//Homo sapiens mRNA for AMMER1 protein.//9.2E-160//736bp//99%/AJ007014
C-NT2RP4001343
C-NT2RP4001345//Homo sapiens mRNA for LCAT-like lysophospholipase (LLPL), complete cds.//2.7E-310//1400bp//100%/AB017494
C-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//1.4E-58//2425bp//59%/U53445
20 C-NT2RP4001353
C-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN).//1.6E-19//222aa//30%/Q08180
C-NT2RP4001373
C-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).//B.2E-17//146aa//35%/P18160
25 C-NT2RP4001379//HYPOTHETICAL 49.1 KD PROTEIN C11D3.06 IN CHROMOSOME 1.//2E-53//436aa//30%/Q10085
C-NT2RP4001407//Homo sapiens mRNA for KIAA0923 protein, complete cds.//0//2716bp//99%/AB023140
C-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//7.7E-190//422aa//82%/Q14141
30 C-NT2RP4001433//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.2E-138//419aa//54%/Q99676
C-NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//2.7E-66//738bp//71%/AF129131
C-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE).//0//962aa//78%/Q02218
35 C-NT2RP4001498//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//1E-27//374aa//29%/P39010
C-NT2RP4001502
C-NT2RP4001507
C-NT2RP4001524
C-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENIC REGION.//5.7E-54//242aa//3.8%/P25656
40 C-NT2RP4001551//Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit mRNA, complete cds.//0//3202bp//99%/AF152961
C-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//4.7E-09//216aa//24%/P96902
C-NT2RP4001567//ARMADILLO SEGMENT POLARITY PROTEIN.//0.00000054//213aa//26.0%/Q02453
45 C-NT2RP4001568//ZINC FINGER PROTEIN GCS1.//1.8E-10//109aa//36%/P35197
C-NT2RP4001571
C-NT2RP4001574//Homo sapiens coat protein gamma-cop mRNA, complete cds.//0//3046bp//99%/AF100756
C-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//0//1087bp//87%/AJ223830
C-NT2RP4001592//ISOLEUCYL-tRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-tRNA LIGASE) (ILERS).//1.7E-141//373aa//47%/P73505
50 C-NT2RP4001610//Homo sapiens mRNA for KIAA0869 protein, partial cds.//0//1897bp//99%/AB020676
C-NT2RP4001614
C-NT2RP4001634
C-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19.//5.1E-46//234aa//32%/P40469
55 C-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//6.4E-19//111aa//45%/P25323
C-NT2RP4001677
C-NT2RP4001679
C-NT2RP4001696//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF)

- 100 KD SUBUNIT).//4E-10//243aa//25%//Q10568
 C-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//3E-10//128aa//32%//Q10282
 C-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//6.4E-17//1168aa//33%//Q09332
 C-NT2RP4001739
 C-NT2RP4001753//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.9E-236//665aa//58%//P51523
 C-NT2RP4001760//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-CIOGENITAL DYSPLASIA PROTEIN).//4.1E-16//263aa//27%//P98174
 C-NT2RP4001790//Homo sapiens mRNA for KIAA1015 protein, complete cds.//0//3144bp//99%//AB023232
 C-NT2RP4001803
 C-NT2RP4001822//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//241aa//30%//O35566
 C-NT2RP4001823//MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.//1.1E-19//77aa//54%//P55083
 C-NT2RP4001828
 C-NT2RP4001838//Homo sapiens CoREST protein (COREST) mRNA, complete cds.//6.3E-99//555bp//73%//AF155595
 C-NT2RP4001861//TRICHOHYALEN.//1E-35//307aa//34%//P37709
 C-NT2RP4001893//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp5640043).//0//1306bp//98%//AL050390
 C-NT2RP4001896//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E1.//0.00000014//345aa//25%//Q00808
 C-NT2RP4001901
 C-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.3E-38//258aa//32%//Q12024
 C-NT2RP400193 8//TRANSCRIPTIONAL REPRESSOR CTCF.//9.8E-60//303aa//38%//P49711
 C-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISO-ASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE).//1.5E-13//211aa//28%//Q43209
 C-NT2RP4001950//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//1.2E-13//356aa//27%//P13816
 C-NT2RP4001953
 C-NT2RP4001966
 C-NT2RP4001975
 C-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//6.9E-24//370aa//27%//Q04652
 C-NT2RP4002052
 C-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13).//1E-137//679aa//40%//Q43143
 C-NT2RP4002071
 C-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3E-150//722aa//39%//Q05481
 C-NT2RP4002081//TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA CHAINS (TFIIA P35 AND P19 SUBUNITS) (TFIIA-42) (TFIIAL).//0.0000067//250aa//31%//P52655
 C-NT2RP4002298
 C-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.5E-63//159aa//53%//P38938
 C-NT2RP4002791
 C-NT2RP4002888//Homo sapiens mRNA; cDNA DKFZp434F172 (from clone DKFZp434F172).//0//2557bp//99%//AL080202
 C-NT2RP4002905
 C-NT2RP5003461//RLR1 PROTEIN.//9.7E-22//177aa//27%//P53552
 C-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.5E-15//280aa//27%//Q00808
 C-NT2RP5003492
 C-NT2RP5003500
 C-NT2RP5003506
 C-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//3.3E-23//219aa//40%//P37116
 C-NT2RP5003524
 C-NT2RP5003534
 C-OVARC1000006//HISTONE H2A.1.//1.1E-55//117aa//99%//P02262
 C-OVARC1000013//APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1).//0.0000042//102aa//32%//

O14727
 C-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//2.6E-295//1393bp//97%//AF058922
 C-OVARC1000035
 C-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE).//
 5 0.0000032//60aa//45 %//P80022
 C-OVARC1000087//HISTONE MACRO-H2A.1.//1.6E-12//174aa//26%//Q02874
 C-OVARC1000091//HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1) (VCAF) (CFF).//
 8.4E-14//259aa//30%//P51610
 C-OVARC1000113
 10 C-OVARC1000139//Homo sapiens CGI-21 protein mRNA, complete cds.//0//1562bp//99%//AF132955
 C-OVARC1000148
 C-OVARC1000151//Homo sapiens partial mRNA for putative protein p38 interacting with transcription factor Sp.1//
 2.5E-95//461bp//98%//AJ242975
 C-OVARC1000168
 15 C-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//1.8E-32//511bp//65%//
 AF068332
 C-OVARC1000212
 C-OVARC1000241//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN)
 (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//8.2E-120//351aa//54%//Q16665
 20 C-OVARC1000288//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)(LEU-
 CINE AMINOPEPTIDASE IV) (LAPIV) (AMINOPEPTIDASE III)(AMINOPEPTIDASE YSCI).//5.4E-53//384aa//
 30%//P14904
 C-OVARC1000304//PROTEIN MOV-10.//1.1E-249//519aa//87%//P23249
 C-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//2.7E-40//154aa//38%//P29363
 25 C-OVARC1000321
 C-OVARC1000326
 C-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//5.9E-14//
 200aa//27%//P40004
 C-OVARC1000347
 30 C-OVARC1000384
 C-OVARC1000411
 C-OVARC1000420
 C-OVARC1000437//TENSIN.//7.9E-181//340aa//84%//Q04205
 C-OVARC1000443//Homo sapiens mRNA; cDNA DKFZp434A073 (from clone DKFZp434A073).//0//1216bp//
 35 99%//AL080126
 C-OVARC1000461
 C-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//1.2E-25//227aa//25%//P11075
 C-OVARC1000466
 C-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPE-
 40 CIFICITY PROTEIN PHOSPHATASE VHR).//3.1E-10//125aa//35%//P51452
 C-OVARC1000479//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//1919bp//99%//AB020636
 C-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.2E-157//892bp//91 %//AF051850
 C-OVARC1000564
 C-OVARC1000576
 45 C-OVARC1000588
 C-OVARC1000605
 C-OVARC1000640
 C-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, com-
 plete cds.//0//1812bp//98%//D43772
 50 C-OVARC1000661
 C-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.1E-46//121aa//79%//P08866
 C-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//1.2E-17//127aa//33%//Q58343
 C-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//1.5E-178//1113bp//86%//AF001533
 C-OVARC1001038//Homo sapiens mRNA for Ariadne-2 protein.//0//1172bp//97%//AJ130978
 55 C-OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.//1E-215//1027bp//98%//AF132946
 C-OVARC1001162
 C-OVARC1001243
 C-OVARC1001296

C-OVARC1001360
 C-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL //6E-148//683bp//
 99%//AJ224819
 C-OVARC1001425
 5 C-PLACE1000005
 C-PLACE1000066//SSU72 PROTEIN //1.1E-39//206aa//43%//P53538
 C-PLACE1000142//3-HYDROXYBUTYRYL-COA DEHYDRATASE (EC 4.2.1.55) (CROTONASE) //2.8E-29//
 134aa//43%//P52046
 10 C-PLACE1000184//Homo sapiens mRNA for KIAA0832 protein, complete cds. //5.5E-312//1411bp//99%//
 AB020639
 C-PLACE1000185
 C-PLACE1000213//Homo sapiens mRNA for KIAA0977 protein, complete cds. //0//1904bp//99%//AB023194
 C-PLACE1000347
 C-PLACE1000374
 15 C-PLACE1000380//Homo sapiens mRNA for KIAA0853 protein, partial cds. //0//2208bp//99%//AB020660
 C-PLACE1000383//Homo sapiens mRNA for MTMR1 protein. //0//753bp//99%//AJ224979
 C-PLACE1000401//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN) //2.7E-30//352aa//31%//
 P15151
 C-PLACE1000406//PTB-ASSOCIATED SPLICING FACTOR (PSF) //1.1E-132//334aa//72%//P23246
 20 C-PLACE1000420//7.8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE) //
 0.000028//134aa//29%//P53368
 C-PLACE1000435
 C-PLACE1000444
 C-PLACE1000562
 25 C-PLACE1000564
 C-PLACE1000580//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-
 BINDING PROTEIN 1) //1.6E-270//437aa//86%//P32455
 C-PLACE1000596//Homo sapiens mRNA for KIAA0850 protein, complete cds. //0//2393bp//99%//AB020657
 C-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds. //2E-55//779bp//67%//
 30 AF044201
 C-PLACE1000636//MALE STERILITY PROTEIN 2 //1.2E-39//261aa//27%//Q08891
 C-PLACE1000716
 C-PLACE1000748
 C-PLACE1000755//Homo sapiens mRNA for Helicase-MOI, complete-cds. //4.6E-250//1189bp//97%//AB028449
 35 C-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds. //0//2002bp//99%//AB014548
 C-PLACE1000798
 C-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN
 YHR148W //2.5E-49//181aa//54%//P32899
 40 C-PLACE1000909//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1 //2.6E-19//404aa//26%//P39010
 C-PLACE1000948
 C-PLACE1000972
 C-PLACE1000977//BETA-CHIMAERIN (BETA-CHIMERIN) //4.4E-22//129aa//35%//Q03070
 C-PLACE1001000
 C-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds. //0//1500bp//99%//AF065485
 45 C-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN) //4.3E-54//257aa//46%//Q04652
 C-PLACE1001383//ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQ-
 UIEM) //3E-33//138aa//42%//Q61103
 C-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 //2.3E-61//
 132aa//46%//Q12929
 50 C-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22_N_12, complete sequence. //0//2118bp//
 99%//AC005412
 C-PLACE1001412
 C-PLACE1001484//Homo sapiens chromosome 20 clone 387E22, WORKING DRAFT SEQUENCE, in unordered
 pieces. //0//1440bp//99%//AL031660
 55 C-PLACE1001503
 C-PLACE1001570
 C-PLACE1001610
 C-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14)

(THIOESTERASE n).//4E-81//263aa//56%//P08635
 C-PLACE1001729
 C-PLACE1001739//PUTATIVE ATP-DEPENDENT RNA HEUCASE PL10.//3.5E-75//439aa//41%//P16381
 C-PLACE1001781//PROBABLE PHOSPHOMANNOMUTASE (EC 5.4.2.8) (PMM).//5.4E-63//427aa//35%//Q57290
 C-PLACE1001810
 C-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//0//1995bp//99%//AF058953
 C-PLACE1001869//L-RIBULOKINASE (EC 2.7.1.16).//2E-27//270aa//31%//P94524
 C-PLACE1001912//Homo sapiens clone 24963 mRNA sequence, complete cds.//0//1196bp//99%//AF131737
 C-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1729bp//99%//AF099935
 C-PLACE1001928
 C-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//1.4E-78//496aa//37%//Q49091
 C-PLACE1002046//LIGATIN (FRAGMENT).//1.7E-240//560aa//80%//Q61211
 C-PLACE1002072
 C-PLACE1002073//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE).//0.0000053//188aa//29%//P49606
 C-PLACE1002140
 C-PLACE1002163
 C-PLACE1002170
 C-PLACE1002433
 C-PLACE1002438//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//0.0000042//133aa//29%//Q13105
 C-PLACE1002465
 C-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//6.7E-214//956bp//94%//AB018256
 C-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//0//1750bp//99%//AF068180
 C-PLACE1002722//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//9E-45//305aa//33%//Q15391
 C-PLACE1002794
 C-PLACE1002815
 C-PLACE1002839
 C-PLACE1002851
 C-PLACE1002941
 C-PLACE1002996
 C-PLACE1003045
 C-PLACE1003092
 C-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//2.6E-79//253aa//60%//Q13268
 C-PLACE1003108
 C-PLACE1003145
 C-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//3.8E-37//143aa//51%//P42743
 C-PLACE1003190//SOF1 PROTEIN.//1.9E-110//325aa//48%//P33750
 C-PLACE1003200
 C-PLACE1003296//Homo sapiens mRNA; cDNA DKFZp434G173 (from clone DKFZp434G173).//0//1706bp//99%//AL080133
 C-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//6.9E-206//396aa//86%//P51522
 C-PLACE1003334
 C-PLACE1003342
 C-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//0//2435bp//99%//U92715
 C-PLACE1003369
 C-PLACE1003602//Homo sapiens mRNA expressed in placenta.//5.9E-278//1275bp//99%//D83200
 C-PLACE1003611
 C-PLACE1003625//ARMADILLO SEGMENT POLARITY PROTEIN.//3.2E-10//380aa//25%//P18824
 C-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//8E-19//208aa//34%//Q08170
 C-PLACE1003711
 C-PLACE1003723

- C-PLACE1003762
C-PLACE1003771
C-PLACE1003784
C-PLACE1003923
5 C-PLACE1003936
C-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN).//
2.4E-124//326aa//73%//P80385
C-PLACE1004104
C-PLACE1004114
10 C-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA
CHAIN 4).//6.1E-181//340aa//96%//P29387
C-PLACE1004149
C-PLACE1004156
C-PLACE1004161
15 C-PLACE1004183//Homo sapiens for TOM1-like protein.//0//1279bp//97%//AJ010071
C-PLACE1004197//BUTYROPOLIN PRECURSOR (BT).//4.5E-10//208aa//27%//Q62556
C-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.//
0//1882bp//99%//AF069493
C-PLACE1004258
20 C-PLACE1004270//TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21.-).//9.7E-36//389aa//31%//O15393
C-PLACE1004277//Homo sapiens two pore domain K⁺ channel (TASK-2) mRNA, complete cds.//0//1498bp//99%//
AF084830
C-PLACE1004289
C-PLACE1004302//SOF1 PROTEIN.//1.9E-110//325aa//48%//P33750
25 C-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//0//1767bp//99%//Y11588
C-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//0//
2512bp//99%//AF100153
C-PLACE1004376
C-PLACE1004388
30 C-PLACE1004405
C-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-).//1.2E-39//385aa//33%//Q63448
C-PLACE1004437//Human NAD⁺-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene
encoding mitochondrial protein, complete cds.//0//985bp//99%//U49283
C-PLACE1004451
35 C-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0000002//218aa//23%//P25823
C-PLACE1004473
C-PLACE1004510//Homo sapiens cofactor of initiator function (Cif150) mRNA, complete//1.3E-209//954bp//
99%//AF026445
C-PLACE1004516
40 C-PLACE1004548
C-PLACE1004564//CLEFTAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100
KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//525aa//99%//Q10568
C-PLACE1004629//PROTEIN OS-9 PRECURSOR.//7.7E-18//264aa//32%//Q13438
C-PLACE1004645
45 C-PLACE1004646//B.taurus mRNA for retinal pigment epithelial membrane receptor p63.//4.4E-42//985bp//59%//
X66277
C-PLACE1004664
C-PLACE1004672
C-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//1.6E-95//191aa//
96%//P12815
50 C-PLACE1004691
C-PLACE1004722
C-PLACE1004736
C-PLACE1004740
55 C-PLACE1004743//PROBABLE N-END-RECOGNIZING PROTEIN (UBIQUITIN-PROTEIN LIGASE E3 COMPO-
NENT) (N-RECOGNIN).//4.4E-35//578aa//27%//O60152
C-PLACE1004751//Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds.//7.1E-224//
790bp//98%//AB022918

- C-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//1.9E-32//259aa//32%/P30337
- C-PLACE1004804//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE).//4.7E-65//695aa//29%/Q01631
- 5 C-PLACE1004814//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//5.9E-19//196aa//36%/Q08170
- C-PLACE1004824
- C-PLACE1004868//MALE STERILITY PROTEIN 2.//3.9E-39//261aa//27%/Q08891
- C-PLACE1004885
- 10 C-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//9.3E-11//94aa//47%/O42643
- C-PLACE1004918//L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDHA).//4.9E-48//198aa//44%/P06151
- C-PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//1853bp//98%/AF099936
- 15 C-PLACE1004934
- C-PLACE1004937//SEL-10 PROTEIN.//6.3E-125//357aa//58%/Q93794
- C-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//2E-14//205aa//26%/Q11073
- C-PLACE1004982
- 20 C-PLACE1005026
- C-PLACE1005027
- C-PLACE1005046
- C-PLACE1005077
- C-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds.//1E-209//1031bp//96%/L40401
- 25 C-PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).//2.6E-56//565aa//30%/Q04652
- C-PLACE1005111
- C-PLACE1005181
- C-PLACE1005187//APAG PROTEIN.//3.8E-13//122aa//36%/P05636
- C-PLACE1005206
- 30 C-PLACE1005232
- C-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E-27//349aa//32%/Q01577
- C-PLACE1005261
- C-PLACE1005266
- C-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds.//3.2E-297//1341bp//100%/AB011182
- 35 C-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.3E-13//269aa//28%/P53352
- C-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//226aa//92%/P08760
- C-PLACE1005308
- C-PLACE1005313
- 40 C-PLACE1005327
- C-PLACE1005335
- C-PLACE1005373//TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//8.6E-09//194aa//27%/O33335
- 45 C-PLACE1005374
- C-PLACE1005480
- C-PLACE1005481
- C-PLACE1005494//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//1649bp//99%/AJ006276
- 50 C-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//5.6E-52//173aa//57%/Q09251
- C-PLACE1005550
- C-PLACE1005554
- C-PLACE1005623
- 55 C-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//0//2130bp//99%/AF083255
- C-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE).//2.1E-148//321aa//83%/P31350

- C-PLACE1005730
C-PLACE1005755
C-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//2.5E-79//209aa//53%//P08635
- 5 C-PLACE1005803
C-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.1E-217//994bp//99%//AF027156
C-PLACE1005851
C-PLACE1005921//AIG1 PROTEIN.//3E-31//284aa//31%//P54120
- 10 C-PLACE1005923
C-PLACE1005925
C-PLACE1005934
C-PLACE1005936
C-PLACE1005951
- 15 C-PLACE1005953//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//6.7E-30//198aa//37%//P43636
C-PLACE1005955//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)//5.4E-54//455aa//32%//P14904
C-PLACE1005966//TRANSCRIPTION INITIATION FACTOR TFIIID 90 KD SUBUNIT (TAFII-90).//0.00000014//254aa//25%//P38129
- 20 C-PLACE1005990
C-PLACE1006011//Homo sapiens mRNA for poly(ADP-ribose) polymerase-2.//0//1564bp//99%//AJ236876
C-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.7E-16//1744bp//99%//X99906
C-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.5E-148//681bp//99%//AF039023
- 25 C-PLACE1006139
C-PLACE1006159
C-PLACE1006167
C-PLACE1006170//Homo sapiens mRNA for KIAA0899 protein, partial cds.//4.5E-293//953bp//99%//AB020706
C-PLACE1006195
- 30 C-PLACE1006198//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//2.7E-116//496aa//48%//Q09747
C-PLACE1006225
C-PLACE1006236
C-PLACE1006239//BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).//2E-16//244aa//31%//P28675
- 35 C-PLACE1006246
C-PLACE1006325//Homo sapiens mRNA; cDNA DKFZp564J142 (from clone DKFZp564J142).//3.8E-278//1271-bp//99%//AL080066
C-PLACE1006335
C-PLACE1006357
- 40 C-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//0//1168bp//99%//AF062085
C-PLACE1006412
C-PLACE1006414
C-PLACE1006438//ZINC FINGER PROTEIN 165.//2.5E-45//122aa//43%//P49910
- 45 C-PLACE1006445
C-PLACE1006470
C-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//7.7E-55//142aa//85%//Q90595
C-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.1E-229//367aa//96%//Q00004
- 50 C-PLACE1006492
C-PLACE1006531
C-PLACE1006552
C-PLACE1006598//Homo sapiens clone NH0310K15, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0//2182bp//99%//AC007383
- 55 C-PLACE1006615
C-PLACE1006626//Homo sapiens mRNA for KIAA0928 protein, partial cds.//0//1760bp//99%//AB023145
C-PLACE1006673
C-PLACE1006678//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.8E-24//734bp//62%//AB015630

- C-PLACE1006704
 C-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//6.9E-13//177aa//33%/Q59263
 C-PLACE1006782
 5 C-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.8E-213//232aa//80%/P08547
 C-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN).//2E-15//188aa//29%/P35123
 10 C-PLACE1006883
 C-PLACE1006901
 C-PLACE1006917//HSH49 PROTEIN.//5.5E-12//97aa//35%/Q99181
 C-PLACE1006932
 C-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III.//6.7E-48//278aa//41%/Q10000
 15 C-PLACE1006956//ATP-DEPENDENT PERMEASE MDL1.//1.3E-86//522aa//36%/P97998
 C-PLACE1006958//Homo sapiens mRNA for heat shock protein apg-1, complete cds.//0//1770bp//99%/AB023421
 C-PLACE1006961
 C-PLACE1006962
 20 C-PLACE1006966
 C-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12) (DER12).//3.2E-35//180aa//33%/Q14542
 C-PLACE1007021
 C-PLACE1007105
 25 C-PLACE1007178
 C-PLACE1007226//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.-) (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1E-42//370aa//31%/P54304
 C-PLACE1007238
 C-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//6.5E-216//1068bp//96%/D50495
 30 C-PLACE1007242
 C-PLACE1007243//UNC-47 PROTEIN.//0.00000017//211aa//27%/P34579
 C-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//0//2052bp//99%/Y15908
 C-PLACE1007274
 35 C-PLACE1007282
 C-PLACE1007301
 C-PLACE1007317//Drosophila melanogaster Adrift (adrift) mRNA, complete cds.//4.1E-17//1037bp//56%/AF117649
 C-PLACE1007342
 40 C-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//0//2366bp//99%/AF096870
 C-PLACE1007367
 C-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13.//0.00000044//127aa//30%/P27715
 45 C-PLACE1007386
 C-PLACE1007402
 C-PLACE1007409//WHITE PROTEIN.//1.1E-64//428aa//32%/Q17320
 C-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP).//8.8E-25//140aa//35%/P27487
 50 C-PLACE1007450
 C-PLACE1007452
 C-PLACE1007460
 C-PLACE1007484
 C-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//5.4E-53//426aa//33%/P52734
 55 C-PLACE1007507
 C-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19).//1.4E-85//385aa//45%/P08728

- C-PLACE1007524
 C-PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds.//8.9e-316//1485bp//98%//AF159164
 C-PLACE1007544
 5 C-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1E-49//361aa//36%//P34537
 C-PLACE1007583
 C-PLACE1007598//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.6E-143//666aa//44%//Q99676
 10 C-PLACE1007618//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0.1713bp//99%//AB023194
 C-PLACE1007621
 C-PLACE1007632//POLIOVIRUS RECEPTOR PRECURSOR.//0.0000001//228aa//31%//P32506
 C-PLACE1007645
 C-PLACE1007649//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0.1952-bp//99%//AB023194
 15 C-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//8.7E-09//279aa//28%//Q26457
 C-PLACE1007690
 C-PLACE1007697//GCN20 PROTEIN.//7.6E-119//171aa//38%//P43535
 C-PLACE1007705//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0.3431bp//99%//AF061243
 C-PLACE1007725
 20 C-PLACE1007729//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.5E-44//231aa//42%//P10265
 C-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//9.2E-294//1504bp//94%//AB014585
 C-PLACE1007746
 C-PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds.//0.1836bp//99%//AB019602
 25 C-PLACE1007810
 C-PLACE1007843
 C-PLACE1007846//Homo sapiens genomic DNA of 21q22.2 Down Syndrome region, segment 3/13.//0.1751bp//99%//AP000010
 C-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//0.3112bp//99%//AB018309
 30 C-PLACE1007897
 C-PLACE1007946//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//2.6E-14//370aa//25%//Q99323
 C-PLACE1007954
 C-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//0.12252bp//99%//AF084530
 35 C-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//0.12300bp//99%//AF079529
 C-PLACE1007969//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.1E-36//202aa//48%//P52272
 40 C-PLACE1007990
 C-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSIN-110) (SYNAPTIC DENSITY PROTEIN PSD-93).//6.1E-14//128aa//39%//Q63622
 C-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.1833bp//99%//AC005628
 45 C-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NUCLEOPORIN) (P105).//4.6E-318//613aa//94%//P52590
 C-PLACE1008095
 C-PLACE1008122
 C-PLACE1008129
 50 C-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//1.3E-24//395aa//31%//Q09531
 C-PLACE1008177//TRICHOHYALIN.//2.3E-29//487aa//26%//P37709
 C-PLACE1008209
 C-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.3E-283//671aa//77%//P53620
 55 C-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-).//2.3E-18//162aa//37%//P12689
 C-PLACE1008280
 C-PLACE1008309

- C-PLACE1008329
 C-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds.//0//1853bp//100%//AB014579
 C-PLACE1008398//GENE 33 POLYPEPTIDE.//7.3E-114//243aa//87%//P05432
 C-PLACE1008401
 5 C-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED PROTEIN) (TAP).//0//698aa//95%//P41541
 C-PLACE1008429//ANKYRIN HOMOLOG PRECURSOR.//3.1E-11//189aa//32%//Q06527
 C-PLACE1008457
 C-PLACE1008465
 10 C-PLACE1008488
 C-PLACE1008524//Human DNA sequence from clone 34B21 on chromosome 6p12.1-21.1. Contains part of a gene for a novel protein with ZU5 domain similar to part of Tight Junction Protein ZO1 (TJP1) and UNC5 Homologs, the gene for a novel BZRP (peripheral benzodiazepine receptor).//0//1980bp//99%//AL031778
 C-PLACE1008531
 15 C-PLACE1008532
 C-PLACE1008533//101 KD MALARIA ANTIGEN (P101) (ACIDIC BASIC REPEAT ANTIGEN).//1.1E-09//62aa//48%//P22620
 C-PLACE1008568
 C-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//7.8E-236//453aa//96%//P37199
 20 C-PLACE1008621
 C-PLACE1008626
 C-PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.//0//1850bp//99%//AJ006591
 C-PLACE1008629
 25 C-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//0//1548bp//100%//AF044333
 C-PLACE1008693
 C-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//0//3002bp//99%//AF038406
 30 C-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBUNIT) (IMPORTIN ALPHA S2).//3.1E-280//533aa//98%//O35345
 C-PLACE1008808//Homo sapiens mRNA for cell cycle checkpoint protein rad1A.//2.3E-269//1225bp//99%//AJ004974
 C-PLACE1008813
 35 C-PLACE1008854
 C-PLACE1008867
 C-PLACE1008887
 C-PLACE1008902
 C-PLACE1008925
 40 C-PLACE1009020//NIFS PROTEIN.//3.9E-55//279aa//41%//P12623
 C-PLACE1009027//Homo sapiens mRNA for doublecortin.//0//1919bp//99%//AJ003112
 C-PLACE1009045
 C-PLACE1009060//BRO1 PROTEIN.//6.7E-19//567aa//24%//P48582
 C-PLACE1009090
 45 C-PLACE1009091
 C-PLACE1009094//FURIN-LIKE PROTEASE 2 PRECURSOR (EC 3.4.21.75) (FURIN 2).//1.9E-44//480aa//30%//P30432
 C-PLACE1009099//ZINC FINGER PROTEIN 41 (FRAGMENT).//1.1E-179//452aa//67%//P51814
 C-PLACE1009110
 50 C-PLACE1009111
 C-PLACE1009130//UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.2.-) (ONCOGENIC PROTEIN-ASSOCIATED PROTEIN E6-AP).//2E-68//181aa//43%//Q05086
 C-PLACE1009158
 C-PLACE1009166
 55 C-PLACE1009174
 C-PLACE1009186
 C-PLACE1009190
 C-PLACE1009230

- C-PLACE1009319//Rattus norvegicus outer membrane protein (OMP25) mRNA, complete cds; nuclear gene for mitochondrial product.//2.1E-132//1229bp//75%//AF107295
- C-PLACE1009328
- C-PLACE1009335
- 5 C-PLACE1009338
- C-PLACE1009368//METAL HOMEOSTASIS FACTOR ATX2.//2.5E-10//151aa//29%//Q12067
- C-PLACE1009375
- C-PLACE1009388
- 10 C-PLACE1009404//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I.//0.000000047//165aa//73%//Q09820
- C-PLACE1009434
- C-PLACE1009443
- C-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//7.8E-71//82aa//89%//P42356
- 15 C-PLACE1009459
- C-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.1E-289//550aa//93%//P54319
- C-PLACE1009476//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//3.9E-40//179aa//37%//P34580
- 20 C-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FACTOR).//8.1E-99//228aa//75%//Q99418
- C-PLACE1009542
- C-PLACE1009571
- C-PLACE1009581
- C-PLACE1009596//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//5.1E-54//291aa//40%//Q00808
- 25 C-PLACE1009607
- C-PLACE1009621
- C-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.3E-60//209aa//41%//P25159
- C-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAPI PROTEIN).//1.5E-285//538aa//99%//P55161
- 30 C-PLACE1009665
- C-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//0//1854bp//100%//AF062534
- C-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN CHROMOSOME I.//7E-33//166aa//43%//Q09876
- C-PLACE1009721//MSF1 PROTEIN.//1.7E-22//176aa//33%//P35200
- 35 C-PLACE1009731//AIG1 PROTEIN.//1.6E-22//274aa//28%//P54120
- C-PLACE1009763//Homo sapiens mRNA for Nedd8-activating enzyme hUba3, complete cds.//4.3E-294//1329bp//100%//AB012190
- C-PLACE1009794
- 40 C-PLACE1009845//Homo sapiens mRNA for KIAA0905 protein, complete cds.//0//2685bp//99%//AB020712
- C-PLACE1009886
- C-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC REGION.//1.9E-108//277aa//43%//P53145
- C-PLACE1009971
- 45 C-PLACE1009992//LIMULUS CLOTTING FACTOR C PRECURSOR (EC 3.4.21.84).//4.6E-59//450aa//34%//P28175
- C-PLACE1009995//Homo sapiens mRNA; cDNA DKFp5640123 (from clone DKFp5640123).//0//1962bp//99%//AL080122
- C-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds.//5.2E-70//736bp//73%//U48288
- 50 C-PLACE1010023
- C-PLACE1010031
- C-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//6E-279//1402bp//94%//X84692
- C-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2019bp//99%//AF065482
- C-PLACE1010076
- 55 C-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.4E-268//506aa//98%//Q62671
- C-PLACE1010102
- C-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//7.3E-114//537aa//44%//O04652
- C-PLACE1010106//Homo sapiens mRNA; cDNA DKFp586M1418 (from clone DKFp586M1418).//0//1974bp//

99%//AL049385
 C-PLACE1010134//TRANSCRIPTION REGULATORY PROTEIN SNF2 (SWI/SNF COMPLEX COMPONENT SNF2) (REGULATORY PROTEIN SWI2) (REGULATORY PROTEIN GAM1) (TRANSCRIPTION FACTOR TYE3).//1.7E-20//156aa//42%//P22082

5 C-PLACE1010148//CYCLIN I (MULTIPLE-BAND POLYPEPTIDE I).//0.00000046//431aa//23%//P35662
 C-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//9.8E-11//95aa//49%//Q01130
 C-PLACE1010202

10 C-PLACE1010261//SEGREGATION DISTORTER PROTEIN.//1.6E-77//214aa//62%//P25722
 C-PLACE1010274//Homo sapiens mRNA; cDNA DKFpZp5640123 (from clone DKFpZp5640123).//0//1964bp//99%//AL080122
 C-PLACE1010293
 C-PLACE1010321//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//1.1E-09//350aa//22%//P52178

15 C-PLACE1010324
 C-PLACE1010329
 C-PLACE1010362//1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE PRECURSOR (EC 3.1.4.10) (PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC).//0.000000002//126aa//29%//P34024
 C-PLACE1010364
 C-PLACE1010383

20 C-PLACE1010481//Homo sapiens mRNA for KIAA0836 protein, partial cds.//0//212bp//99%//AB020643
 C-PLACE1010491
 C-PLACE1010492
 C-PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induced by progesterone), complete cds.//0//1981bp//99%//AB022718
 C-PLACE1010529
 C-PLACE1010547//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.00000012//616aa//24%//P253_86
 C-PLACE1010599//Homo sapiens Pex14 mRNA for peroxisomal membrane anchor protein, complete cds.//0//1904bp//99%//AB017546

30 C-PLACE1010616
 C-PLACE1010622//TROPONIN T, CARDIAC MUSCLE ISOFORMS (TNTC).//0.00000016//120aa//28%//P02642
 C-PLACE1010629
 C-PLACE1010630
 C-PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS13.//5.7E-75//423aa//39%//Q01755
 C-PLACE1010714
 C-PLACE1010720//Homo sapiens mRNA for chromosome-associated polypeptide-C, complete cds.//4E-299//1091bp//99%//AB019987

40 C-PLACE1010743//Homo sapiens myosin-IXb splice variant (Myo9b) mRNA, partial cds.//8.9E-91//668bp//82%//AF020267
 C-PLACE1010771//M.musculus HCNGP mRNA.//7.4E-168//966bp//89%//X68061
 C-PLACE1010786
 C-PLACE1010800
 C-PLACE1010811

45 C-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.3E-143//407aa//58%//Q05481
 C-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//0//1885bp//99%//AB011182
 C-PLACE1010900
 C-PLACE2000050
 C-PLACE4000522//NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (XOTCH PROTEIN)-//2.4E-191//828aa//48%//P21783

50 C-PLACE4000590
 C-PLACE4000638
 C-PLACE4000650//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).//7.9E-17//201aa//34%//P49816

55 C-Y79AA1001647

Homology Search Result Data 7.

[0315] The result of the homology search of the SwissProt using the 5'-end sequence (54 clones selected in EXAM-
 PLE 16).

[0316] Data include

the name of clone,
 definition of the top hit data,
 the P-value: the length of the compared sequence: identity (%), and
 the organism and the Accession No. of the top hit data, as in the order separated by //.

[0317] Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000497//METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G)//0.13//52//38//P25860
 F-HEMBA1001750//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THI-
 OLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME
 64E)//2.2e-28//104//59//Q24574
 F-HEMBA1003854//VERPROLIN//0.012//138//31//P37370
 F-HEMBA1004193//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3) (FRAGMENT)//0.93//39//
 33//Q37131
 F-HEMBA1004600//HIGH POTENTIAL IRON-SULFUR PROTEIN, ISOZYME 2 (HIPIP 2)//0.90//20//50//P38524
 F-HEMBA1005572//ZINC FINGER PROTEIN 124 (HZF-16)//7.6e-46//141//58//Q15973
 F-HEMBA1006038//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENT)//0.0033//32//46//P70560
 F-HEMBA1006092//VERPROLIN//1.0//62//35//P37370
 F-HEMBA1006406//MATING PHEROMONE ER-10 PRECURSOR (EUPLOMONE R10)//0.30//41//36//P12350
 F-HEMBA1006650//MATING-TYPE PHEROMONE BAP1(2) PRECURSOR//0.089//21//52//Q02593
 F-HEMBA1006812//HEAT SHOCK PROTEIN HTGA (HEAT SHOCK PROTEIN HTPY)//0.38//156//30//P28697
 F-HEMBA1006672
 F-HEMBA1001197//DNA-BINDING PROTEIN 65 (PROTEIN GP65)//1.0//30//36//P16012
 F-HEMBA1001871//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S1)//3.7e-54//
 241//47//P47853
 F-MAMMA1001252//HYPOTHETICAL 9.1 KD PROTEIN IN NIRQ 3'REGION (ORF3)//0.59//48//39//Q51483
 F-MAMMA1002094
 F-NT2RM4000634//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11)//0.26//58//27//P06333
 F-NT2RM4000657//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC
 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT)//8.9e-20//83//48//P10895
 F-NT2RM4000783//ZINC FINGER PROTEIN (FRAGMENT)//1.0//42//40//P19326
 F-NT2RM4000857//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN
 PRECURSOR (ALS)//6.0e-23//207//32//Q02833
 F-NT2RM4001178//HOMEBOX PROTEIN OTX3 (ZOTX3)//0.012//156//28//Q90267
 F-NT2RM4002420//GLUTAMIC ACID-RICH PROTEIN PRECURSOR//0.0012//81//37//P13816
 F-NT2RP2000198//CREB-BINDING PROTEIN//0.29//98//37//Q92793
 F-NT2RP2000551//PROTEIN Q300//0.00017//23//60//Q02722
 F-NT2RP2000680//HYPOTHETICAL PROTEIN MJ0401//1.0//41//29//Q57844
 F-NT2RP2001214//MALE SPECIFIC SPERM PROTEIN MST84DC//0.27//13//61//Q01644
 F-NT2RP2001460//PROTEIN KINASE C-LIKE (EC 2.7.1.-)//0.089//99//29//Q99014
 F-NT2RP2001756//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT)//4.0e-13//177//
 28//P16372
 F-NT2RP2002056//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5'REGION//0.37//12//75//P53820
 F-NT2RP2002677//NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)//0.99//61//32//Q42616
 F-NT2RP2002755//OCTAPEPTIDE-REPEAT PROTEIN T2//1.3e-10//90//35//Q06666
 F-NT2RP2002843//CYTOCHROME B//0.78//103//26//P48884
 F-NT2RP2003101//ATPASE INHIBITOR, MITOCHONDRIAL HOMOLOG//0.40//28//46//P37209
 F-NT2RP2003799//HYPOTHETICAL PROTEIN MJ0116.1//0.80//55//32//P81303
 F-NT2RP2004095
 F-NT2RP2004732
 F-NT2RP2004920//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE//0.18//18//55//Q48251
 F-NT2RP2005454

F-NT2RP2005776//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE) (FRAGMENT)//17.4e-38//136//41//P51003

F-NT2RP2005806//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR//14.0e-08//180//28//P32323

F-NT2RP2005882

F-NT2RP3001282//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB//0.0022//69//39//P39217

F-NT2RP3001723//TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3)//0.00035//127//31//P15276

F-NT2RP3002099//NONHISTONE CHROMOSOMAL PROTEIN HMG-17//0.97//71//28//P05204

F-NT2RP3003155//CCAAT DISPLACEMENT PROTEIN (HOMEOBOX PROTEIN CLOX) (CLOX-1) (FRAGMENT)//0.064//110//34//P39881

F-NT2RP3004028//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT)//0.020//95//29//P15583

F-OVARC1000008//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//2.8e-05//165//29//P17437

F-OVARC1000724//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT)//0.035//152//30//P10162

F-OVARC1000751//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (VMW118 PROTEIN)//0.38//124//31//P28284

F-OVARC1001029

F-PLACE1000814//EC PROTEIN HOMOLOG 2 (FRAGMENT)//0.45//61//24//Q42377

F-PLACE1003030//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29)//0.70//121//32//P47845

F-PLACE1005549//RHO1 GDP-GTP EXCHANGE PROTEIN 1 (PROTEIN KINASE C SUPPRESSOR SKC1)//3.2e-08//205//24//P53046

F-PLACE1007218//IG KAPPA CHAIN V-III REGION (PC 7210)//0.99//52//38//P01668

Homology Search Result Data 8.

[0318] The result of the homology search of the GenBank using the clone sequence of 5'-end (54 clones selected in EXAMPLE 16.) except EST and STS.

[0319] Data include

the name of clone,

definition of the top hit data,

the P-value: the length of the compared sequence: identity (%), and

the Accession No. of the top hit data, as in the order separated by //.

[0320] Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000497

F-HEMBA1001750//Human mitochondrial genes for several tRNAs (Phe, Val, Leu) and 12S and 16S ribosomal RNAs//6.6e-101//473//99//V00710

F-HEMBA1003854//Homo sapiens clone RG270D13, *** SEQUENCING IN PROGRESS ***, 18 unordered pieces//1.7e-05//412//61//AC005081

F-HEMBA1004193//Human BAC clone RG343H22 from 7q31, complete sequence//0.77//466//59//AC002386

F-HEMBA1004860//Human pigment epithelium-derived factor gene, complete cds.//6.7e-07//492//57//U29953

F-HEMBA1005572//HZF-16=Kruppel-related zinc finger gene homolog [alternatively spliced] [human, hepatoblastoma cell line, HEP-G2, mRNA, 2080 nt]//2.9e-47//341//77//S54641

F-HEMBA1006038//Human DNA sequence from clone 989H11 on chromosome 22q13.1-13.2, complete sequence//0.28//436//59//Z83851

F-HEMBA1006092//Human chromosome 16p13.11 BAC clone CIT987SK-29B12 complete sequence//0.28//309//60//U95738

F-HEMBA1006406//HS_2268_B2_C07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=14 Row=F, genomic survey sequence//3.7e-69//340//99//AQ070566

F-HEMBA1006650//H.sapiens CpG island DNA genomic MseI fragment, clone 5h5, forward read cpG5h5.f1a.//9.4e-24//143//96//Z55730

F-HEMBA1006812//X.laevis xUBFalpal mRNA for upstream binding factor 2//0.96//234//64//X59863

- F-HEMBB1000672//CIT-HSP-2350H6.TF CIT-HSP Homo sapiens genomic clone 2350H6, genomic survey sequence.//1.1e-68//375//94//AQ059158
- F-HEMBB1001197//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//2.8e-10//229//66//U95760
- 5 F-HEMBB1001871//Equus caballus dermatan sulfate proteoglycan II mRNA, complete cds.//1.2e-27//619//62//AF038127
- F-MAMMA1001252
- F-MAMMA1002094//H.sapiens CpG island DNA genomic MseI fragment, clone 184g7, forward read cpq184g7.ft1a.//3.4e-29//167//97//Z59993
- 10 F-NT2RM4000634//Chionoecetes opilio (clone COP41) DNA microsatellite repeat regions.//1.4e-21//230//73//L49136
- F-NT2RM4000657//Human mRNA for phospholipase C, complete cds.//0.029//245//61//D42108
- F-NT2RM4000783//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence.//3.7e-36//324//70//AC005199
- 15 F-NT2RM4000857//RPC11-49P19.TJ RPC1-11 Homo sapiens genomic clone RPC1-11-49P19, genomic survey sequence.//1.5e-62//322//97//AQ051961
- F-NT2RM4001178//Streptomyces coelicolor cosmid 7H1.//0.0025//296//62//AL021411
- F-NT2RM4002420//Homo sapiens chromosome 17, clone hRPK_63_A_1, complete sequence.//0.00013//121//76//AC005670
- 20 F-NT2RP2000198//Human platelet glycoprotein IX mRNA, 3' end.//0.016//246//62//M25827
- F-NT2RP2000551//Rattus norvegicus microsatellite sequence clone 82G9.//2.0e-08//223//69//AJ233812
- F-NT2RP2000660//Homo sapiens chromosome 19, cosmid R30953, complete sequence.//0.0073//209//66//AC005622
- F-NT2RP2001214
- 25 F-NT2RP2001460//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.0//80//76//AC005189
- F-NT2RP2001756//CIT-HSP-237P31.TR CIT-HSP Homo sapiens genomic clone 237P31, genomic survey sequence.//3.0e-38//220//94//AQ110589
- F-NT2RP2002056//Genomic sequence from Human 17, complete sequence.//1.2e-80//317//91//AC002094
- 30 F-NT2RP2002677//Homo sapiens chromosome 10 clone CIT987SK-1031G15 map 10q25, *** SEQUENCING IN PROGRESS ***, 1 ordered pieces.//0.032//141//70//AC006097
- F-NT2RP2002755//Homo sapiens genomic DNA of 21q22.2 Down Syndrome region, segment 9/13.71.8e-22//377//69//AP000018
- 35 F-NT2RP2002843//Homo sapiens BAC clone RG030L05 from 7q22, complete sequence.//6.5e-16//311//63//AC005050
- F-NT2RP2003101//Human FMR1 gene, 5' end.//0.32//105//67//L19476
- F-NT2RP2003799//Human DNA for 5' terminal region of LINE-1 transposable element clone CGL1-4.//1.6e-33//119//96//X52233
- 40 F-NT2RP2004095//HS_3083_A1_A02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3083 Col=3 Row=A, genomic survey sequence.//1.0e-14//154//79//AQ106698
- F-NT2RP2004732//CIT-HSP-631P16.TP CIT-HSP Homo sapiens genomic clone 631P16, genomic survey sequence.//2.3e-20//120//99//B79035
- F-NT2RP2004920//Plasmodium falciparum MAL3P4, complete sequence.//0.030//397//59//AL008970
- 45 F-NT2RP2005454//Plasmodium falciparum chromosome 2, section 47 of 73 of the complete sequence.//0.97//455//56//AE001410
- F-NT2RP2005776//H.sapiens PAP mRNA.//1.0e-33//451//68//X76770
- F-NT2RP2005806//Mus musculus sex determining protein (Sry) gene, complete cds.//0.029//412//60//U70652
- 50 F-NT2RP2005882//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//9.4e-25//155//90//Z93242
- F-NT2RP3001282//RPC11-52L16.TJ RPC1-11 Homo sapiens genomic clone RPC1-11-52L16, genomic survey sequence.//3.2e-21//122//100//AQ052775
- F-NT2RP3001723//H.sapiens CpG island DNA genomic MseI fragment, clone 13g5, reverse read cpq13g5.ft1a.//2.2e-18//163//85//Z56771
- 55 F-NT2RP3002099//Homo sapiens chromosome 17, clone hCIT.296_K_1, complete sequence.//1.1e-76//351//86//AC005180
- F-NT2RP3003155
- F-NT2RP3004028//Sequence 1 from patent US 5618695.//3.3e-13//217//70//I40055

F-OVARC1000008//0.0040//674//57//M82636

F-OVARC1000724//Herpes simplex virus type I immediate early (IE) gene 3 for transcriptional activator IE175 (= ICP 4)//1.1e-07//519//59//X06461

F-OVARC1000751//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence//1.7e-21//509//62//AC004221

F-OVARC1001029//Human DNA sequence from clone 19408 on chromosome 6q24.1-25.3 Contains STS and GSSs, complete sequence//1.1e-05//388//61//AL031769

F-PLACE1000814//Homo sapiens BAC clone GS011E15 from 5q31, complete sequence//1.4e-84//1717//178//AC002427

F-PLACE1003030

F-PLACE1005549//Human guanine nucleotide regulatory protein (NET1) mRNA, complete cds//4.9e-56//709//68//U02081

F-PLACE1007218//Homo sapiens chromosome 20 clone RP3-387E22, *** SEQUENCING IN PROGRESS ***, in unordered pieces//3.1e-39//214//98//AL031660

Homology Search Result Data 9.

[0321] The result of the homology search of the GenBank using the clone sequence of 3'-end (54 clones selected in EXAMPLE 16.) except EST and STS.

[0322] Data include

the name of clone,

definition of the top hit data,

the P-value: the length of the compared sequence: identity (%), and

the Accession No. of the top hit data, as in the order separated by //.

[0323] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

[0324] Data are not shown for the clones in which the P-value was higher than 1.

R-HEMBA1000497//***ALU WARNING: Human Alu-J subfamily consensus sequence//1.4e-38//185//84//U14567

R-HEMBA1001750//Hansenuita wingel mitochondrial DNA, complete sequence//1.7e-07//399//59//D31785

R-HEMBA1003854//Human DNA sequence from clone 224A6 on chromosome 1p35.1-36.23 Contains part of a gene similar to Mouse Wnt-4 protein, the gene for CDC42 (cell division cycle 42 (GTP-binding protein, 25kD)), ESTs, STSs, GSSs and a CpG Island, complete sequence//1.4e-75//309//85//AL031281

R-HEMBA1004193//***ALU WARNING: Human Alu-J subfamily consensus sequence//1.1e-34//188//81//U14567

R-HEMBA1004860//Homo sapiens 12q13.1 PAC RPC13-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence//1.3e-06//239//66//AC004241

R-HEMBA1005572//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2, complete sequence//3.1e-21//341//67//AJ010598

R-HEMBA1006038//Homo sapiens chromosome 19, cosmid R34094, complete sequence//1.7e-24//307//171//AC004678

R-HEMBA1006092//H. Sapiens mRNA for alpha2-subunit of soluble guanylyl cyclase//0.76//246//62//X63282

R-HEMBA1006406//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4 Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence//1.3e-31//297//77//AL023574

R-HEMBA1006650//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence//1.8e-15//350//65//AC003071

R-HEMBA1006812//Homo sapiens chromosome X clone RP3-424J12, *** SEQUENCING IN PROGRESS ***, in unordered pieces//1.8e-55//430//81//Z82207

R-HEMBA1000672//Homo sapiens clone UWGC:y54c283 from 6p21, complete sequence//9.1e-39//437//171//AC006166

R-HEMBA1001197//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence//1.5e-37//275//85//AC004593

R-HEMBA1001871//Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces//0.00097//410//59//AC004688

R-MAMMA1001252//Homo sapiens clone 201104, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces//2.9e-13//364//64//AC004529

R-MAMMA1002094//HS_3163_A1_A09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=17 Row=A, genomic survey sequence//5.9e-41//256//91//AQ141441

- R-NT2RM4000634//Homo sapiens chromosome 19, cosmid R30783, complete sequence.//1.6e-21//283//73//AC005258
- R-NT2RM4000657
- R-NT2RM4000783
- 5 R-NT2RM4000857//RPCI11-63K2.TK RPCI-11 Homo sapiens genomic clone RPCI-11-63K2, genomic survey sequence.//4.0e-07//62//98//AQ203073
- R-NT2RM4001178
- R-NT2RM4002420
- 10 R-NT2RP2000198//Homo sapiens Chromosome 16 BAC clone CIT987-SK37914 -complete genomic sequence, complete sequence.//0.58//108//67//AC002307
- R-NT2RP2000551//Homo sapiens DNA, pseudoautosomal boundary-like sequence PABL2.//6.2e-72//391//87//D30043
- R-NT2RP2000660//Homo sapiens chromosome 17, clone hRPK.640_1_15, complete sequence.//0.0058//166//69//AC005324
- 15 R-NT2RF2001214//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//0.93//117//65//U49822
- R-NT2RP2001460
- R-NT2RP2001756//CIT-HSP-2382021.TR CIT-HSP Homo sapiens genomic clone 2382021, genomic survey sequence.//3.4e-91//507//92//AQ114228
- 20 R-NT2RP2002056//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//0.00022//225//69//Z97181
- R-NT2RP2002677//CIT-HSP-2349K20.TF CIT-HSP Homo sapiens genomic clone 2349K20, genomic survey sequence.//3.1e-29//178//94//AQ062168
- R-NT2RP2002755//Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X *.//5.3e-39//449//72//Z81014
- 25 R-NT2RP2002843//Homo sapiens chromosome 17, clone hRPK.22_N_12, complete sequence.//0.0097//498//59//AC005412
- R-NT2RP2003101//CIT-HSP-238301.TR CIT-HSP Homo sapiens genomic clone 238301, genomic survey sequence.//1.2e-32//344//75//AQ196754
- 30 R-NT2RP2003799//I3.6e-05//408//60//AL010237
- R-NT2RP2004095//Plasmodium falciparum chromosome 4 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.//2.1e-10//455//61//AL034557
- R-NT2RP2004732//Human DNA sequence from clone 703H14 on chromosome 1q23.2-24.3 Contains 3' end of a novel gene, ESTs, CA repeat(D1S445), STS, GSSs, complete sequence.//5.1e-51//383//74//AL031287
- 35 R-NT2RP2004920//Homo sapiens chromosome 5, P1 clone 878H11 (LBNL H45), complete sequence.//0.062//315//61//AC005219
- R-NT2RP2005454//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs, polymorphic CA repeat, CpG island, genomic fragments.//0.75//246//63//Z86062
- 40 R-NT2RP2005776//Homo sapiens PAC clone DJ1189D06 from 7p15.3-p14, complete sequence.//0.91//232//61//AC005232
- R-NT2RP2005806//Human neurofibromatosis type 1 (NF1) gene, intron 19a, complete sequence.//1.3e-19//405//66//U37368
- R-NT2RP2005882//Plasmodium falciparum MAL3P1, complete sequence.//1.1e-09//533//60//Z97348
- 45 R-NT2RP3001282//Plasmodium falciparum MAL3P8, complete sequence.//0.00026//499//58//AL034560
- R-NT2RP3001723//Human BAC clone RG354L07 from 7q31, complete sequence.//0.00035//337//61//AC002466
- R-NT2RP3002099//Homo sapiens chromosome 17, clone hCIT.296_K_1, complete sequence.//1.8e-44//307//86//AC005180
- R-NT2RP3003155
- 50 R-NT2RP3004028//F14A6-Sp6 IGF Arabidopsis thaliana genomic clone F14A6, genomic survey sequence.//0.95//95//65//B21351
- R-OVARC1000008
- R-OVARC1000724//Homo sapiens BAC clone RG017K18 from 7q31, complete sequence.//0.91//83//71//AC005161
- 55 R-OVARC1000751//HS_2222_A2_C09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=18 Row=E, genomic survey sequence.//2.8e-12//176//72//AQ033143
- R-OVARC1001029//Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore X library) and PAC RPCI1-93D11 (from Roswell Park Cancer Center) complete sequence.//1.2e-09//165//75//AC002357

R-PLACE1000814//Homo sapiens BAC clone GS465N13 from 7p15-p21, complete sequence.//6.2e-52//514//175//AC004744

R-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//9.6e-33//225//90//AF032387

R-PLACE10e5549//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17, complete sequence.//0.037//323//6//AB007644

R-PLACE1007218//Homo sapiens chromosome 20 clone RP3-387E22, *** SEQUENCING IN PROGRESS ***, in unordered pieces.//1.1e-88//497//91//AL031660

Homology Search Result Data 10.

[0325] The result of the homology search of the Human Unigene using the clone sequence of 5'-end (54 clones selected in EXAMPLE 16.) .

[0326] Data include

the name of clone,
title of the top hit data,
the P-value: the length of the compared sequence: identity (%), and
the Accession No. of the top hit data, as in the order separated by //.

[0327] Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000497//ou15a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1626332 3' mRNA sequence.//1.0//186//65//AI018130

F-HEMBA1001750//Human mRNA for TI-227H.//2.5e-101//473//99//D50525

F-HEMBA1003854//Homo sapiens mRNA for KIAA1031 protein, partial cds.//7.2e-06//103//80//AB028954

F-HEMBA1004193//Homo sapiens mRNA for TL132.//0.75//334//59//AJ012755

F-HEMBA1004860//my07e01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1271064 3' similar to contains Alu repetitive element; mRNA sequence.//3.7e-06//140//70//AA749151

F-HEMBA1005572//HZF-16=Kruppel-related zinc finger gene homolog [alternatively spliced] [human, hepatoblastoma cell line, HEP-G2, mRNA, 2080 nt].//1.1e-48//341//77//S54641

F-HEMBA1006038//Homo sapiens gene for insulin receptor substrate-2, complete cds.//0.036//297//60//AB000732

F-HEMBA1006092//ab80f12.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853295 3' similar to contains Alu repetitive element; mRNA sequence.//0.65//150//63//AA663266

F-HEMBA1006406//ws26e11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2498348 3' similar to TR:002710 002710 GAG POLYPROTEIN; mRNA sequence.//1.4e-32//518//67//AI989639

F-HEMBA1006650//Homo sapiens Arp2/3 protein complex subunit p20-Arc (ARC20) mRNA, complete cds.//1.3e-19//136//90//AF006087

F-HEMBA1006812//zh49f01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415417 3' mRNA sequence.//1.3e-120//579//98//W80404

F-HEMBA100672//Homo sapiens mRNA for KIAA1040 protein, partial cds.//0.00047//706//57//AB028963

F-HEMBA1001197//tq45e03.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2211772 3' similar to TR:001940 001940 STRAWBERRY NOTCH1; mRNA sequence.//1.2e-16//117//92//AI580023

F-HEMBA1001871//Human chondroitin/dermatan sulfate proteoglycan (PG40) core protein mRNA, complete cds.//4.6e-26//527//62//M14219

F-MAMMA1001252

F-MAMMA1002094

F-NT2RM4000634//DKFZp434D1813_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1813 5' mRNA sequence.//9.7e-16//226//69//AL040136

F-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//7.6e-179//817//99//AB028992

F-NT2RM4000783//wd82t06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338115 3' mRNA sequence.//1.8e-20//470//65//AI703299

F-NT2RM4000857//Homo sapiens KIAA0416 mRNA, partial cds.//1.9e-46//749//65//AB007876

F-NT2RM4001178//Homo sapiens protein tyrosine phosphatase (PAC-1) mRNA, complete cds.//0.0024//254//63//L11329

F-NT2RM4002420//wg39f11.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367501 3' similar to contains element L1 L1 repetitive element; mRNA sequence.//1.4e-13//127//84//AI742251

F-NT2RP2000198//Human mRNA for platelet glycoprotein IX.//0.0033//241//62//X52997
 F-NT2RP2000551//ze37d12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361175 3', mRNA sequence.//5.0e-07//116//71//AA017066
 F-NT2RP2000660//qx01g11.x1 NCI_CGAP_Br14 Homo sapiens cDNA clone IMAGE:1999364 3', mRNA sequence.//0.0271//120//65//AI225283
 F-NT2RP2001214
 F-NT2RP2001460//wb50h10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309155 3', mRNA sequence.//0.0013//89//78//AI851878
 F-NT2RP2001756//zw54e12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773902 3' similar to contains element TAR1 repetitive element ; mRNA sequence.//2.3e-18//120//93//AA427992
 F-NT2RP2002056//tw44g09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2262592 3' similar to contains Alu repetitive element; mRNA sequence.//2.4e-07//99//79//AI811687
 F-NT2RP2002677
 F-NT2RP2002755//zj83d10.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:461491 3' similar to contains element TAR1 repetitive element ; mRNA sequence.//1.9e-19//229//76//AA705059
 F-NT2RP2002843//wl88d12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2514551 3' similar to TR: P79522 P79522 MHC CLASS 1 REGION PROLINE RICH PROTEIN.; mRNA sequence.//8.2e-15//1314//67//AI964055
 F-NT2RP2003101//wi65a03.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398156 3', mRNA sequence.//0.38//106//68//AI761333
 F-NT2RP2003799//Homo sapiens mRNA; cDNA DKFZp564C142 (from clone DKFZp564C142).//2.5e-29//124//91//AL049979
 F-NT2RP2004095
 F-NT2RP2004732//Homo sapiens mRNA for KIAA0884 protein, partial cds.//2.6e-109//533//96//AB020691
 F-NT2RP2004920//wz68d10.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2563219 3' similar to TR: 000172 000172 LINE-1 REVERSE TRANSCRIPTASE ; mRNA sequence.//0.0020//220//61//AI969546
 F-NT2RP2005454//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0.058//143//69//AB023194
 F-NT2RP2005776//H.sapiens PAP mRNA.//4.3e-35//451//68//X76770
 F-NT2RP2005806//HSZ78328 Human fetal brain S. Meier-Ewert Homo sapiens cDNA clone 2.48 (CEPH) 3', mRNA sequence.//2.0e-05//385//62//Z78328
 F-NT2RP2005882//Human mRNA for KIAA0364 gene, complete cds.//7.3e-23//141//94//AB002362
 F-NT2RP3001282
 F-NT2RP3001723//ws73d05.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2503593 3' similar to contains MSR1.t1 TAR1 TAR1 repetitive element ; mRNA sequence.//2.6e-07//245//66//AW008782
 F-NT2RP3002099//yg49d01.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:36239 3', mRNA sequence.//0.58//164//64//R46086
 F-NT2RP3003155
 F-NT2RP3004028//Homo sapiens mRNA for KIAA1074 protein, complete cds.//1.3e-29//488//66//AB028997
 F-OVARC1000008//Homo sapiens mRNA for KIAA0665 protein, complete cds.//0.00032//430//59//AB014565
 F-OVARC1000724//Homo sapiens mRNA for KIAA0641 protein, complete cds.//0.0054//426//58//AB014541
 F-OVARC1000751//Human Tis11d gene, complete cds.//4.6e-12//527//62//U07802
 F-OVARC1001029//qv29c05.x1 NCI_CGAP_Ov31 Homo sapiens cDNA clone IMAGE:1982984 3' similar to contains element L1 repetitive element ; mRNA sequence.//0.0012//145//68//AI252422
 F-PLACE1000814//ak42f05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408641 3', mRNA sequence.//7.1e-31//275//76//AA668469
 F-PLACE1003030
 F-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A.//1.2e-57//737//67//AJ010046
 F-PLACE1007218//yo34a08.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:179798 3', mRNA sequence.//2.2e-21//216//76//H52716

Homology Search Result Data 11.

[0328] The result of the homology search of the Human Unigene using the clone sequence of 3'-end (54 clones selected in EXAMPLE 16.).

[0329] Data include

the name of clone,

title of the top hit data,
the P-value: the length of the compared sequence: identity (%), and
the Accession No. of the top hit data, as in the order separated by //.

- 5 [0330] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.
[0331] Data are not shown for the clones in which the P-value was higher than 1.
- R-HEMBA1000497//hp09h02.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1115859 similar to contains
Alu repetitive element; contains element MER22 repetitive element ; mRNA sequence.//6.2e-38//185//83//
10 AA614254
R-HEMBA1001750//yy71b10.s1 Soares_multiple_sclerosis_2NbHMSHP Homo sapiens cDNA clone IMAGE:
278971 3', mRNA sequence.//0.00451193//63//N63303
R-HEMBA1003854//Homo sapiens mRNA; cDNA DKFZp564F133 (from clone DKFZp564F133).//3.4e-72//310//
80//AL049263
15 R-HEMBA1004193//tr01e08.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2217062 3' similar to con-
tains Alu repetitive element; contains element MER4 repetitive element ; mRNA sequence.//1.5e-33//186//81//
AI914747
R-HEMBA1004860//qh16b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844819 3', mRNA
sequence.//0.017//118//69//AI218308
20 R-HEMBA1005572//hw16h05.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2403033 3', mRNA se-
quence.//4.6e-111//522//99//AI861830
R-HEMBA1006038//DKFZp434E1117_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E1117 5',
mRNA sequence.//1.2e-22//295//72//AL041450
25 R-HEMBA1006092//qt30d09.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE: 1949489
3' similar to contains element PTR5 repetitive element ; mRNA sequence.//1.4e-87//422//98//AI337963
R-HEMBA1006406//Homo sapiens mRNA for KIAA0752 protein, partial cds.//4.1e-30//291//76//AB018295
R-HEMBA1006650//H. sapiens mRNA for serine/threonine protein kinase EMK.//3.1e-09//319//62//X97630
R-HEMBA1006812//Human mRNA for KIAA0118 gene, partial cds.//3.1e-52//337//87//ID42087
R-HEMBA100672//Homo sapiens mRNA; cDNA DKFZp434M011 (from clone DKFZp434M011).//3.2e-48//276//
30 74//AL096734
R-HEMBA1001197//zt35b11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724317 5' similar
to contains Alu repetitive element; mRNA sequence.//9.9e-44//275//88//AA410788
R-HEMBA1001871//hwg20c02.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:
2365634 3', mRNA sequence.//6.3e-104//501//98//AI741321
35 R-MAMMA1001252//aa61h04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825463 3' similar to con-
tains Alu repetitive element; contains element XTR repetitive element ; mRNA sequence.//9.0e-19//127//91//
AA504355
R-MAMMA1002094//wd28h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2329511 3', mR-
NA sequence.//2.5e-68//328//99//AI936520
40 R-NT2RM4000634//DKFZp434F2016_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434F2016 3',
mRNA sequence.//8.2e-20//185//81//AL041146
R-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//5.7e-62//335//94//AB028992
R-NT2RM4000783
R-NT2RM4000857//Human megakaryocyte stimulating factor mRNA, complete cds.//0.00074//360//61//U70136
45 R-NT2RM4001178//tk08e03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2150428 3', mRNA se-
quence.//0.77//96//62//AI457506
R-NT2RM4002420//w58b04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2429071 3', mRNA se-
quence.//2.4e-85//438//94//AI857508
R-NT2RP2000198//nxt19b11.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1256541 3', mRNA se-
50 quence.//1.9e-45//270//91//AA738352
R-NT2RP2000551//tgh0h11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2115141 3', mRNA se-
quence.//3.3e-53//311//85//AI417680
R-NT2RP2000660//ns42a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1186258 3', mRNA se-
quence.//4.3e-26//142//97//AA805691
55 R-NT2RP2001214//tw65g08.x1 NCI_CGAP_Ui3 Homo sapiens cDNA clone IMAGE:2264606 3' similar to contains
element MSR1 repetitive element ; mRNA sequence.//1.5e-57//289//97//AI600174
R-NT2RP2001460
R-NT2RP2001756//zw54e12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773902 3'

similar to TR:G456660 G456660 ZINC FINGER PROTEIN ZFP-1 ; mRNA sequence.//6.0e-13//85//96//AA427992
 R-NT2RP2002056//yh26a12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130846 3', mRNA
 sequence.//0.0016//208//65//R22302
 R-NT2RP2002677//Homo sapiens mRNA for KIAA0524 protein, partial cds.//3.4e-26//339//71//AB011096
 5 R-NT2RP2002755//qd50d10.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1732915 3',
 mRNA sequence.//1.5e-26//419//66//A1190698
 R-NT2RP2002843//at31f08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2373639 3' similar to
 contains L1.11 L1 repetitive element; mRNA sequence.//1.8e-45//463//74//A1749673
 R-NT2RP2003101//ty24h05.x1 NCI_CGAP_Ui3 Homo sapiens cDNA clone IMAGE:2280057 3', mRNA se-
 10 quence.//7.5e-73//347//99//A1758824
 R-NT2RP2003799//Homo sapiens mRNA for KIAA0751 protein, complete cds.//0.0026//247//65//AB018294
 R-NT2RP2004095//zv08c02.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:753026 3' similar to con-
 tains element MER32 repetitive element ; mRNA sequence.//9.6e-07//188//66//AA436455
 R-NT2RP2004732//tu60a07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2255412 3' similar to con-
 15 tains Alu repetitive element; contains element L1 repetitive element ; mRNA sequence.//4.3e-25//414//68//
 A1678956
 R-NT2RP2004920//wd13h02.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2328051 3', mRNA se-
 quence.//6.8e-91//483//93//A1694022
 R-NT2RP2005454//yy77g09.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:
 20 279616 3', mRNA sequence.//0.0070//325//59//N48302
 R-NT2RP2005776//qq97d06.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1939307 3',
 mRNA sequence.//7.5e-08//89//82//A1338419
 R-NT2RP2005806//wc29h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2316625 3' similar to con-
 tains MER2.b3 MER2 repetitive element ; mRNA sequence.//3.2e-16//235//71//A1671398
 25 R-NT2RP2005882//wo31f09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2456969 3', mRNA se-
 quence.//0.00095//352//59//A1925528
 R-NT2RP3001282//wg35b03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:
 2367053 3', mRNA sequence.//1.7e-113//555//97//A1769199
 R-NT2RP3001723//wo48e06.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2458594 3', mRNA se-
 30 quence.//4.2e-98//471//98//A1926617
 R-NT2RP3002099//DKFZp564L227_s1 564 (synonym: htfbr2) Homo sapiens cDNA clone DKFZp564L227 3', mR-
 NA sequence.//9.2e-50//329//87//AL037910
 R-NT2RP3003155//zp07a07.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595668
 3', mRNA sequence.//1.4e-30//159//99//AA173172
 35 R-NT2RP3004028//Homo sapiens protein kinase C-alpha mRNA, partial 3' UTR.//0.43//66//75//AF035504
 R-OVARC1000008//wa69e12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2301454 3', mRNA
 sequence.//1.0e-77//376//98//A1699393
 R-OVARC1000724//tf94b10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2106907 3', mRNA se-
 quence.//0.71//27//100//A1380236
 40 R-OVARC1000751//log93d04.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455847 3', mRNA se-
 quence.//3.5e-13//274//63//AA863306
 R-OVARC1001029//yz96e02.r1 Soares_melanocyte_2NbHM Homo sapiens cDNA clone IMAGE:290906 5' similar
 to contains Alu repetitive element; contains element PTR5 repetitive element ; mRNA sequence.//3.5e-13//175//74//
 N99464
 45 R-PLACE1000814//tg94a08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112086 3' similar
 to contains Lt.12 L1 L1 repetitive element; mRNA sequence.//2.2e-18//285//69//A1424789
 R-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete
 cds.//4.0e-34//225//90//AF032387
 50 R-PLACE1005549//tm26b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157693 3', mRNA
 sequence.//0.91//127//66//A1480253
 R-PLACE1007218//lyq06e01.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:196152 5'
 similar to contains Alu repetitive element; contains LTR4 repetitive element; mRNA sequence.//2.4e-36//245//87//
 R92256

Homology Search Result Data 12.

[0332] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequenc-
 es. Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology,

and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.

- C-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE-TRNA LIGASE) (LEURS).//6.4E-99//457aa//45%//Q09996
- 5 C-HEMBA1000020//Homo sapiens beta 2 gene.//7.5E-264//1194bp//95%//X02344
- C-HEMBA1000129//HYTOTHEICAL HELICASE C8A4.08C IN CHROMOSOME 1.//3.8E-25//166aa//36%//Q09884
- C-HEMBA1000201//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//1612bp//99%//AJ011738
- 10 C-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//1E-86//146aa//56%//Q61221
- C-HEMBA1000231
- C-HEMBA1000264
- C-HEMBA1000280
- C-HEMBA1000282
- 15 C-HEMBA1000303//"Mus musculus Plenty of SH3s (POSH) mRNA, complete cds."//7.1E-254//1440bp//87%//AF030131
- C-HEMBA1000333//"Homo sapiens mRNA for KIAA0874 protein, partial cds."//4.8E-253//1148bp//99%//AB020681
- C-HEMBA1000351
- 20 C-HEMBA1000356//Homo sapiens mRNA; cDNA DKFpZp566C243 (from clone DKFpZp566C243).//3.3E-287//815bp//98%//AL050274
- C-HEMBA1000396
- C-HEMBA1000411//ANKYRIN.//5.7E-12//127aa//38%//Q02357
- C-HEMBA1000442
- 25 C-HEMBA1000456
- C-HEMBA1000504
- C-HEMBA1000518//PECANEX PROTEIN.//2.1E-19//227aa//38%//P18490
- C-HEMBA1000519
- C-HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.//2.4E-44//292aa//36%//Q01755
- 30 C-HEMBA1000542//"Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds."//2.2E-194//663bp//83%//D89340
- C-HEMBA1000545
- C-HEMBA1000557
- C-HEMBA1000592//"Homo sapiens sorting nexin 6 (SNX6) mRNA, complete cds."//0//1465bp//99%//AF121856
- 35 C-HEMBA1000594
- C-HEMBA1000604
- C-HEMBA1000622
- C-HEMBA1000637
- 40 C-HEMBA1000655
- C-HEMBA1000657//"Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds."//7.2E-156//1366bp//76%//U35776
- C-HEMBA1000749
- C-HEMBA1000769
- 45 C-HEMBA1000773
- C-HEMBA1000774
- C-HEMBA1000822
- C-HEMBA1000843
- C-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD).//1E-78//119aa//87%//P51689
- 50 C-HEMBA1000870
- C-HEMBA1000908
- C-HEMBA1000934
- C-HEMBA1000972
- C-HEMBA1000986
- 55 C-HEMBA1000991
- C-HEMBA1001008
- C-HEMBA1001059//"Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 14."//4.8E-169//786bp//99%//U06088

- C-HEMBA1001094
C-HEMBA1001302//"Homo sapiens calcium binding protein precursor, mRNA, complete cds."//9.6E-258//682bp//94%//AF153686
- 5 C-HEMBA1001330
C-HEMBA1001497
C-HEMBA1001569//SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2).//2.3E-53//110aa//100%//P19065
C-HEMBA1001570
C-HEMBA1001620//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.6E-166//506aa//60%//P42803
- 10 C-HEMBA1001640
C-HEMBA1001655
C-HEMBA1001672//"Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds."//0//1707bp//98%//AF072247
- 15 C-HEMBA1001711
C-HEMBA1001723//"Rattus norvegicus G beta-like protein GBL mRNA, complete cds."//4.7E-172//1240bp//81%//AF051155
C-HEMBA1001746//"Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds."//7.6E-59//998bp//64%//AF098066
- 20 C-HEMBA1001781
C-HEMBA1001804//"Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds."//0//1637bp//99%//AF125158
C-HEMBA1001822//"Mus musculus Ese2L protein mRNA, complete cds."//1.9E-235//1329bp//89%//AF132479
- 25 C-HEMBA1001824
C-HEMBA1001866//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//5.7E-51//234aa//41%//Q09332
C-HEMBA1001910
C-HEMBA1001913//GCN20 PROTEIN.//2.3E-81//158aa//50%//P43535
- 30 C-HEMBA1001921//"Homo sapiens germinal center kinase related protein kinase mRNA, complete cds."//0//1850bp//99%//AF000145
C-HEMBA1001939
C-HEMBA1001950//"Homo sapiens mRNA for KIAA0971 protein, complete cds."//0//1974bp//99%//AB023188
- 35 C-HEMBA1001967//"Homo sapiens NY-REN-57 antigen mRNA, partial cds."//0//1721bp//99%//AF155114
C-HEMBA1002035//Homo sapiens mRNA; cDNA DKFZp586E0518 (from clone DKFZp586E0518).//0//2149bp//99%//AL050089
- 40 C-HEMBA1002092//"Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds."//1.3E-271//1583bp//88%//U92703
C-HEMBA1002102//ANKYRIN.//4.40E-10//106aa//35%//Q02357
C-HEMBA1002150
C-HEMBA1002151//"Rattus norvegicus p34 mRNA, complete cds."//1.1E-153//1059bp//82%//AF178669
- 45 C-HEMBA1002189
C-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//2.2E-199//392aa//89%//P47226
C-HEMBA1002229
C-HEMBA1002241//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//3.70E-06//95aa//33%//P46087
- 50 C-HEMBA1002341//"Homo sapiens mRNA for KIAA0771 protein, partial cds."//0//1514bp//99%//AB018314
C-HEMBA1002417//"Homo sapiens chromosome 19, cosmid R28784, complete sequence."//1.4E-299//294bp//100%//AC005954
C-HEMBA1002547//"Homo sapiens agrin precursor mRNA, partial cds."//0//1605bp//97%//AF016903
- 55 C-HEMBA1002703
C-HEMBA1002779
C-HEMBA1002816
C-HEMBA1002970

C-HEMBA1002999//"Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.
"./1.4E-171/1552bp/75%/U20286

5 C-HEMBA1003021
C-HEMBA1003077//SLIT PROTEIN PRECURSOR./2.6E-15/199aa/31%/P24014
C-HEMBA1003079
C-HEMBA1003273
C-HEMBA1003304
C-HEMBA1003309
10 C-HEMBA1003376
C-HEMBA1003384
C-HEMBA1003531
C-HEMBA1003548
C-HEMBA1003556
C-HEMBA1003571
15 C-HEMBA1003579
C-HEMBA1003684//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN)./2E-73/526aa/32%/Q13105
C-HEMBA1003692
C-HEMBA1003720
C-HEMBA1003725
20 C-HEMBA1003729
C-HEMBA1003758
C-HEMBA1003773//"Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.
"./5.8E-81/511bp/86%/U17343
C-HEMBA1003783//"Mus musculus bromodomain-containing protein BP75 mRNA, complete cds."./

25 1.1E-190/1204bp/84%/AF084259
C-HEMBA1003799
C-HEMBA1003804
C-HEMBA1003805//"Mus musculus KH domain RNA binding protein QKI-5A mRNA, complete cds."./

30 0/988bp/95%/AF090402
C-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1)./8.10E-31/134aa/52%/P40484
C-HEMBA1003856
C-HEMBA1003866//"Mus musculus semaphorin 1A mRNA, complete cds."./1.2E-105/1192bp/70%/

35 AF030430
C-HEMBA1003879
C-HEMBA1003880
C-HEMBA1003893
C-HEMBA1003908
C-HEMBA1003937
40 C-HEMBA1003942
C-HEMBA1003958
C-HEMBA1003976
C-HEMBA1003978//"Homo sapiens mRNA for KIAA0840 protein, partial cds."./0/1530bp/100%/

45 AB020647
C-HEMBA1003985
C-HEMBA1004011
C-HEMBA1004024
C-HEMBA1004038
C-HEMBA1004045
C-HEMBA1004048
50 C-HEMBA1004111//"Homo sapiens mRNA for KIAA1276 protein, partial cds."./1.00E-163/751bp/

99%/AB033102
C-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT)./1.6E-166/416aa/72%/Q14141
C-HEMBA1004138
C-HEMBA1004143
55 C-HEMBA1004150
C-HEMBA1004168//"Homo sapiens geminin mRNA, complete cds."./3.9E-208/951 bp/99%/

AF067855
C-HEMBA1004200

C-HEMBA1004202//RAS-RELATED PROTEIN RAB-13.//6.2E-30//208aa//37%//P51153
 C-HEMBA1004203//NUCLEOLAR PROTEIN NOP2.//1.5E-12//258aa//29%//P40991
 C-HEMBA1004238
 C-HEMBA1004248//"Homo sapiens insulin induced protein 2 mRNA, complete cds."//8.20E-175//
 5 552bp//97%//AF125392
 C-HEMBA1004272
 C-HEMBA1004274
 C-HEMBA1004275//"Homo sapiens mRNA for KIAA1111 protein, partial cds."//0//1341bp//99%//
 AB029034
 10 C-HEMBA1004286//"Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds."//
 0//1982bp//99%//AF022795
 C-HEMBA1004312
 C-HEMBA1004321//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.3E-93//357aa//42%//Q99676
 15 C-HEMBA1004323
 C-HEMBA1004327
 C-HEMBA1004330
 C-HEMBA1004341
 C-HEMBA1004366
 C-HEMBA1004372
 20 C-HEMBA1004389//"Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.
 "//0//1437bp//99%//AF125158
 C-HEMBA1004394
 C-HEMBA1004408//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CY-
 CLOPHILIN-10).//3.2E-32//148aa//52%//P52017
 25 C-HEMBA1004429
 C-HEMBA1004460
 C-HEMBA1004461
 C-HEMBA1004502
 C-HEMBA1004554
 30 C-HEMBA1004560
 C-HEMBA1004610
 C-HEMBA1004629
 C-HEMBA1004632
 C-HEMBA1004637
 35 C-HEMBA1004670
 C-HEMBA1004672
 C-HEMBA1004697
 C-HEMBA1004711
 C-HEMBA1004725
 40 C-HEMBA1004730
 C-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN
 LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.9E-39//143aa//52%//P42743
 C-HEMBA1004751
 C-HEMBA1004752
 45 C-HEMBA1004889//"Human C3f mRNA, complete cds."//6.70E-24//341aa//26%//U72515
 C-HEMBA1004934
 C-HEMBA1004944
 C-HEMBA1004973
 C-HEMBA1004977
 50 C-HEMBA1005009//"Homo sapiens BAF53a (BAF53a) mRNA, complete cds."//0//1813bp//99%//
 AF041474
 C-HEMBA1005083
 C-HEMBA1005113
 C-HEMBA1005133
 55 C-HEMBA1005185
 C-HEMBA1005219//NUCLEAR PROTEIN SNF7.//5.3E-10//189aa//25%//P39929
 C-HEMBA1005252//"Homo sapiens mRNA for KIAA0585 protein, partial cds."//1.2E-268//1215bp//
 99%//AB011157

C-HEMBA1005296
 C-HEMBA1005314
 C-HEMBA1005331
 C-HEMBA1005394
 5 C-HEMBA1005403
 C-HEMBA1005423//"Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.
 "./2E-213//537bp//99%//AF041248
 C-HEMBA1005468
 C-HEMBA1005469
 10 C-HEMBA1005474
 C-HEMBA1005517
 C-HEMBA1005518
 C-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1).//3.1E-154//285aa//99%//Q60809
 C-HEMBA1005558//NUCLEAR PROTEIN SNF7.//6.40E-16//170aa//31%//P39929
 15 C-HEMBA1005576//"Homo sapiens mRNA for KIAA0463 protein, partial cds."./1.1E-181//835bp//
 99%//AB007932
 C-HEMBA1005582//"TROPOMYOSIN 1, NON-MUSCLE ISOFORM (TROPOMYOSIN II) (CYTOSKELETAL
 TROPOMYOSIN)."./0.00000009//213aa//27%//P09492
 C-HEMBA1005583
 20 C-HEMBA1005595//"DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) "./2.3E-54//562aa//29%//P34036
 C-HEMBA1005609//Homo sapiens mRNA; cDNA DKFZp564K133 (from clone DKFZp564K133).//2.2e-315//
 1448bp//99%//AL050012
 C-HEMBA1005621//"Homo sapiens Mad2B protein (MAD2B) mRNA, complete cds."./2.9E-224//
 1031bp//99%//AF139365
 25 C-HEMBA1005666
 C-HEMBA1005680
 C-HEMBA1005685
 C-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT).//
 4.4E-17//167aa//34%//P25296
 30 C-HEMBA1005746
 C-HEMBA1005755
 C-HEMBA1005813
 C-HEMBA1005822
 C-HEMBA1005834
 35 C-HEMBA1005884
 C-HEMBA1005891
 C-HEMBA1005909
 C-HEMBA1005911
 C-HEMBA1005931
 40 C-HEMBA1005963
 C-HEMBA1005991
 C-HEMBA1006005
 C-HEMBA1006031//"Homo sapiens mRNA for putative phospholipase, complete cds."./0//1413bp//
 99%//AB019435
 45 C-HEMBA1006067
 C-HEMBA1006081
 C-HEMBA1006091
 C-HEMBA1006100
 C-HEMBA1006108//"Homo sapiens mRNA for KIAA0943 protein, partial cds."./4.8E-245//764bp//
 99%//AB023160
 50 C-HEMBA1006121
 C-HEMBA1006130//SEL-10 PROTEIN.//0.000000043//219aa//25%//Q93794
 C-HEMBA1006155
 C-HEMBA1006158//"Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.".
 //0//1551bp//99%//AF048693
 55 C-HEMBA1006182
 C-HEMBA1006198//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//1.9E-19//215aa//39%//P05142
 C-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//0//1615bp//99%//AF070557

C-HEMBA1006253//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR./0.00000002//
 62aa//53%//P42698
 C-HEMBA1006259
 C-HEMBA1006272//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.3E-123//200aa//73%//P10265
 5 C-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANS-
 FERASE).//1E-210//490aa//77%//P25500
 C-HEMBA1006283//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2./0.000000012//176aa//
 30%//P32505
 C-HEMBA1006284
 10 C-HEMBA1006291//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-).//4.2E-12//215aa//23%//P70473
 C-HEMBA1006293
 C-HEMBA1006309//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION.//1.4E-48//
 248aa//43%//P38821
 C-HEMBA1006349
 15 C-HEMBA1006364
 C-HEMBA1006381
 C-HEMBA1006398//"Human L1 element L1.6 putative p150 gene, complete cds."./2E-277//1729bp//
 85%//U93563
 C-HEMBA1006445//"Homo sapiens putative tumor suppressor NOEY2 mRNA, complete cds."./1.4E-
 20 270//1224bp//100%//U96750
 C-HEMBA1006483
 C-HEMBA1006492
 C-HEMBA1006497
 C-HEMBA1006502
 25 C-HEMBA1006507//"Homo sapiens mRNA for KIAA0666 protein, partial cds."./0//2334bp//99%//
 AB014566
 C-HEMBA1006535
 C-HEMBA1006559//"Mus musculus PRAJA1 (Praja1) mRNA, complete cds."./2.8E-206//1107bp//83
 %//U06944
 30 C-HEMBA1006566
 C-HEMBA1006579
 C-HEMBA1006583
 C-HEMBA1006612
 C-HEMBA1006624//DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG./0.000000069//109aa//
 35 38%//Q58323
 C-HEMBA1006643
 C-HEMBA1006674
 C-HEMBA1006682
 C-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMC1-TFG2
 40 INTERGENIC REGION.//3.3E-22//241aa//31%//P53196
 C-HEMBA1006717
 C-HEMBA1006744
 C-HEMBA1006754
 C-HEMBA1006767
 45 C-HEMBA1006789
 C-HEMBA1006832
 C-HEMBA1006885//"Homo sapiens gene for Proline synthetase associated, complete cds."./0//
 1467bp//96%//AB018566
 C-HEMBA1006900
 50 C-HEMBA1006926
 C-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.//1.8E-226//1039bp//99%//
 AJ010841
 C-HEMBA1006973//"Homo sapiens rab3-GAP regulatory domain mRNA, complete cds."./5.6E-143//
 740bp//94%//AF004828
 55 C-HEMBA1006993
 C-HEMBA1007002
 C-HEMBA1007062
 C-HEMBA1007080

EP 1 074 617 A2

C-HEMBA1007087//HYPOTHETICAL PROTEIN MJ0162.//2E-45//304aa//32%//Q57626
 C-HEMBA1007112//Homo sapiens mRNA; cDNA DKFZp586C1817 (from clone DKFZp586C1817).//0//1619bp//99%//AL117450
 5 C-HEMBA1007194//"Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds."://0//1588bp//99%//AF139658
 C-HEMBA1007206
 C-HEMBA1007256
 C-HEMBA1007267
 C-HEMBA1007281
 10 C-HEMBA1007300//"Homo sapiens 3',5'-cyclic nucleotide phosphodiesterase 10A1 (PDE10A) mRNA, splice variant 1, complete cds."://0//1519bp//99%//AF127479
 C-HEMBA1007301
 C-HEMBA1007319
 C-HEMBA1007320
 15 C-HEMBA1007327
 C-HEMBA1007347
 C-HEMBA1000005
 C-HEMBA1000030
 C-HEMBA1000048
 20 C-HEMBA1000099
 C-HEMBA1000141
 C-HEMBA1000198
 C-HEMBA1000217//"Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds."://0//1038bp//99%//AF090385
 25 C-HEMBA1000218
 C-HEMBA1000274
 C-HEMBA1000312
 C-HEMBA1000402
 C-HEMBA1000420
 30 C-HEMBA1000480
 C-HEMBA1000530
 C-HEMBA1000550
 C-HEMBA1000556//"Homo sapiens mRNA for KIAA0750 protein, complete cds."://6.3E-74//1213bp//64%//AB018293
 35 C-HEMBA1000586
 C-HEMBA1000592
 C-HEMBA1000593//"Homo sapiens transferrin receptor 2 alpha (TFR2) mRNA, complete cds."://1.3E-107//503bp//99%//AF067864
 C-HEMBA1000649
 40 C-HEMBA1000693//"Homo sapiens neuroan1 mRNA, complete cds."://0//2952bp//94%//AF040723
 C-HEMBA1000822
 C-HEMBA1000826
 C-HEMBA1000890
 C-HEMBA1000915//SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (EC 3.4.21.-).//1.10E-08//129aa//31%//P29122
 45 C-HEMBA1001008
 C-HEMBA1001020//"Homo sapiens mRNA for KIAA0889 protein, complete cds."://0//1812bp//98%//AB020696
 C-HEMBA1001051
 50 C-HEMBA1001112//"Homo sapiens sec61 homolog mRNA, complete cds."://6E-145//961bp//83%//AF077032
 C-HEMBA1001221
 C-HEMBA1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).//5.4E-93//196aa//54%//P46938
 C-HEMBA1001282//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//7E-43//394aa//34%//P16157
 55 C-HEMBA1001302
 C-HEMBA1001335
 C-HEMBA1001337

C-HEMBB1001356
 C-HEMBB1001364
 C-HEMBB1001366
 C-HEMBB1001367
 5 C-HEMBB1001527
 C-HEMBB1001537
 C-HEMBB1002359
 C-HEMBB1002415
 10 C-HEMBB1002457
 C-HEMBB1002492
 C-HEMBB1002495
 C-HEMBB1002502
 C-HEMBB1002550//HYPOTHETICAL UOG-1 PROTEIN.//5E-28//266aa//33%//P27544
 15 C-HEMBB1002600//"Homo sapiens tetraspan NET-5 mRNA, complete cds."//0//1417bp//99%//
 AF089749
 C-HEMBB1002607//"Homo sapiens vitamin D3 receptor interacting protein (DRIP80) mRNA, complete cds.
 "//2E-136//660bp//98%//AF105421
 C-HEMBB1002684
 C-HEMBB1002692
 20 C-HEMBB1002697
 C-HEMBB1002705//"Homo sapiens CGI-27 protein mRNA, complete cds."//7.80E-285//841bp//96%//
 AF132961
 C-MAMMA1000019
 C-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FM05).//8.2E-198//868bp//99%//
 25 Z47553
 C-MAMMA1000025
 C-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//1.5E-90//323aa//48%//P47226
 C-MAMMA1000069
 C-MAMMA1000084
 30 C-MAMMA1000139
 C-MAMMA1000163
 C-MAMMA1000171
 C-MAMMA1000173//"Homo sapiens src homology 3 domain-containing protein HIP-55 mRNA, complete
 cds."//2.6E-164//1044bp//87%//AF197060
 35 C-MAMMA1000277
 C-MAMMA1000278
 C-MAMMA1000284//P.walti mRNA for mp associated protein 55.//2.2E-109//864bp//76%//X99836
 C-MAMMA1000309
 C-MAMMA1000312
 40 C-MAMMA1000313
 C-MAMMA1000361
 C-MAMMA1000388//"Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds."//
 0//1466bp//99%//AB015132
 C-MAMMA1000395
 45 C-MAMMA1000410
 C-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//2.00E-30//119aa//
 53%//Q09232
 C-MAMMA1000421
 C-MAMMA1000422
 50 C-MAMMA1000468
 C-MAMMA1000472
 C-MAMMA1000490
 C-MAMMA1000524
 C-MAMMA1000567
 55 C-MAMMA1000612//"Rattus norvegicus G beta-like protein GBL mRNA, complete cds."//1E-95//
 1115bp//72%//AF051155
 C-MAMMA1000623
 C-MAMMA1000625//GYP7 PROTEIN.//2.1E-41//198aa//40%//P48365

- C-MAMMA1000664
C-MAMMA1000670
C-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.-)//4.4E-33//250aa//33%//P42660
- 5 C-MAMMA1000713//L-RIBULOKINASE (EC 2.7.1.16)//7.70E-17//246aa//29%//P94524
C-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1)//1E-77//395aa//45%//014846
C-MAMMA1000734//Homo sapiens mRNA for SEC63 protein.//0//1587bp//99%//AJ011779
- 10 C-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//9E-299//1033aa//55%//P87115
C-MAMMA1000746
C-MAMMA1000775
C-MAMMA1000824//ACTIN.//6.2E-20//284aa//28%//P53500
C-MAMMA1000831
- 15 C-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4)//7.8E-40//101aa//54%//027540
C-MAMMA1000842
C-MAMMA1000843
C-MAMMA1000856
C-MAMMA1000865
- 20 C-MAMMA1000875
C-MAMMA1000906
C-MAMMA1000908
C-MAMMA1000914
C-MAMMA1000956//Homo sapiens CLDN8 gene for claudin-8.//0//1767bp//99%//AJ250711
- 25 C-MAMMA1000968
C-MAMMA1000979
C-MAMMA1001008//"Homo sapiens aspartic-like protease mRNA, complete cds."//2.50E-276//1263bp//99%//AF117892
C-MAMMA1001021
- 30 C-MAMMA1001041//"SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) "//1.6E-16//113aa//41%//Q01082
C-MAMMA1001059//Homo sapiens mRNA for DEAD Box Protein 5.//0//1440bp//99%//AJ237946
C-MAMMA1001075//"Homo sapiens CGI-72 protein mRNA, complete cds."//1.3E-18//397bp//98%//AF151830
- 35 C-MAMMA1001078
C-MAMMA1001091
C-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN).//4E-49//125aa//68%//P51521
C-MAMMA1001110
C-MAMMA1001126
- 40 C-MAMMA1001139//SRE-2 PROTEIN.//5.80E-35//239aa//38%//Q09273
C-MAMMA1001143
C-MAMMA1001154
C-MAMMA1001181//ABC1 PROTEIN HOMOLOG PRECURSOR.//1.30E-07//81aa//45%//Q92338
C-MAMMA1001215
- 45 C-MAMMA1001244
C-MAMMA1001259//"Mus musculus F-box protein FBX18 mRNA, partial cds."//2.3E-271//1414bp//89%//AF184275
C-MAMMA1001260//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//2.1E-52//630aa//30%//P34537
- 50 C-MAMMA1001343
C-MAMMA1001411//Homo sapiens mRNA; cDNA DKFZp56400823 (from clone DKFZp56400823).//0//2131bp//99%//AL080121
C-MAMMA1001419
C-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) (FRAGMENT).//6.5E-129//260aa//92%//P52623
- 55 C-MAMMA1001510
C-MAMMA1001522
C-MAMMA1001576//"Human gamma-tubulin mRNA, complete cds."//7.5E-276//1561bp//90%//

M61764
 C-MAMMA1001604
 C-MAMMA1001620
 C-MAMMA1001635
 5 C-MAMMA1001649
 C-MAMMA1001686
 C-MAMMA1001692
 C-MAMMA1001743//Y BOX BINDING PROTEIN-1 (Y-BOX TRANSCRIPTION FACTOR).//B.5E-32//171aa//36%//
 P21573
 10 C-MAMMA1001754//"Homo sapiens CGI-11 protein mRNA, complete cds."//0//1837bp//98%//
 AF132945
 C-MAMMA1001757
 C-MAMMA1001764
 C-MAMMA1001768//CELL DIVISION CYCLE PROTEIN 48 HOMOLOG MJ1156.//3.8E-45//351aa//38%//Q58556
 15 C-MAMMA1001771//M.musculus mRNA for semaphorin B.//2.60E-200//1272bp//79%//X85991
 C-MAMMA1001790
 C-MAMMA1001837//ZINC FINGER PROTEIN 29 (ZFP-29).//2.6E-77//507aa//38%//Q07230
 C-MAMMA1001868
 C-MAMMA1001868//TRICHOHYALIN.//2.7E-19//359aa//25%//P22793
 20 C-MAMMA1001970
 C-MAMMA1002042
 C-MAMMA1002068
 C-MAMMA1002153
 C-MAMMA1002156
 25 C-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN).//6E-66//157aa//70%//P15880
 C-MAMMA1002174
 C-MAMMA1002209
 C-MAMMA1002219//"Homo sapiens mRNA for KIAA1067 protein, partial cds."//1.1E-181//861bp//
 98%//AB028990
 30 C-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EX-
 CHANGE FACTOR).//8.8E-217//310aa//86%//P70541
 C-MAMMA1002243
 C-MAMMA1002268//"Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds."//1E-190//
 1624bp//76%//AF068748
 35 C-MAMMA1002269
 C-MAMMA1002292
 C-MAMMA1002294
 C-MAMMA1002297//Homo sapiens mRNA for Rab6 GTPase activating protein.//1.1E-214//881bp//97%//
 AJ011679
 40 C-MAMMA1002312
 C-MAMMA1002329//M.musculus mRNA for semaphorin B.//3.80E-45//332bp//84%//X85991
 C-MAMMA1002333
 C-MAMMA1002351//FERRIPYOCHELIN BINDING PROTEIN.//0.000078//127aa//26%//P40882
 C-MAMMA1002353
 45 C-MAMMA1002355
 C-MAMMA1002356
 C-MAMMA1002362
 C-MAMMA1002380
 C-MAMMA1002384
 50 C-MAMMA1002427
 C-MAMMA1002470//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1E-11//128aa//36%//
 P47623
 C-MAMMA1002485//"Homo sapiens stannocalcin-related protein mRNA, complete cds."//0//1822bp//
 99%//AF098462
 55 C-MAMMA1002494
 C-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION.//1.2E-34//
 337aa//31%//P43571
 C-MAMMA1002530//"Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete

cds."//0//1910bp//99%//AF065214
 C-MAMMA1002554
 C-MAMMA1002585//"Homo sapiens mRNA for KIAA0860 protein, complete cds."//0//1405bp//99%//
 5 AB020667
 C-MAMMA1002598
 C-MAMMA1002619//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15)
 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-
 ZYME)//9.5E-16//159aa//37%//Q09931
 10 C-MAMMA1002655//"Homo sapiens mRNA for ganglioside sialidase, complete cds."//0//1515bp//
 99%//AB008185
 C-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COALIGASE) (ACYL-AC-
 TIVATING ENZYME)//1.1E-45//618aa//26%//P27550
 C-MAMMA1002673
 15 C-MAMMA1002684//"Homo sapiens mRNA for KIAA0214 protein, complete cds."//0//3174bp//99%//
 D86987
 C-MAMMA1002711
 C-MAMMA1002769//"Homo sapiens cell cycle progression restoration 8 protein (CPR8) mRNA, complete
 cds."//2.2E-25//330bp//77%//AF011794
 C-MAMMA1002775
 20 C-MAMMA1002782
 C-MAMMA1002796
 C-MAMMA1002807
 C-MAMMA1002838
 C-MAMMA1002842//"Mus musculus c-Cb1 associated protein CAP mRNA, complete cds."//2.6E-58//
 25 373bp//81%//U58883
 C-MAMMA1002869//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN)//1.4E-160//
 305aa//85%//P48059
 C-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN)//5.7E-30//214aa//
 35%//P48060
 30 C-MAMMA1002886
 C-MAMMA1002890
 C-MAMMA1002938//"Homo sapiens mRNA for KIAA0698 protein, complete cds."//8.4E-252//1139bp//
 100%//AB014598
 C-MAMMA1002964
 35 C-MAMMA1003011//HESTONE MACRO-H2A.1//2.7E-123//370aa//66%//Q02874
 C-MAMMA1003013//DNA POLYMERASE BETA (EC 2.7.7.7)//7.4E-46//332aa//36%//P06746
 C-MAMMA1003015
 C-MAMMA1003019
 C-MAMMA1003035//RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C (EC 4.2.1.70) (PSEU-
 40 DOURIDYLATE SYNTHASE) (URACIL HYDROLYASE)//1.9E-13//108aa//33%//P23851
 C-MAMMA1003039
 C-MAMMA1003044
 C-MAMMA1003049
 C-MAMMA1003056
 45 C-MAMMA1003057//MD6 PROTEIN//3.1E-225//419aa//97%//Q60584
 C-MAMMA1003066
 C-MAMMA1003099
 C-MAMMA1003104
 C-MAMMA1003113//"Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds."//
 50 1.1E-234//1178bp//86%//AF071316
 C-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA)//2.2E-105//217aa//89%//P46735
 C-MAMMA1003135
 C-MAMMA1003146//Homo sapiens mRNA for GalT3 protein.//4.3E-218//996bp//99%//Y15062
 C-MAMMA1003150//"Homo sapiens mRNA for KIAA1096 protein, partial cds."//0//1342bp//99%//
 55 AB029019
 C-MAMMA1003166//"Homo sapiens MLL septin-like fusion protein (MSF) mRNA, complete cds."//
 3.10E-158//592bp//97%//AF123052
 C-NT2RM1000032

- C-NT2RM1000035//"Human mRNA for KIAA0199 gene, partial cds."//0//2948bp//99%//D83782
 C-NT2RM1000039//HYPOTHETICAL 41.4 KD PROTEIN IN SRLQ-HYPF INTERGENIC REGION (EC 1.18.1.-)
 (ORF4) (ORF2).//2.90E-14//299aa//25%//P37596
 C-NT2RM1000055//"Homo sapiens mRNA for KIAA0829 protein, partial cds."//0//3111bp//99%//
 5 AB020636
 C-NT2RM1000059
 C-NT2RM1000062
 C-NT2RM1000119//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CAL-
 CINEURIN REGULATORY SUBUNIT).//1.2E-10//150aa//28%//P87072
 10 C-NT2RM1000119
 C-NT2RM1000127
 C-NT2RM1000131//"Homo sapiens mRNA for KIAA0792 protein, complete cds."//0//2980bp//99%//
 AB018335
 C-NT2RM1000132//"Homo sapiens NADH:ubiquinone oxidoreductas NDUF56 subunit mRNA, nuclear gene
 15 encoding mitochondrial protein, complete cds."//7.8E-110//516bp//99%//AF044959
 C-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3.3E-3 8//469aa//27%//P49902
 C-NT2RM1000185//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CAL-
 CINEURIN REGULATORY SUBUNIT).//1.2E-10//150aa//28%//P87072
 C-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE
 20 SPAC10F6.02C.//1.1E-10//94aa//47%//D42643
 C-NT2RM1000199//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2476bp//99%//
 AJ245820
 C-NT2RM1000244//"Homo sapiens TRAF4 associated factor 1 mRNA, partial cds."//2E-126//592bp//
 99%//U81002
 25 C-NT2RM1000252//H. sapiens E-MAP-115 mRNA.//9.7E-35//569bp//64%//X73882
 C-NT2RM1000256//"Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete
 cds."//0//3012bp//99%//AB016789
 C-NT2RM1000260//"Human mRNA for KIAA0130 gene, complete cds."//0//3139bp//98%//D50920
 C-NT2RM1000271
 30 C-NT2RM1000300
 C-NT2RM1000314//"Human mRNA for KIAA0159 gene, complete cds."//0//4349bp//99%//D63880
 C-NT2RM1000354//"Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.
 "//7.4E-245//2101bp//68%//AF111423
 C-NT2RM1000355//"Homo sapiens transmembrane protein BRI (BRI) mRNA, complete cds."//0//
 35 1599bp//99%//AF152462
 C-NT2RM1000365
 C-NT2RM1000377//"Homo sapiens dual specificity phosphatase MKP5 (MKP5) mRNA, complete cds."//
 3.2E-196//1016bp//94%//AF179212
 C-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//
 40 0.000000019//677aa//31%//P53915
 C-NT2RM1000399
 C-NT2RM1000430//"Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds."//
 1.4E-185//1486bp//81%//AF084928
 C-NT2RM1000555//"Homo sapiens mRNA for KIAA0885 protein, complete cds."//0//2885bp//99%//
 45 AB020692
 C-NT2RM1000563//TRANSMISSION-BLOCKING TARGET ANTIGEN S230 PRECURSOR.//0.0000068//199aa//
 30%//Q08372
 C-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.5E-75//301aa//39%//P43636
 C-NT2RM1000661//"Homo sapiens translation initiation factor 4e mRNA, complete cds."//4.3E-210//
 50 960bp//99%//AF038957
 C-NT2RM1000666//DNA-BINDING PROTEIN A.//2.2E-09//165aa//34%//P16989
 C-NT2RM1000672
 C-NT2RM1000691//Homo sapiens mRNA for PLU-1 protein.//0//3104bp//99%//AJ132440
 C-NT2RM1000699
 55 C-NT2RM1000741//"Homo sapiens mRNA for KIAA0567 protein, partial cds."//1.1E-295//1338bp//
 99%//AB011139
 C-NT2RM1000742//"Homo sapiens AC133 antigen mRNA, complete cds."//0//3524bp//99%//
 AF027208

- C-NT2RM1000746//"Homo sapiens polyamine modulated factor-1 (PMF1) mRNA, complete cds."//6.70E-227//11043bp//99%//AF141310
- C-NT2RM1000770//DXS6673E PROTEIN.//1.4E-39//194aa//48%//Q14202
- 5 C-NT2RM1000772//VEGETATTOLE INCOMPATIBILITY PROTEIN HET-E-1.//7.3E-15//280aa//27%//Q00808
- C-NT2RM1000780
- C-NT2RM1000800//Mus musculus partial mRNA for B-IND1 protein (B-ind1 gene).//1.1E-98//571bp//89%//Z97207
- C-NT2RM1000802
- C-NT2RM1000811//"Homo sapiens AC133 antigen mRNA, complete cds."//0//3524bp//99%//AF027208
- 10 C-NT2RM1000826//"Homo sapiens mRNA for KIAA0885 protein, complete cds."//0//2885bp//99%//AB020692
- C-NT2RM1000829
- C-NT2RM1000850//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//9.7E-42//333aa//36%//P16157
- 15 C-NT2RM1000852//"Homo sapiens putative ATP-dependent RNA helicase ROK1 mRNA, complete cds."//0//2206bp//99%//AF077033
- C-NT2RM1000857//"Homo sapiens mRNA for KIAA0962 protein, partial cds."//0//3716bp//99%//AB023179
- 20 C-NT2RM1000874//"Homo sapiens death effector domain-containing testicular molecule mRNA, complete cds."//1.4E-244//1113bp//99%//AF043733
- C-NT2RM1000882//"Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds."//4.30E-122//1394bp//69%//AF126799
- C-NT2RM1000885//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1.8E-56//630aa//30%//P34537
- 25 C-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//1020aa//89%//P70700
- C-NT2RM1000898//"ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR)"//8.9E-26//229aa//29%//P02583
- C-NT2RM1000905//"Homo sapiens HSPC021 mRNA, complete cds."//0//1480bp//99%//AF077207
- 30 C-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//1E-15//266aa//26%//P46577
- C-NT2RM1000927
- C-NT2RM1000962
- C-NT2RM1000978
- 35 C-NT2RM1001003//"Homo sapiens alpha-catenin-like protein (CTNNA1) mRNA, complete cds."//0//2230bp//99%//AF030233
- C-NT2RM1001043
- C-NT2RM1001066
- 40 C-NT2RM1001072//"1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-148)"//8.3E-47//259aa//35%//P08487
- C-NT2RM1001085//"Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds."//3.7E-32//460bp//64%//AF053768
- C-NT2RM1001102//"Human HEM45 mRNA, complete cds."//2.3E-27//482bp//63%//U88964
- 45 C-NT2RM1001105
- C-NT2RM1001139//Homo sapiens mRNA; cDNA DKFZp564F0522 (from clone DKFZp564F0522).//0//1756bp//99%//AL049943
- C-NT2RM2000420
- 50 C-NT2RM2000566//"Homo sapiens integrin alpha-7 mRNA, complete cds."//0//2519bp//96%//AF032108
- C-NT2RM2000609
- C-NT2RM2000612//"Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds."//2.6E-106//1069bp//74%//U35776
- C-NT2RM2000735//ZINC FINGER PROTEIN 43 (UZINC PROTEIN HTF6).//2.9E-103//249aa//73%//P28160
- 55 C-NT2RM2001588
- C-NT2RM2001605//Homo sapiens mRNA for PLU-1 protein.//0//3114bp//99%//AJ132440
- C-NT2RM2001613//"Homo sapiens sec61 homolog mRNA, complete cds."//0//2601bp//99%//AF084458

- C-NT2RM2001632//KES 1 PROTEIN.//1.40E-31//342aa//34%//P35844
 C-NT2RM2001648//"Homo sapiens sec61 homolog mRNA, complete cds."//0//2421bp//99%//AF084458
- 5 C-NT2RM2001652//"Homo sapiens guanine nucleotide exchange factor mRNA, complete cds."//0//2608bp//99%//AF111162
 C-NT2RM2001659//ZINC/CADMIUM RESISTANCE PROTEIN.//3.4E-39//161aa//34%//P20107
 C-NT2RM2001664//"Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds."//0//2471bp//99%//AF044195
- 10 C-NT2RM2001668//"Homo sapiens putative WHSC1 protein (WHSC1) mRNA, alternative splice product ending in intron 11, complete cds."//6.2E-16//464bp//62%//AF083391
 C-NT2RM2001671//"Oryctolagus cuniculus sarcolemmal associated protein (SLAP1) mRNA, complete cds."//0//1843bp//94%//U21155
 C-NT2RM2001675
 C-NT2RM2001681
- 15 C-NT2RM2001688//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME 1.//4.60E-20//253aa//30%//Q09674
 C-NT2RM2001695//Homo sapiens clone H63 unknown mRNA.//0//2016bp//99%//AF103804
 C-NT2RM2001696
 C-NT2RM2001698//"Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds."//6.2E-253//1170bp//99%//AB028600
- 20 C-NT2RM2001700//"ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3.99.-) (VL-CAD) (FRAGMENT)."//5.7E-130//536aa//49%//P50544
 C-NT2RM2001716
 C-NT2RM2001723
- 25 C-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//7.2E-16//381aa//27%//Q09931
 C-NT2RM2001743//"Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds."//0//1498bp//99%//AF011792
- 30 C-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210.//8.8E-11//119aa//36%//Q92609
 C-NT2RM2001760//"Homo sapiens sec61 homolog mRNA, complete cds."//0//2379bp//99%//AF084458
 C-NT2RM2001768
 C-NT2RM2001771//ZINC FINGER PROTEIN 135.//6.4E-154//394aa//64%//P52742
- 35 C-NT2RM2001782//"Homo sapiens GDP-mannose pyrophosphorylase A (GMPPA) mRNA, complete cds."//0//1470bp//99%//AF135422
 C-NT2RM2001784
 C-NT2RM2001785//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2146bp//99%//AL050118
- 40 C-NT2RM2001813
 C-NT2RM2001823//CHD1 PROTEIN.//1.8E-106//631aa//39%//P32657
 C-NT2RM2001839//"Homo sapiens calumein (Calu) mRNA, complete cds."//0//2415bp//97%//AF013759
 C-NT2RM2001840
 C-NT2RM2001855
- 45 C-NT2RM2001867//"Homo sapiens mRNA for KIAA0943 protein, partial cds."//0//967bp//99%//AB023160
 C-NT2RM2001879
 C-NT2RM2001983//"Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds."//0//1658bp//98%//AF089816
- 50 C-NT2RM2002145//"Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds."//8.5E-191//1524bp//81%//AF084928
 C-NT2RM40000027
 C-NT2RM40000030//LAS1 PROTEIN.//5.6E-12//184aa//32%//P36146
- 55 C-NT2RM40000046//GOLIATH PROTEIN (G1 PROTEIN).//0.000008//112aa//31%//Q06003
 C-NT2RM4000155//"THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE--TRNA LIGASE) (THRRS)."//1.2E-157//321aa//61%//P26639
 C-NT2RM4000156//H.sapiens HPBRII-7 gene.//3.6E-21//785bp//60%//X67336

- C-NT2RM4000167//"Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds."//0//1946bp//99%//AF071592
- C-NT2RM4000199
- C-NT2RM4000200
- 5 C-NT2RM4000202//ZINC FINGER PROTEIN MOK-2 (HOK-2)//4.9E-32//170aa//41%//Q16600
- C-NT2RM4000233//"Mus musculus semaphorin Via mRNA, complete cds."//3.4E-231//1395bp//86%//AF030430
- C-NT2RM4000244
- 10 C-NT2RM4000251
- C-NT2RM4000265
- C-NT2RM4000324
- C-NT2RM4000327
- C-NT2RM4000356//RAS-RELATED PROTEIN RAB-17 //5.9E-80//213aa//75%//P35292
- C-NT2RM4000425
- 15 C-NT2RM4000433//"Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds."//4.1E-271//2085bp//77%//AF062476
- C-NT2RM4000514
- C-NT2RM4000531//ZINC FINGER PROTEIN 29 (ZFP-29) //2.4E-89//389aa//43%//007230
- C-NT2RM4000532
- 20 C-NT2RM4000534
- C-NT2RM4000603
- C-NT2RM4000611//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//2.9E-09//108aa//31%//Q00808
- C-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) //2.7E-146//420aa//60%//P27550
- 25 C-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL1374 //1.2E-28//180aa//30%//P74168
- C-NT2RM4000689
- C-NT2RM4000698
- C-NT2RM4000700
- C-NT2RM4000712//"Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds."//1E-136//1104bp//77%//AF022789
- 30 C-NT2RM4000717
- C-NT2RM4000733//TRANSCRIPTION TERMINATION FACTOR RHO.//0.0000041//207aa//29%//P52154
- C-NT2RM4000734//"Homo sapiens mRNA for KIAA0760 protein, partial cds."//0//2273bp//99%//AB018303
- 35 C-NT2RM4000741//"Homo sapiens hSGT1 mRNA for hSgt1p, complete cds."//0//2184bp//99%//D88208
- C-NT2RM4000751//ZINC FINGER PROTEIN 184 (FRAGMENT) //3.9E-125//301aa//53%//Q99676
- C-NT2RM4000764
- C-NT2RM4000778
- 40 C-NT2RM4000787
- C-NT2RM4000790
- C-NT2RM4000795//"Homo sapiens mRNA for KIAA0951 protein, complete cds."//0//1847bp//96%//AB023168
- C-NT2RM4000796
- 45 C-NT2RM4000798//"Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 mRNA, complete cds."//0//2603bp//99%//AF084521
- C-NT2RM4000813
- C-NT2RM4000820//VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45 SUBUNIT) //1.10E-24//138aa//44%//P40682
- 50 C-NT2RM4000833
- C-NT2RM4000848
- C-NT2RM4000852
- C-NT2RM4000855
- C-NT2RM4000887
- 55 C-NT2RM4000895
- C-NT2RM4000950
- C-NT2RM4000979
- C-NT2RM4001002//Homo sapiens mRNA; cDNA DKFZp586G0518 (from clone DKFZp586G0518) //0//2259bp//

- 100%//AL050092
C-NT2RM4001032
C-NT2RM4001047//M025 PROTEIN //8E-140//333aa//80%//Q06138
C-NT2RM4001054//"Homo sapiens sec61 homolog mRNA, complete cds."//3.1E-190//1315bp//81%//
5 AF077032
C-NT2RM4001084//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I.//0.000000032//
165aa//33%//Q09820
C-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME II.//5.9E-86//292aa//
48%//Q09417
10 C-NT2RM4001140//HOMEOBOX PROTEIN MSH-D.//1E-11//103aa//38%//Q01704
C-NT2RM4001151
C-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN.//4.1E-197//445aa//78%//Q27969
C-NT2RM4001160
C-NT2RM4001187
15 C-NT2RM4001191//"Homo sapiens clone 24963 mRNA sequence, complete cds."//0//1950bp//99%//
AF131737
C-NT2RM4001200//ZINC FINGER PROTEIN 135.//9.5E-135//375aa//60%//P52742
C-NT2RM4001203//"Homo sapiens mRNA for KIAA0839 protein, partial cds."//0//3047bp//99%//
AB020646
20 C-NT2RM4001204//"Homo sapiens mRNA for KIAA1089 protein, partial cds."//0//2349bp//99%//
AB029012
C-NT2RM4001217//"Homo sapiens nuclear matrix protein NRP/B (NRPB) mRNA, complete cds."//
7.3E-148//1409bp//72%//AF059611
C-NT2RM4001256//"Xenopus laevis putative Zic3 binding protein mRNA, complete cds."//4.30E-55//
25 289bp//77%//AF129131
C-NT2RM4001258
C-NT2RM4001309
C-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-LIKE (EC 2.7.1.137) (PI3-KINASE) (PTDINS-
3-KINASE) (PI3K).//3.50E-35//124aa//65%//P54676
30 C-NT2RM4001316//"ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR (EC
1.3.99.3) (MCAD)."//2.3E-31//334aa//30%//P08503
C-NT2RM4001320//"Homo sapiens mRNA for Neuroblastoma, complete cds."//1.8E-39//728bp//64%//
D89016
C-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).//1E-28//171aa//37%//P32626
35 C-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HOL1 INTERGENIC REGION.//8.1E-
30//265aa//33%//P53742
C-NT2RM4001347//"Homo sapiens NY-REN-25 antigen mRNA, partial cds."//0//2300bp//99%//
AF155103
C-NT2RM4001371//"Homo sapiens IDN3 mRNA, partial cds."//0//2524bp//99%//AB019494
40 C-NT2RM4001382//"Homo sapiens RanBP7/importin 7 mRNA, complete cds."//2.2E-237//1079bp//
99%//AF098799
C-NT2RM4001384
C-NT2RM4001410
C-NT2RM4001411//"Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA,
45 complete cds."//0//1962bp//87%//AF020526
C-NT2RM4001412//"Homo sapiens nGAP mRNA, complete cds."//0//1918bp//99%//AF047711
C-NT2RM4001414
C-NT2RM4001437
C-NT2RM4001444//SOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS).//
50 1.4E-118//444aa//46%//P73505
C-NT2RM4001454
C-NT2RM4001455
C-NT2RM4001483//ZINC FINGER PROTEIN 136.//5.1E-106//357aa//55%//P52737
C-NT2RM4001489//"Homo sapiens mRNA for KIAA0685 protein, complete cds."//0//1810bp//99%//
55 AB014585
C-NT2RM4001522
C-NT2RM4001557//"Homo sapiens mRNA for KIAA1040 protein, partial cds."//0//1547bp//97%//
AB028963

- C-NT2RM4001565
C-NT2RM4001566//"Homo sapiens mRNA for KIAA1114 protein, complete cds."//0//1900bp//99%//AB029037
- 5 C-NT2RM4001582//"Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds."//1.5E-284//1082bp//90%//AF071317
C-NT2RM4001592//"Homo sapiens mRNA for KIAA1122 protein, partial cds."//0//2170bp//99%//AB032948
C-NT2RM4001594
C-NT2RM4001597//M.musculus red-1 gene.//2.1E-171//1414bp//78%//X92750
- 10 C-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).//2.6E-32//203aa//39%//Q12600
C-NT2RM4001629//"MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LARGE HOMOLOG 3) "//1.5E-93//278aa//38%//Q13368
C-NT2RM4001650
C-NT2RM4001662
- 15 C-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REGION.//2.7E-84//410aa//42%//P37339
C-NT2RM4001682
C-NT2RM4001710
C-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT).//8.9E-141//354aa//72%//Q14141
- 20 C-NT2RM4001715
C-NT2RM4001731//"Homo sapiens mRNA for KIAA1004 protein, partial cds."//0//1922bp//100%//AB023221
C-NT2RM4001746
C-NT2RM4001754
- 25 C-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.1.-).//4.1E-186//639aa//58%//Q05512
C-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1).//7.9E-66//311aa//35%//Q03164
C-NT2RM4001810//"Homo sapiens mRNA for KIAA0863 protein, complete cds."//0//2377bp//99%//AB020670
- 30 C-NT2RM4001813//LECTIN BRA-2.//0.0000048//114aa//30%//P17346
C-NT2RM4001823//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//2.9E-55//325aa//37%//P28160
C-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.9E-161//481aa//56%//P51523
C-NT2RM4001836
- 35 C-NT2RM4001841//"Homo sapiens mRNA for KIAA0920 protein, complete cds."//0//1861bp//98%//AB023137
C-NT2RM4001842
C-NT2RM4001856
- 40 C-NT2RM4001858//T-BOX CONTAINING PROTEIN TBX6L (FRAGMENT).//6.5E-22//126aa//46%//P79779
C-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//4.3E-244//1248bp//94%//Y17711
C-NT2RM4001876//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//6.5E-23//184aa//36%//Q15404
C-NT2RM4001880//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-).//5.9E-09//268aa//26%//P47486
- 45 C-NT2RM4001922//"Homo-sapiens mRNA for KIAA0957 protein, complete cds."//0//2165bp//99%//AB023174
C-NT2RM4001930//"Homo sapiens dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl glucosyltransferase (ALG6) mRNA, complete cds."//0//1930bp//99%//AF102851
C-NT2RM4001940//"Homo sapiens timeless homolog mRNA, complete cds."//0//2087bp//99%//AF098162
- 50 C-NT2RM4001953
C-NT2RM4001965
C-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//2.6E-261//1563bp//84%//X99330
C-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.8E-112//457aa//47%//P51523
- 55 C-NT2RM4001984
C-NT2RM4001987//"NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM 180) [CONTAINS: N-CAM 140]."//3.2E-17//281aa//30%//P16170
C-NT2RM4002013//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1

INTERGENIC REGION.//6.9E-94//589aa//35%/P42935

C-NT2RM4002018

C-NT2RM4002034//"Homo sapiens hiwi mRNA, partial cds."//1.9E-53//1585bp//60%/AF104260

C-NT2RM4002044

5 C-NT2RM4002054

C-NT2RM4002063//"Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds."//0//1865bp//99%/U82267

C-NT2RM4002066//"Homo sapiens thyroid hormone receptor-associated protein complex component TRAP230 mRNA, complete cds."//1.50E-211//1123bp//71%/AF117755

10 C-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//2.8E-105//556aa//41%/Q04652

C-NT2RM4002128

C-NT2RM4002140

C-NT2RM4002145//SLIT PROTEIN PRECURSOR.//1.40E-09//127aa//33%/P24014

15 C-NT2RM4002161//"Homo sapiens laforin (EPM2A) mRNA, complete cds."//0//2671bp//99%/AF084535

C-NT2RM4002174//MRP PROTEIN.//9.1E-68//264aa//51%/P21590

C-NT2RM4002189//"GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)."//6.2E-33//688aa//27%/P08640

20 C-NT2RM4002205//"ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)."//3E-37//122aa//72%/Q07803

C-NT2RM4002213//"Homo sapiens protein phosphatase methylesterase-1 (PME-1) mRNA, complete cds."//0//2452bp//100%/AF157028

C-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//3.7E-19//147aa//41%/P40809

25 C-NT2RM4002251//"ALPHA-1,3-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYL-TRANSFERASE (EC 2.4.1.101) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE I) (GNT-I) (GLCNAC-TI)."//2.2E-36//320aa//38%/P27808

C-NT2RM4002256

C-NT2RM4002266

C-NT2RM4002281

30 C-NT2RM4002287

C-NT2RM4002294

C-NT2RM4002301

C-NT2RM4002323//ANTIGEN GOR (FRAGMENT).//0.000000001//154aa//33 %/P48778

C-NT2RM4002339

35 C-NT2RM4002344

C-NT2RM4002373//"Homo sapiens mRNA for KIAA0649 protein, complete cds."//0//2666bp//99%/AB014549

C-NT2RM4002374

C-NT2RM4002383

40 C-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-TIVATING ENZYME).//1.3E-29//275aa//30%/P27095

C-NT2RM4002438//"Xenopus laevis putative Zic3 binding protein mRNA, complete cds."//1.1E-49//611bp//70%/AF129131

C-NT2RM4002446

45 C-NT2RM4002452

C-NT2RM4002457

C-NT2RM4002460//"ENV POLYPROTEIN (COAT POLYPROTEIN) [CONTAINS: COAT PROTEINS GP70, GP20]."//0.0000016//226aa//24%/P51515

C-NT2RM4002493

50 C-NT2RM4002527//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.9E-15//366aa//27%/Q00808

C-NT2RM4002532//PROTEIN HOM1.//2E-16//276aa//28%/P55137

C-NT2RM4002558//"Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds."//0//1797bp//99%/AF055899

C-NT2RM4002567

55 C-NT2RM4002593

C-NT2RM4002594//MSP1 PROTEIN HOMOLOG.//2.7E-68//236aa//58%/P54815

C-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//2.3E-101//488aa//45%/032038

C-NT2RP1000324
 C-NT2RP1000363//"Homo sapiens mRNA for KIAA0638 protein, partial cds."//0//1345bp//99%//
 AB014538
 C-NT2RP1000418
 5 C-NT2RP1000513//"Human NifU-like protein (hNifU) mRNA, partial cds."//6.50E-171//516bp//99%//
 U47101
 C-NT2RP1000721
 C-NT2RP1000730
 C-NT2RP1000767
 10 C-NT2RP1000836
 C-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//5.2E-20//306aa//
 33%//Q09531
 C-NT2RP1000943
 C-NT2RP1001033//"Homo sapiens delta-tubulin mRNA, complete cds."//2.10E-285//1290bp//100%//
 15 AF201333
 C-NT2RP1001073//"Homo sapiens U6 snRNA-associated Sm-like protein Lsm5 mRNA, complete cds.
 "//8.1E-107//504bp//99%//AF182291
 C-NT2RP1001199
 C-NT2RP1001248
 20 C-NT2RP1001253//"Homo sapiens oscillin (hLn) mRNA, complete cds."//0//2020bp//99%//AF029914
 C-NT2RP1001286
 C-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//32%//Q12024
 C-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//32%//Q12024
 C-NT2RP1001310//"Homo sapiens mitochondrial carrier homolog 1 isoform a mRNA, partial cds; nuclear
 25 gene for mitochondrial product."//0//1732bp//99%//AF176006
 C-NT2RP1001361//"Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA,
 complete cds."//6.5E-116//541bp//100%//AF070652
 C-NT2RP1001385//HYPOTHETICAL 48.8 KD PROTEIN IN SSU81-SCS2 INTERGENIC REGION.//2.7E-22//
 284aa//25%//P40074
 30 C-NT2RP1001432
 C-NT2RP2000040//"Homo sapiens mRNA for KIAA0747 protein, partial cds."//0//2648bp//99%//
 AB013290
 C-NT2RP2000076//Homo sapiens partial mRNA for polyhomeotic 2 protein (PH2 gene).//7.9E-20//265bp//73%//
 AJ242730
 35 C-NT2RP2000098
 C-NT2RP2000108
 C-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//9.7E-41//278aa//36%//P40556
 C-NT2RP2000258//ACTIVATOR 1 140 KD SUBUNIT (REPLICATION FACTOR C LARGE SUBUNIT) (A1 140 KD
 SUBUNIT) (RF-C 140 KD SUBUNIT) (ACTIVATOR 1 LARGE SUBUNIT) (DNA-BINDING PROTEIN PO-GA).//
 40 7.1E-12//213aa//23%//P35251
 C-NT2RP2000289
 C-NT2RP2000327
 C-NT2RP2000337
 C-NT2RP2000420//ZINC FINGER PROTEIN 165.//8.5E-33//155aa//52%//P49910
 45 C-NT2RP2000459
 C-NT2RP2000498
 C-NT2RP2000758
 C-NT2RP2001137
 C-NT2RP2001149
 50 C-NT2RP2001168//VERPROLIN.//1.5E-09//143aa//33%//P37370
 C-NT2RP2001173//"Homo sapiens mRNA for KIAA0480 protein, complete cds."//0//1780bp//99%//
 AB007949
 C-NT2RP2001174//GASTRULA ZINC FINGER PROTEIN XLGCF46.1 (FRAGMENT).//6E-10//88aa//38%//
 P18722
 55 C-NT2RP2001196
 C-NT2RP2001226
 C-NT2RP2001268//"Homo sapiens mRNA for KIAA0810 protein, partial cds."//0//3301bp//98%//
 AB018353

- C-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-ALPHA HOMOLOG) (BRAIN PROTEIN 147) (FRAGMENT).//4.4E-91//179aa//99%//P28663
C-NT2RP2001295//ZINC/CADMIUM RESISTANCE PROTEIN.//8.3E-39//161aa//34%//P20107
C-NT2RP2001312
- 5 C-NT2RP2001327//"TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN)."//5.5E-116//311aa//71%//Q13829
C-NT2RP2001328
C-NT2RP2001366
- 10 C-NT2RP2001378//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//2E-11//403aa//25%//Q02817
C-NT2RP2001392//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//8.4E-192//581aa//54%//P93647
C-NT2RP2001394//Homo sapiens mRNA for SCML2 protein.//0//2068bp//99%//Y18004
C-NT2RP2001420//"Mus musculus nuclear protein NIP45 mRNA, complete cds."//9E-112//742bp//82%//U76759
- 15 C-NT2RP2001450
C-NT2RP2001467
C-NT2RP2001506
C-NT2RP2001511//"Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds."//3.2E-297//2206bp//75%//AF093097
- 20 C-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1.//0//2502bp//99%//Y14494
C-NT2RP2001536//"Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds."//0//2326bp//99%//AF035586
C-NT2RP2001560//NAV2 PROTEIN.//0.0000015//219aa//27%//Q60992
C-NT2RP2001576//HYPOTHETICAL 62.2 KD PROTEIN C4G8.12C IN CHROMOSOME I.//8.2E-29//294aa//31%//Q09837
- 25 C-NT2RP2001581
C-NT2RP2001597//"RYANODINE RECEPTOR, CARDIAC MUSCLE."//0.00000036//127aa//36%//P30957
C-NT2RP2001628
- 30 C-NT2RP2001663//ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).//1.1E-47//126aa//53%//P42897
C-NT2RP2001748//FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS) (FARNESYL DI-PHOSPHATE SYNTHETASE) (DIMETHYLLALLYLTRANSFERASE (EC 2.5.1.1) / GERANYLTRANSFERASE (EC 2.5.1.10)) (KIAA0032).//5.40E-47//96aa//97%//P14324
- 35 C-NT2RP2001813
C-NT2RP2001883//"Homo sapiens CGI-01 protein mRNA, complete cds."//0//2306bp//99%//AF132936
C-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5.//2.3E-38//395aa//30%//P53946
C-NT2RP2001947
- 40 C-NT2RP2001985//"Homo sapiens high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha mRNA, complete cds."//2.00E-38//435bp//67%//AF090989
C-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//6.5E-129//279aa//85%//Q08469
C-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//1.7E-47//247aa//52%//P35331
- 45 C-NT2RP2002058//"Homo sapiens WD repeat protein WDR3 (WDR3) mRNA, complete cds."//0//2510bp//99%//AF083217
C-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.71.5E-294//1334bp//99%//AF052183
C-NT2RP2002078//PECANEX PROTEIN.//1.8E-09//195aa//32%//P18490
- 50 C-NT2RP2002079//"HISTONE H1, GONADAL."//4.4E-11//214aa//34%//P02256
C-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//3389bp//99%//AJ007509
C-NT2RP2002185//"Homo sapiens ubiquitin mRNA, complete cds."//0//1789bp//99%//AF176069
C-NT2RP2002193//"Homo sapiens PIAS3 mRNA for protein inhibitor of activated STAT3, complete cds."//0//2809bp//99%//AB021868
- 55 C-NT2RP2002231
C-NT2RP2002235
C-NT2RP2002252//"Mus musculus (clone pVZmSin3A9) mSin3A9 mRNA, complete cds."//0//3118bp//91%//L38621

- C-NT2RP2002292
C-NT2RP2002408
C-NT2RP2002442//HESA PROTEIN.//2.8E-14//163aa//30%//P46037
C-NT2RP2002464//DNA CROSS-LINK REPAIR PROTEIN PS02/SNM1.//6.50E-07//171aa//27%//P30620
5 C-NT2RP2002498
C-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC1744).//4.6E-144//537aa//49%//Q02386
C-NT2RP2002520//"Homo sapiens transcription factor RFX-B (RFXB) mRNA, complete cds."//3.70E-34//668bp//61%//AF105427
C-NT2RP2002549
10 C-NT2RP2002609//2-HYDROXYMUCONIC SEMIALDEHYDE HYDROLASE (EC 3.1.1.-) (HMSH).//2.80E-08//109aa//37%//P19076
C-NT2RP2002706
C-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1.//4.9E-85//489aa//43%//P55194
C-NT2RP2002800
15 C-NT2RP2002880//GLUCOSE REPRESSION MEDIATOR PROTEIN.//0.000039//206aa//23%//P14922
C-NT2RP2002891
C-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II.//4.1E-87//395aa//40%//Q18964
C-NT2RP2002939//ZINC FINGER PROTEIN 136.//5.4E-70//282aa//42%//P52737
20 C-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//716aa//91%//P70700
C-NT2RP2003034
C-NT2RP2003099
C-NT2RP2003137//UBIQUITIN.//0.000026//70aa//30%//P13117
25 C-NT2RP2003157//"Homo sapiens CGI-74 protein mRNA, complete cds."//0//2037bp//99%//AF151832
C-NT2RP2003158//"Homo sapiens mRNA for proteasome subunit p58, complete cds."//0//2091bp//99%//D67025
C-NT2RP2003165
30 C-NT2RP2003243//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//99%//AJ242978
C-NT2RP2003277//"Homo sapiens mRNA for KIAA0625 protein, partial cds."//0//3788bp//99%//AB014525
C-NT2RP2003286//PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4) (RNA-3'-PHOSPHATE CYCLASE) (RNA CYCLASE).//4.1E-88//374aa//47%//Q23400
35 C-NT2RP2003297
C-NT2RP2003307//KINESIN LIGHT CHAIN (KLC).//2.2E-199//550aa//70%//Q07866
C-NT2RP2003308//CROOKED NECK PROTEIN.//5.4E-244//622aa//67%//P17886
C-NT2RP2003347//BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN HOMOLOG.//0.000022//261aa//24%//P48754
40 C-NT2RP2003391//Homo sapiens mRNA for nuclear transport receptor.//0//1509bp//99%//AJ133769
C-NT2RP2003393
C-NT2RP2003445
C-NT2RP2003466//"Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds."//0//2194bp//99%//AF126799
45 C-NT2RP2003480//"Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds."//0//3012bp//99%//AF125158
C-NT2RP2003506//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//5.4E-14//106aa//46%//P04175
50 C-NT2RP2003511
C-NT2RP2003513//"Human mRNA for KIAA0270 gene, partial cds."//0//2137bp//97%//D87460
C-NT2RP2003567//"Homo sapiens mRNA for KIAA0462 protein, partial cds."//0//2343bp//99%//AB007931
C-NT2RP2003604//"Homo sapiens alpha-catenin-like protein (CTNNA1) mRNA, complete cds."//0//2442bp//99%//AF030233
55 C-NT2RP2003691
C-NT2RP2003713//"Homo sapiens ubiquitin-specific protease 3 (USP3) mRNA, complete cds."//0//2018bp//99%//AF073344

- C-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//0//869aa//80%/P53620
- C-NT2RP2003764
- C-NT2RP2003769
- 5 C-NT2RP2003777
- C-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//3.7E-21//137aa//43%/Q11076
- C-NT2RP2003857//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).//0.0000016//117aa//29%/Q91955
- 10 C-NT2RP2003981//"Homo sapiens mRNA for KIAA0804 protein, partial cds."//0//3046bp//99%/AB018347
- C-NT2RP2003984//Homo sapiens mRNA; cDNA DKFZp564A026 (from clone DKFZp564A026).//0//2514bp//99%/AL050367
- 15 C-NT2RP2004041//SYNAPSINS IA AND IB.//0.00000074//159aa//32%/P17599
- C-NT2RP2004066//"Human DNA sequence from clone 134019 on chromosome 1p36.11-36.33. complete sequence."//0//2410bp//99%/AL034555
- C-NT2RP2004081
- C-NT2RP2004124
- C-NT2RP2004152
- 20 C-NT2RP2004165
- C-NT2RP2004187//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).//5.6E-31//424aa//28%/J007231
- C-NT2RP2004239//"Homo sapiens lok mRNA for protein kinase, complete cds."//0//3044bp//99%/AB015718
- 25 C-NT2RP2004245
- C-NT2RP2004364
- C-NT2RP2004365
- C-NT2RP2004366//"Homo sapiens mRNA for KIAA0986 protein, partial cds."//0//2790bp//97%/AB023203
- 30 C-NT2RP2004373
- C-NT2RP2004476//"Homo sapiens cyclin L ania-6a mRNA, complete cds."//0//2075bp//99%/AF180920
- C-NT2RP2004551
- C-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03.//3E-117//625aa//40%/Q09903
- 35 C-NT2RP2004600
- C-NT2RP2004664//"Homo sapiens mRNA for KIAA0460 protein, partial cds."//0//2368bp//99%/AB007929
- C-NT2RP2004743
- C-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).//1.3E-26//190aa//41.-%//P38692
- 40 C-NT2RP2004816//"Homo sapiens H beta 58 homolog mRNA, complete cds."//0//2144bp//96%/AF054179
- C-NT2RP2004861
- C-NT2RP2004897
- 45 C-NT2RP2004933//"Homo sapiens mRNA for ZIP-kinase, complete cds."//0//2103bp//99%/AB007144
- C-NT2RP2004978//ACTIN-LIKE PROTEIN ARP8.//3.3E-47//353aa//30%/Q12386
- C-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL ADDITION ENZYME) (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFERASE).//4E-91//218aa//44%/Q92089
- 50 C-NT2RP2005162//"Homo sapiens aspartyl aminopeptidase mRNA, complete cds."//0//1615bp//99%/AF005050
- C-NT2RP2005204//"Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds."//0//1262bp//99%/AF090385
- C-NT2RP2005227
- 55 C-NT2RP2005287
- C-NT2RP2005288//"Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds."//0//2992bp//99%/AF060219
- C-NT2RP2005490//"Mus musculus D3Mm3e (D3Mm3e) mRNA, complete cds."//1.8E-175//1102bp//

- 83%//AF053628
C-NT2RP2005539//"Homo sapiens mRNA for KIAA0850 protein, complete cds."//0//1560bp//99%//AB020657
- 5 C-NT2RP2005605//QUEUINE TRNA-RIBOSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSGLYCOSYLASE) [GUANINE INSERTION ENZYME].//8.2E-23//164aa//28%//032053
C-NT2RP2005722//"Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds."//0//2545bp//99%//AB011414
C-NT2RP2005732
- 10 C-NT2RP2005784//"Homo sapiens ubiquitin-conjugating enzyme variant Kua (UBE2V) mRNA, complete cds."//0//2191bp//92%//AF155120
C-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//2.3E-39//318aa//31%//P40004
C-NT2RP2005859//"Homo sapiens mRNA for KIAA0863 protein, complete cds."//0//1649bp//99%//AB020670
- 15 C-NT2RP2006023
C-NT2RP2006334//Homo sapiens mRNA; cDNA DKFZp434J154 (from clone DKFZp434J154).//0//2318bp//99%//AL080155
C-NT2RP2006441
C-NT2RP3000002
- 20 C-NT2RP3000050//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.2E-150//490aa//53%//Q05481
C-NT2RP3000055
C-NT2RP3000068
C-NT2RP3000080
- 25 C-NT2RP3000085//ACETYL-/PROPIONYL-COENZYME A CARBOXYLASE ALPHA CHAIN [CONTAINS: BIOTIN CARBOXYLASE (EC 6.3.4.14); BIOTIN CARBOXYL CARRIER PROTEIN (BCCP)].//1.9E-123//436aa//50%//P46401
C-NT2RP3000092
C-NT2RP3000109//P54 PROTEIN PRECURSOR.//0.0000065//358aa//22%//P13692
- 30 C-NT2RP3000134
C-NT2RP3000149
C-NT2RP3000197
C-NT2RP3000207//"GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)."//2.9E-11//721aa//23%//P08640
- 35 C-NT2RP3000233//"Human DNA sequence from clone 22D12 on chromosome Xq21.1-21.33. Contains a novel protein similar to Drosophila Kelch (Ring Canal formation, KEL) and a heterogenous set of other types of proteins. Contains ESTs and GSSs, complete sequence."//0//1462bp//99%//AL035424
C-NT2RP3000235
C-NT2RP3000247
- 40 C-NT2RP3000267
C-NT2RP3000299//"Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds."//0//2730bp//82%//D29766
C-NT2RP3000324
C-NT2RP3000341//"Homo sapiens mitochondrial inner membrane preprotein translocase Tim17a mRNA, nuclear gene encoding mitochondrial protein, complete cds."//1.5E-246//1124bp//99%//AF106622
- 45 C-NT2RP3000393//"Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds."//5.8E-266//1373bp//86%//AF061817
C-NT2RP3000441//"Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds."//3.40E-42//645bp//67%//AF093066
- 50 C-NT2RP3000449
C-NT2RP3000451
C-NT2RP3000456
C-NT2RP3000542
C-NT2RP3000561
- 55 C-NT2RP3000562//"Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds."//0//2165bp//99%//AF093097
C-NT2RP3000578//HES1 PROTEIN.//1.3E-22//229aa//27%//P35843
C-NT2RP3000590//UVS-2 PROTEIN.//1.3E-22//458aa//24%//P33288

- C-NT2RP3000592
C-NT2RP3000622
C-NT2RP3000624
C-NT2RP3000685
- 5 C-NT2RP3000736//HYPOTHETICAL PROTEIN KIAA0140.//1.2E-166//305aa//99%//014153
C-NT2RP3000742//"1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA
1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT)."//4.1E-165//
371aa//49%//P10895
- 10 C-NT2RP3000753
C-NT2RP3000826
C-NT2RP3000865
C-NT2RP3000875//MEVALONATE KINASE (EC 2.7.1.36) (MK).//7.7E-87//175aa//98%//Q03426
C-NT2RP3001007
C-NT2RP3001055
- 15 C-NT2RP300111//"Homo sapiens TRF-proximal protein mRNA, complete cds."//1.50E-149//731bp//
97%//AF097725
C-NT2RP3001120//ZINC FINGER PROTEIN 136.//7.8E-170//512aa//58%//P52737
C-NT2RP3001126
C-NT2RP3001150//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000031//207aa//29%//P52154
- 20 C-NT2RP3001232
C-NT2RP3001268//"Homo sapiens zinc finger protein ZNF228 (ZNF228) mRNA, complete cds."//0//
3606bp//99%//AF198358
C-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein.//
1.3E-99//669bp//83%//Y18101
- 25 C-NT2RP3001274//"Homo sapiens mRNA for KIAA1037 protein, partial cds."//0//2254bp//99%//
AB028960
C-NT2RP3001281
C-NT2RP3001297
C-NT2RP3001318
- 30 C-NT2RP3001338//ZINC FINGER PROTEIN 81 (FRAGMENT).//2.4E-16//175aa//28%//P51508
C-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PRO-
TEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN).//3.6E-25//129aa//34%//P32089
C-NT2RP3001374
C-NT2RP3001428//NUCLEOPROTEIN TPR.//1.4E-128//152aa//99%//P12270
- 35 C-NT2RP3001432
C-NT2RP3001447
C-NT2RP3001449//"Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the
alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A,
-B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA,
40 Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal
Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae)
bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G
protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs,
complete sequence."//0//1827bp//99%//AL031282
- 45 C-NT2RP3001453//ANTIGEN PEPTIDE TRANSPORTER 2 (APT2) (HISTOCOMPATIBILITY ANTIGEN MODIFI-
ER 2).//3.2E-90//157aa//59%//P36371
C-NT2RP3001459
C-NT2RP3001527//"Human Spl40 protein (Spl40) mRNA, complete cds."//4.4E-290//793bp//93%//
U63420
- 50 C-NT2RP3001538//HYPOTHETICAL 39.0 KD PROTEIN T2.8D9.3 IN CHROMOSOME II.//9.10E-10//158aa//
31%//Q10022
C-NT2RP3001580//"Mus musculus strain C57BL/J germ cell-less protein (Gd) mRNA, complete cds."/
//0//1730bp//85%//AF163665
C-NT2RP3001587//"Human anthracycline-associated resistance ARX mRNA, complete cds."//0//
2617bp//99%//U35832
- 55 C-NT2RP3001589
C-NT2RP3001607
C-NT2RP3001608

- C-NT2RP3001671//"Homo sapiens mRNA for KIAA0850 protein, complete cds."//0//2310bp//99%//AB020657
- C-NT2RP3001672//"Homo sapiens Sex comb on midleg homolog 1 isoform 2 (SCMH1) mRNA, complete cds."//0//2836bp//99%//AF149046
- 5 C-NT2RP3001678
- C-NT2RP3001688//"Homo sapiens glucocorticoid modulatory element binding protein-1 (GMEB1) mRNA, complete cds."//0//1695bp//99%//AF099013
- C-NT2RP3001690//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.00000024//481aa//21%//P25386
- 10 C-NT2RP3001698
- C-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR.//3.4E-33//161aa//32%//P54356
- C-NT2RP3001716
- C-NT2RP3001752
- 15 C-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.8E-117//462aa//55%//P52272
- C-NT2RP3001844
- C-NT2RP3001854//Homo sapiens mRNA; cDNA DKFZp564G013 (from clone DKFZp564G013).//0//1528bp//99%//AL050011
- 20 C-NT2RP3001855//HOMEOBOX PROTEIN PKNOX1 (HOMEOBOX PROTEIN PREP-1).//8.1E-125//302aa//60%//P55347
- C-NT2RP3001898//"Homo sapiens mRNA for UDP-N-acetylglucosamine: alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV, complete cds."//0//1587bp//100%//AB000624
- C-NT2RP3001931
- C-NT2RP3001969//TRICHOHYALIN.//2.7E-11//442aa//23%//P37709
- 25 C-NT2RP3002002
- C-NT2RP3002004//H.sapiens mRNA for FAST kinase.//1.50E-192//11475bp//94%//X86779
- C-NT2RP3002007//SAP1 PROTEIN.//1.1E-68//474aa//32%//P39955
- C-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//5.30E-25//139aa//48%//Q09232
- 30 C-NT2RP3002045//"Homo sapiens mRNA for KIAA0899 protein, partial cds."//0//33 85bp//99%//AB020706
- C-NT2RP3002056//"Homo sapiens Rb binding protein homolog mRNA, partial cds."//0//2374bp//99%//AF083249
- 35 C-NT2RP3002062//"Homo sapiens mRNA for KIAA0873 protein, partial cds."//0//3764bp//99%//AB020680
- C-NT2RP3002081//"Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds."//4.1E-233//1896bp//69%//AF111423
- C-NT2RP3002097
- 40 C-NT2RP3002108//DEC1 PROTEIN (MDM20 PROTEIN).//7.90E-09//181aa//22%//Q12387
- C-NT2RP3002142
- C-NT2RP3002146
- C-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING PROTEIN GST1-HS).//2.8E-253//474aa//93%//P15170
- 45 C-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP7.1.9E-151//223aa//91%//Q02614
- C-NT2RP3002166
- C-NT2RP3002181
- C-NT2RP3002244
- C-NT2RP3002248
- 50 C-NT2RP3002273//SCD6 PROTEIN.//1.30E-09//295aa//28%//P45978
- C-NT2RP3002276
- C-NT2RP3002304
- C-NT2RP3002501//THREONINE DEHYDRATASE CATABOLIC (EC 4.2.1.16) (THREONINE DEAMINASE).//3.70E-43//318aa//37%//P05792
- 55 C-NT2RP3002529//Homo sapiens mRNA for leucocyte vacuolar protein sorting.//0//2276bp//99%//AJ133421
- C-NT2RP3002566
- C-NT2RP3002587
- C-NT2RP3002590
- C-NT2RP3002631

- C-NT2RP3002650//"Mus musculus growth suppressor 1L (Gros1) mRNA, complete cds."./0//2109bp//87%//AF165163
- C-NT2RP3002663//"Homo sapiens putative glycolipid transfer protein mRNA, complete cds."./8.10E-263//1243bp//97%//AF103731
- 5 C-NT2RP3002671//ELONGATION FACTOR 2 (EF-2)./2.50E-73//179aa//36%//P13060
- C-NT2RP3002763
- C-NT2RP3002861
- C-NT2RP3002911
- C-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN)./2E-111//551aa//42%//Q04652
- 10 C-NT2RP3002953//"Homo sapiens protocadherin beta 5 (PCDH-beta5) mRNA, complete cds."./0//2388bp//99%//AF152498
- C-NT2RP3002988//"Homo sapiens Ikb kinase-b (IKK-beta) mRNA, complete cds."./1.8E-292//1325bp//99%//AF080158
- C-NT2RP3003008
- 15 C-NT2RP3003101//"Mouse mRNA for tetracycline transporter-like protein, complete cds."./3.6E-83//807bp//72%//D88315
- C-NT2RP3003204
- C-NT2RP3003278
- C-NT2RP3003282//"Homo sapiens dynamin (DNM) mRNA, complete cds."./0//2596bp//98%//L36983
- 20 C-NT2RP3003290//"Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds."./1.5E-310//1468bp//82%//AB033922
- C-NT2RP3003302
- C-NT2RP3003313//"Homo sapiens thyroid hormone receptor-associated protein complex component TRAP80 mRNA, complete cds."./0//2476bp//99%//AF117657
- 25 C-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (R052)./1.3E-35//178aa//44%//Q62191
- C-NT2RP3003344
- C-NT2RP3003353//HYPOTHETICAL 26.2 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION./2.80E-07//161aa//28%//P40084
- 30 C-NT2RP3003377
- C-NT2RP3003385//"Mus musculus SKD3 mRNA, complete cds."./0//2133bp//85%//U09874
- C-NT2RP3003433
- C-NT2RP3003490//"Homo sapiens mRNA for KIAA0725 protein, partial cds."./0//2437bp//99%//AB018268
- 35 C-NT2RP3003491//"Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds."./5.6E-36//842bp//62%//AF091624
- C-NT2RP3004206//CROOKED NECK PROTEIN./1.4E-220//567aa//67%//P17886
- C-NT2RP3004207//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene)./0//2445bp//100%//AJ245820
- 40 C-NT2RP3004209//"Homo sapiens ubiquitin processing protease (Ubp-M) mRNA, complete cds."./0//2320bp//99%//AF126736
- C-NT2RP3004242//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-CIOGENITAL DYSPLASIA PROTEIN HOMOLOG)./4.7E-13//118aa//33%//P52734
- C-NT2RP3004246
- 45 C-NT2RP3004258//"Homo sapiens ZIS1 mRNA, complete cds."./0//1861bp//99%//AF065391
- C-NT2RP3004262//"Homo sapiens heat shock protein hsp40-3 mRNA, complete cds."./2.4E-248//1126bp//100%//AF088982
- C-NT2RP3004341
- C-NT2RP3004378
- 50 C-NT2RP3004424//Homo sapiens mRNA for stromal antigen 3 (STAG3 gene)./1E-66//364bp//93%//AJ007798
- C-NT2RP3004428
- C-NT2RP3004451
- C-NT2RP3004454//"Homo sapiens mRNA for KIAA0448 protein, complete cds."./0//2875bp//99%//AB007917
- 55 C-NT2RP3004472//GERM CELL-LESS PROTEIN./1.6E-61//170aa//40%//Q01820
- C-NT2RP3004498//"Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds."./2E-249//1777bp//80%//U83176
- C-NT2RP3004504//M.musculus mRNA for CPEB protein./1.9E-295//893bp//92%//Y08260

- C-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1)//3.7E-37//190aa//39%//P40484
 C-NT2RP3004534//"Mouse oncogene (ect2) mRNA, complete cds."//01/2075bp//87%//L11316
 C-NT2RP4000528//NPL4 PROTEIN.//9.8E-86//515aa//37%//P33755
 5 C-NT2RP4000907//"Mouse NLR-1 mRNA for leucine-rich-repeat protein, complete cds."//01/2127bp//86%//U45913
 C-NT2RP4001029//"Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds."//01/1711bp//90%//U20086
 C-NT2RP4001336//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN//0.000016//186aa//29%//U24076
 10 C-NT2RP4001389//KES1 PROTEIN.//1.70E-31//342aa//34%//P35844
 C-NT2RP4001442
 C-NT2RP4001529//"Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds."//1.70E-255//1148bp//90%//U20086
 15 C-NT2RP4001656//VACUOLAR BIOGENESIS PROTEIN END1 (PEP5 PROTEIN)//1.10E-45//310aa//27%//P12868
 C-OVARC1000106//"TROPOMYOSIN 1, FUSION PROTEIN 33."//0.000032//165aa//27%//P49455
 C-OVARC1000198
 C-OVARC1000682//"PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B)."//1.1E-209//293aa//95%//P39098
 20 C-OVARC1000703
 C-OVARC1000722//"Homo sapiens chromosome 1q21-q23 beta-1,4-galactosyltransferase mRNA, complete cds."//01/759bp//98%//AF038661
 C-OVARC1000730
 C-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN.//0.00000017//78aa//48%//P25159
 25 C-OVARC1000781
 C-OVARC1000787
 C-OVARC10008347//Homo sapiens mRNA for atopy related autoantigen CALCJ.//2.8E-258//1183bp//99%//Y17711
 C-OVARC1000846//NUCLEOLIN (PROTEIN C23).//0.0000097//109aa//30%//P08199
 C-OVARC1000850//"Homo sapiens PB39 mRNA, complete cds."//01/2095bp//99%//AF045584
 30 C-OVARC1000862//M. musculus mRNA for FT1.//5.9E-226//1498bp//81%//Z67963
 C-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).//2.2E-50//206aa//52%//P40484
 C-OVARC1000883
 C-OVARC1000886
 C-OVARC1000912
 35 C-OVARC1000915//"Homo sapiens histone deacetylase 5 mRNA, complete cds."//1.60E-121//591bp//97%//AF132608
 C-OVARC1000924
 C-OVARC1000964
 C-OVARC1000984
 40 C-OVARC1001004
 C-OVARC1001010
 C-OVARC1001011
 C-OVARC1001032
 C-OVARC1001044
 45 C-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSOR.//1.9E-35//76aa//98%//P43490
 C-OVARC1001068//"Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds."//01/1819bp//99%//AF082657
 C-OVARC1001074
 C-OVARC1001092//"Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F185707 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))."//2E-214//769bp//97%//AJ005897
 50 C-OVARC1001107//"Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds."//6.1E-276//594bp//98%//AF167572
 C-OVARC1001154//"Homo sapiens clone 24720 epithelin 1 and 2 mRNA, complete cds."//2.3E-296//1561bp//93%//AF055008
 55 C-OVARC1001161
 C-OVARC1001167
 C-OVARC1001170

- C-OVARC1001171//"Homo sapiens translation initiation factor 3 47 kDa subunit mRNA, complete cds."
//5.7E-151//436bp//92%//U94855
- C-OVARC1001173
- C-OVARC1001176
- 5 C-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2.//1.1E-11//221aa//25%//P48510
- C-OVARC1001188
- C-OVARC1001232//"CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT)."//5.10E-22//83aa//37%//Q10568
- C-OVARC1001270
- 10 C-OVARC1001271//NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1).//0.0000014//224aa//26%//P25976
- C-OVARC1001306//N-MYC PROTO-ONCOGENE PROTEIN.//0.00000073//247aa//27%//P18444
- C-OVARC1001344
- C-OVARC1001369
- 15 C-OVARC1001372//"Homo sapiens mRNA for KIAA0897 protein, partial cds."//0//840bp//97%//AB020704
- C-OVARC1001391
- C-OVARC1001399
- C-OVARC1001417//"Homo sapiens thyroid hormone receptor-associated protein complex component TRAP170 mRNA, complete cds."//0//1715bp//99%//AF135802
- 20 C-OVARC1001419//"Homo sapiens GOK (STIM1) mRNA, complete cds."//4.9E-48//586bp//69%//U52426
- C-OVARC1001436//ENL PROTEIN.//0.0000009//81aa//39%//Q03111
- C-OVARC1001453
- 25 C-OVARC1001476//"Mus musculus YGR163w mRNA homologue, complete cds."//1.80E-187//510bp//89%//AB017616
- C-OVARC1001480
- C-OVARC1001489
- C-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE PROTEIN 1).//0//777aa//91%//P98161
- 30 C-OVARC1001525
- C-OVARC1001555//NGG1-INTERACTING FACTOR 3.//4.4E-19//130aa//40%//P53081
- C-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//0//1167bp//100%//AF031165
- 35 C-OVARC1001600
- C-OVARC1001610//"Homo sapiens choline/ethanolaminephosphotransferase (CEPT1) mRNA, complete cds."//0//1870bp//99%//AF068302
- C-OVARC1001702
- 40 C-OVARC1001703//"Mus musculus ARL-6 interacting protein-2 (Aip-2) mRNA, complete cds."//3.5E-16//399bp//61%//AF133670
- C-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).//2.80E-10//106aa//38%//Q62267
- C-OVARC1001713//ENDOPEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).//4.4E-40//195aa//41%//P07106
- 45 C-OVARC1001726//APICAL-LIKE PROTEIN (APXL PROTEIN).//4.3E-16//116aa//43%//Q13796
- C-OVARC1001731//"TROPOMYOSIN ALPHA CHAIN, FIBROBLAST ISOFORM F2."//4E-122//282aa//65%//P08942
- C-OVARC1001745
- C-OVARC1001762//"N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA-AMINO, ACETYLTRANSFERASE 1)."//6.4E-85//514aa//34%//P12945
- 50 C-OVARC1001766//"Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds."//0//963bp//99%//U97670
- C-OVARC1001767//"Homo sapiens mRNA for KIAA0675 protein, complete cds."//0//2083bp//99%//AB014575
- 55 C-OVARC1001768
- C-OVARC1001791
- C-OVARC1001795
- C-OVARC1001802

- C-OVARC1001809//"Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds."//2.7E-190//1624bp//76%//AF068748
- C-OVARC1001828
- C-OVARC1001846
- 5 C-OVARC1001861
- C-OVARC1001879
- C-OVARC1001880
- C-OVARC1001883
- C-OVARC1001916
- 10 C-OVARC1001928
- C-OVARC1001942//"N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA-AMINO, ACETYLTRANSFERASE 1)."//3.1E-81//497aa//35%//P12945
- C-OVARC1001943//"Mus musculus DEBT-91 mRNA, complete cds."//0//2035bp//87%//AF143859
- C-OVARC1001950
- 15 C-OVARC1001987//"Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds."//2.3E-220//652bp//84%//AF061817
- C-OVARC1002050//"Homo sapiens mRNA for actin binding protein ABP620, complete cds."//0//1019bp//99%//AB029290
- C-OVARC1002082
- 20 C-OVARC1002107
- C-OVARC1002127//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER 2 (BRAIN DIGOXIN CARRIER PROTEIN) (BRAIN-SPECIFIC ORGANIC ANION TRANSPORTER) (OATP-B1).//5.4E-52//306aa//35%//035913
- C-OVARC1002138//SAP1 PROTEIN.//7.6E-60//126aa//59%//P39955
- 25 C-OVARC1002156
- C-OVARC1002158
- C-PLACE100004//"Homo sapiens IDN3-B mRNA, complete cds."//0//2365bp//99%//AB019602
- C-PLACE1000040//TRANSFORMING PROTEIN P21/K-RAS 2B.//1.4E-17//185aa//32%//P08643
- C-PLACE1000048
- 30 C-PLACE1000050
- C-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//7.9E-54//190bp//94%//L22154
- C-PLACE100008//"Human SEC7 homolog Tic (TIC) mRNA, complete cds."//0//2077bp//99%//U63127
- C-PLACE1000094
- 35 C-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//1.8E-62//158aa//81%//P20290
- C-PLACE1000214
- C-PLACE1000236
- 40 C-PLACE1000246
- C-PLACE1000292
- C-PLACE1000308
- C-PLACE1000332
- C-PLACE1000453
- C-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.60E-47//207aa//46%//P51522
- 45 C-PLACE1000599
- C-PLACE1000610//MSN5 PROTEIN.//0.0000026//136aa//26%//P52918
- C-PLACE1000653//"Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds."//0//1992bp//99%//AF180371
- 50 C-PLACE1000656//"Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNc110F1857Q7 (RZPD Berlin))."//2.1E-277//1260bp//99%//AJ005896
- C-PLACE1000706//"Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds."//0//1366bp//99%//AF119043
- C-PLACE1000712
- 55 C-PLACE1000749
- C-PLACE1000769//"Homo sapiens CGI-18 protein mRNA, complete cds."//0//1985bp//98%//AF132952
- C-PLACE1000786//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-

CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//7.10E-09//59aa//47%//P52734
 C-PLACE1000849
 C-PLACE1000856//"Homo sapiens mRNA for KIAA0974 protein, partial cds."//0//1310bp//100%//
 AB023191
 5 C-PLACE1000931
 C-PLACE1000987//"Homo sapiens mRNA for KIAA0724 protein, complete cds."//0//1749bp//99%//
 AB018267
 C-PLACE1001010
 C-PLACE1001015
 10 C-PLACE1001024
 C-PLACE1001062//"Homo sapiens PAC clone DJ1049N15 from 7q31.2-7q32, complete sequence."//
 2.7E-32//470bp//71%//AC006020
 C-PLACE1001104
 C-PLACE1001168
 15 C-PLACE1001171//MYOTUBULARIN.//7.1E-84//198aa//73%//Q13496
 C-PLACE1001185//"Homo sapiens mRNA for KIAA0943 protein, partial cds."//0//1668bp//99%//
 AB023160
 C-PLACE1001238//"Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds."//
 2E-202//1333bp//80%//D14336
 20 C-PLACE1001280
 C-PLACE1001294//M.musculus GEG-154 mRNA.//4.3E-221//1057bp//78%//X71642
 C-PLACE1001304//"Homo sapiens zinc finger protein dp mRNA, complete cds."//0//2421bp//99%//
 AF153201
 C-PLACE1001311
 25 C-PLACE1001323
 C-PLACE1001351
 C-PLACE1001414
 C-PLACE1001440
 C-PLACE1001456
 30 C-PLACE1001517//"Homo sapiens gene for glycosylphosphatidylinositol anchor attachment 1 (GPA1),
 complete cds."//4.60E-112//392bp//87%//AB002137
 C-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1).//5.7E-130//244aa//99%//Q60809
 C-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.4E-118//429aa//48%//
 P51523
 35 C-PLACE1001634
 C-PLACE1001640
 C-PLACE1001672//PROBABLE AMINOTRANSFERASE T01B11.2 (EC 2.6.1.-).//4.3E-66//174aa//45%//P91408
 C-PLACE1001705
 C-PLACE1001716
 40 C-PLACE1001720
 C-PLACE1001745
 C-PLACE1001748//"Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds."//0//2602bp//99%//
 AF061243
 C-PLACE1001771//Homo sapiens mRNA for transient receptor potential protein
 45 TRP6.//0//2900bp//99%//AJ006276
 C-PLACE1001799
 C-PLACE1001845//"Mus musculus cyclin ania-6a mRNA, complete cds."//3.30E-31//925bp//62%//
 AF159159
 C-PLACE1001897
 50 C-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).//6.5E-58//112aa//100%//
 076094
 C-PLACE1002157
 C-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX COMPONENT
 SWI3) (TRANSCRIPTION FACTOR TYE2).//0.00005//179aa//23%//P32591
 55 C-PLACE1002227
 C-PLACE1002259
 C-PLACE1002319
 C-PLACE1002395//"Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds."//7.9E-

- 100//966bp//75%//AB030505
 C-PLACE1002477
 C-PLACE1002493//"Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds.
 "//1.7E-113//545bp//98%//AF042273
 5 C-PLACE1002500
 C-PLACE1002514
 C-PLACE1002532//HOMEODOMAIN PROTEIN DLX-5.//1.2E-152//289aa//96%//P70396
 C-PLACE1002537
 10 C-PLACE1002571//ACTIN-LIKE PROTEIN 13E.//5E-99//386aa//48%//P45890
 C-PLACE1002583//"GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2 PRECURSOR (GLUTAMATE
 RECEPTOR 6) (GLUR-6) (GLUTAMATE RECEPTOR BETA-2) (GLUR BETA-2) (FRAGMENT)."//5.6E-34//
 76aa//98%//P39087
 C-PLACE1002598//OLIGORIBONUCLEASE (EC 3.1.-.-).//5.5E-17//76aa//56%//P45340
 C-PLACE1002625
 15 C-PLACE1002655//ADSEVERIN (SCINDERIN)(SC).//2.5E-278//543aa//92%//Q28046
 C-PLACE1002768
 C-PLACE1002782//"Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds."//3.8E-43//
 385bp//77%//U50927
 20 C-PLACE1002816//HISTONE DEACETYLASE HDA1.//2.20E-48//217aa//46%//P53973
 C-PLACE1002853
 C-PLACE1002908//"Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds."//0//
 1654bp//99%//AB028600
 C-PLACE1002962
 C-PLACE1002968
 25 C-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4).//1.4E-78//496aa//37%//Q49091
 C-PLACE1003025
 C-PLACE1003027//"Homo sapiens mRNA for KIAA0516 protein, partial cds."//2.1e-314//1417bp//
 100%//AB011088
 C-PLACE1003044//"Homo sapiens mRNA for KIAA0829 protein, partial cds."//0//1382bp//96%//
 30 AB020636
 C-PLACE1003176
 C-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//4.9E-76//309aa//47%//
 Q15391
 C-PLACE1003256
 35 C-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN.//7.9E-22//70aa//47%//P21541
 C-PLACE1003343
 C-PLACE1003361
 C-PLACE1003366//"Homo sapiens otoferlin (OTOF) mRNA, complete cds."//1.4E-78//542bp//67%//
 AF107403
 40 C-PLACE1003373
 C-PLACE1003375
 C-PLACE1003394//"Sprague-Dawley (clone LRB13) RAB14 mRNA, complete cds."//2.30E-150//
 774bp//94%//M83680
 45 C-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//1.3E-40//278aa//36%//P40556
 C-PLACE1003454
 C-PLACE1003478
 C-PLACE1003516
 C-PLACE1003519//H.sapiens hnRNP-E2 mRNA.//5.1E-218//905bp//99%//X78136
 C-PLACE1003521//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//0.0000011//101aa//32%//
 50 Q09475
 C-PLACE1003528
 C-PLACE1003537//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHE-
 ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-
 NENT).//7.7E-68//404aa//33%//P32802
 55 C-PLACE1003566
 C-PLACE1003584
 C-PLACE1003593
 C-PLACE1003605//HAP5 TRANSCRIPTIONAL

ACTIVATOR.//0.00000023//82aa//35%//Q02516
 C-PLACE1003618
 C-PLACE1003638
 C-PLACE1003738//ZINC FINGER PROTEIN 135.//9.6E-118//350aa//46%//P52742
 5 C-PLACE1003760//"Homo sapiens tetraspanin TM4-A mRNA, complete cds."//5.2E-289//1313bp//97%//AF133423
 C-PLACE1003768
 C-PLACE1003795
 C-PLACE1003886
 10 C-PLACE1003888//"Homo sapiens mRNA for KIAA1092 protein, partial cds."//0//2057bp//99%//AB029015
 C-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE).//1.4E-243//584aa//74%//P17812
 C-PLACE1003915//"PROBABLE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19) (ARGININE- -TRNA LIGASE) (ARGRS) "//2.4E-108//581aa//40%//Q05506
 15 C-PLACE1004118
 C-PLACE1004256//"Mus musculus short coiled coil protein SCOCO (Scoc) mRNA, complete cds."//2E-93//960bp//76%//AF115778
 C-PLACE1004274
 C-PLACE1004284
 20 C-PLACE1005331
 C-PLACE1005739//Homo sapiens mRNA; cDNA DKFZp564A032 (from clone DKFZp564A032).//0//2190bp//99%//AL050267
 C-PLACE1005828
 25 C-PLACE1005876//"CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT)."//0//730aa//99%//Q10568
 C-PLACE1005890//BEM46 PROTEIN (FRAGMENT) //9.9E-42//224aa//43%//P54069
 C-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).//2E-28//236aa//30%//P98110
 30 C-PLACE1007053
 C-PLACE1007068
 C-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).//5.3E-26//309aa//30%//Q04652
 C-PLACE1009921
 35 C-PLACE1010401
 C-PLACE1010856
 C-PLACE1010857
 C-PLACE1010917
 C-PLACE1010925
 40 C-PLACE1010926//"Homo sapiens mRNA for KIAA0554 protein, partial cds."//0//1160bp//100%//AB011126
 C-PLACE1010942//"Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds."//0//1440bp//99%//AF114487
 C-PLACE1010944
 45 C-PLACE1010954
 C-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//5.3E-98//297aa//48%//P45890
 C-PLACE1011026
 C-PLACE1011046//"1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1 (EC 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PLC-154)."//0//646aa//97%//P10894
 50 C-PLACE1011054
 C-PLACE1011057
 C-PLACE101109//"ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)."//1.50E-22//63aa//88%//Q07803
 C-PLACE101114//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//2.9E-71//190aa//44%//Q03532
 55 C-PLACE1011133
 C-PLACE1011143
 C-PLACE1011165
 C-PLACE1011185//INSERTION ELEMENT IS1 PROTEIN INSB.//1.3E-89//167aa//100%//P03830

- C-PLACE1011219//PROBABLEOXIDOREDUCTASE (EC 1.-.-.-).//3.2E-12//1212aa//29%//Q03326
C-PLACE1011221
- C-PLACE1011263//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp5640043).//0//2487bp//99%//AL050390
- 5 C-PLACE1011325
C-PLACE1011332//"Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds."//7.2E-151//697bp//99%//AF102265
- C-PLACE1011340//"Homo sapiens IDN3-B mRNA, complete cds."//1.20E-74//380bp//97%//AB019602
- 10 C-PLACE1011399//"Homo sapiens CGI-72 protein mRNA, complete cds."//3.2E-90//427bp//99%//AF151830
- C-PLACE1011433//"Homo sapiens mRNA for KIAA0530 protein, partial cds."//0//1946bp//99%//AB011102
- C-PLACE1011452
- 15 C-PLACE1011465
C-PLACE1011472//"Homo sapiens mRNA for KIAA0712 protein, complete cds."//0//2022bp//99%//AB018255
- C-PLACE1011477//"Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds."//0//2040bp//99%//AF065482
- 20 C-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//4.90E-11//147aa//32%//P52178
- C-PLACE1011520
- C-PLACE1011563
- C-PLACE1011567
- 25 C-PLACE1011576//"Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds."//0//1791bp//82%//L11672
- C-PLACE1011586
- C-PLACE1011643
- C-PLACE1011649
- 30 C-PLACE1011664//CROOKED NECK PROTEIN.//1.6E-187//505aa//64%//P17886
- C-PLACE1011682
- C-PLACE1011719
- C-PLACE1011729
- C-PLACE1011858//Homo sapiens mRNA; cDNA DKFZp586C021 (from clone DKFZp586C021).//0//1490bp//99%//AL050287
- 35 C-PLACE1011874
C-PLACE1011875//"Homo sapiens mRNA for KIAA0580 protein, partial cds."//4.1E-112//524bp//100%//AB011152
- C-PLACE1011923//"Homo sapiens serum-inducible kinase mRNA, complete cds."//0//2782bp//99%//AF059617
- 40 C-PLACE1011982
C-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//2.6E-42//104aa//49%//Q09475
- C-PLACE2000015//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN).//1.1E-116//364aa//45%//P42566
- 45 C-PLACE2000017
C-PLACE2000021//"Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, complete cds."//2.7E-107//981bp//74%//AF082556
- C-PLACE2000047
- 50 C-PLACE2000062//"Homo sapiens mRNA for type II membrane protein similar to HIV gp120-binding C-type lectin, complete cds, clone:HP01347."//6.3E-166//656bp//94%//AB015629
- C-PLACE2000100
- C-PLACE2000111
- C-PLACE2000172
- 55 C-PLACE2000187
C-PLACE2000216//"Dog nonerythroid beta-spectrin mRNA, 3' end."//3.2E-253//1799bp//83%//L02897
- C-PLACE2000246//"Homo sapiens mRNA for KIAA0795 protein, partial cds."//4.60E-172//796bp//99%//AB018338

- C-PLACE2000317
 C-PLACE2000341//"Homo sapiens sodium-dependent multivitamin transporter (SMVT) mRNA, complete cds."//1554bp//99%//AF069307
 C-PLACE2000366
- 5 C-PLACE2000373//F-SPONDIN PRECURSOR.//8.6E-16//371aa//28%//P35446
 C-PLACE2000394
 C-PLACE2000398//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//6.3E-37//90aa//98%//P10586
- 10 C-PLACE2000411//"Homo sapiens mRNA for KIAA1037 protein, partial cds."//2515bp//99%//AB028960
 C-PLACE2000425
 C-PLACE2000427//PROBABLE HELICASE MOT1.//1.2E-26//200aa//27%//P32333
 C-PLACE2000433
- 15 C-PLACE2000438//"POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN- UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALACTOSAMINYLTRANSFERASE)(GALNAC-T1)."//2.1E-86//348aa//41%//Q10472
 C-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//2.5E-25//165aa//40%//P33450
- 20 C-PLACE2000477//"Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds."//6.7E-127//671bp//94%//AF072733
 C-PLACE3000009
 C-PLACE3000020//"Homo sapiens type III adenylyl cyclase (AC-III) mRNA, complete cds."//0//2253bp//99%//AF033861
 C-PLACE3000103
- 25 C-PLACE3000142
 C-PLACE3000145//TENSIN.//1E-108//277aa//75%//Q04205
 C-PLACE3000156
 C-PLACE3000157
 C-PLACE3000197
 C-PLACE3000208
- 30 C-PLACE3000226//"Homo sapiens mRNA for KIAA0962 protein, partial cds."//0//4805bp//99%//AB023179
 C-PLACE3000242//"Homo sapiens mRNA for KIAA1114 protein, complete cds."//0//2786bp//96%//AB029037
- 35 C-PLACE3000363
 C-PLACE3000405
 C-PLACE3000416//"Homo sapiens mRNA for actin binding protein ABP620, complete cds."//1.80E-141//565bp//98%//AB029290
 C-PLACE3000477
- 40 C-PLACE4000106//"Homo sapiens mRNA for KIAA0462 protein, partial cds."//0//6702bp//99%//AB007931
 C-PLACE4000323
 C-PLACE4000326//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1).//8.10E-24//319aa//31%//P30771
- 45 C-PLACE4000369//"Homo sapiens mRNA for KIAA1025 protein, partial cds."//0//4830bp//99%//AB028948
 C-PLACE4000445//Homo sapiens mRNA; cDNA DKFZp434C212 (from clone DKFZp434C212).//0//2565bp//99%//AL080196
 C-PLACE4000558//"Homo sapiens mRNA for KIAA0729 protein, partial cds."//0//1051bp//97%//AB018272
- 50 C-PLACE4000581//FIBROPELIN I PRECURSOR (EPIDERMAL GROWTH FACTOR-RELATED PROTEIN 1) (UEGF-1).//9.3E-70//226aa//52%//P10079
 C-PLACE4000593
 C-PLACE4000612//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//7.1E-154//340aa//40%//P21414
- 55 C-PLACE4000670
 C-THYRO1000026
 C-THYRO1000085//"PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B."//2E-72//155aa//92%//

Q06710
 C-THYRO1000107
 C-THYRO1000111
 C-THYRO1000132//"Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA,
 5 complete cds."://1.1E-158//824bp//95%//U97018
 C-THYRO1000156
 C-THYRO1000173//"Homo sapiens AP-mu chain family member mu1B (HSMU1B) mRNA, complete cds.
 "://0//1713bp//99%//AF020797
 C-THYRO1000186
 10 C-THYRO1000187
 C-THYRO1000241
 C-THYRO1000279
 C-THYRO1000327//"Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds."
 //0//1567bp//99%//AF124145
 15 C-THYRO1000452
 C-THYRO1000471
 C-THYRO1000484
 C-THYRO1000502
 C-THYRO1000505
 20 C-THYRO1000585//"Homo sapiens protein associated with Myc mRNA, complete cds."://0//1901bp//
 99%//AF075587
 C-THYRO1000596
 C-THYRO1000662//"Homo sapiens XPV mRNA for DNA polymerase eta, complete cds."://0//2341 bp//
 99%//AB024313
 25 C-THYRO1000666//Mus musculus mRNA for kinesin like protein 9.//0//2001bp//86%//AJ132889
 C-THYRO1000715
 C-THYRO1000734
 C-THYRO1000748//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//3.30E-96//335aa//52%//
 P98171
 30 C-THYRO1000756//"ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (EC
 2.4.99.-) (ST6GALNACII) (STY) "://1.8E-55//243aa//42%//Q64686
 C-THYRO1000777
 C-THYRO1000783//"Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete
 cds."://2.4E-157//1656bp//70%//U37373
 35 C-THYRO1000787
 C-THYRO1000793
 C-THYRO1000796
 C-THYRO1000843
 C-THYRO1000852//"Human branched chain aminotransferase precursor (BCATm) mRNA, nuclear gene en-
 40 coding mitochondrial protein, complete cds."://3.3E-147//790bp//93%//U68418
 C-THYRO1000865
 C-THYRO1000895
 C-THYRO1000926//"Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.
 "://0//2387bp//99%//AF079529
 45 C-THYRO1000951//DIHYDROXYACETONE KINASE 2 (EC 2.7.1.29) (GLYCERONE KINASE).//5E-83//566aa//
 37%//P43550
 C-THYRO1000952
 C-THYRO1000983//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN
 LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//6.30E-17//143aa//39%//P35132
 50 C-THYRO1001003//UBIQUITIN-CONJUGATING ENZYME E2-21.2 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN
 LIGASE) (UBIQUITIN CARRIER PROTEIN).//5.90E-14//84aa//41%//P52491
 C-THYRO1001031
 C-THYRO1001062
 C-THYRO1001100//ZINC FINGER X-LINKED PROTEIN ZXDA (FRAGMENT).//1.2E-67//245aa//62%//P98168
 55 C-THYRO1001133
 C-THYRO1001134//"Homo sapiens CGI-78 protein mRNA, complete cds."://0//1898bp//99%//
 AF151835
 C-THYRO1001173

C-THYRO1001213
 C-THYRO1001321
 C-THYRO1001322
 C-THYRO1001365
 5 C-THYRO1001401
 C-THYRO1001411
 C-THYRO1001434
 C-THYRO1001534
 10 C-THYRO1001541
 C-THYRO1001559
 C-THYRO1001570
 C-THYRO1001595
 C-THYRO1001605
 C-THYRO1001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//0//1784bp//
 15 99%//AJ002190
 C-THYRO1001656//"Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds."//4.1E-
 273//1947bp//82%//AF175968
 C-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//0//1820bp//99%//
 AJ225089
 20 C-THYRO1001673
 C-THYRO1001703//NIFR3-LIKE PROTEIN.//2.90E-32//282aa//32%//P45672
 C-THYRO1001706
 C-THYRO1001738//TUBULIN-TYROSINE LIGASE (EC 6.3.2.25) (TTL).//2.4E-20//217aa//30%//P38584
 C-THYRO1001745
 25 C-THYRO1001793
 C-THYRO1001809//MYOCYTE NUCLEAR FACTOR (MNF).//1.4E-74//158aa//89%//P42128
 C-THYRO1001895
 C-THYRO1001907
 C-VESEN1000122
 30 C-Y79AA1000037//DNA-BINDING PROTEIN BMI-1.//2.4E-30//80aa//60%//P25916
 C-Y79AA1000059//"Homo sapiens immunophilin homolog ARA9 mRNA, complete cds."//2.9E-70//
 1040bp//65%//U78521
 C-Y79AA1000065
 C-Y79AA1000131
 35 C-Y79AA1000181//"Homo sapiens CGI-01 protein mRNA, complete cds."//0//1858bp//99%//
 AF132936
 C-Y79AA1000202
 C-Y79AA1000214//"Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds."//7.1E-71//
 345bp//100%//AF081192
 40 C-Y79AA1000230
 C-Y79AA1000258
 C-Y79AA1000268//"Mus musculus Nip21 mRNA, complete cds."//2.10E-50//648bp//64%//AF035207
 C-Y79AA1000313//CALPHOTIN.//0.000011//336aa//23%//Q02910
 C-Y79AA1000332//SEL-10 PROTEIN.//0.000000067//219aa//25 %//Q93794
 45 C-Y79AA1000355
 C-Y79AA1000368//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//4E-20//261 aa//27%//P25343
 C-Y79AA1000420
 C-Y79AA1000469//"Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, com-
 plete cds."//8.30E-252//1207bp//85%//U41736
 50 C-Y79AA1000480
 C-Y79AA1000540
 C-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE
 CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA
 C SUBUNIT).//0//652aa//98%//P17427
 55 C-Y79AA1000574//Homo sapiens clone H17 unknown mRNA.//0//1932bp//99%//AF103801
 C-Y79AA1000627//"Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds."//2E-287//203
 1bp//82%//AF060503
 C-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1.//5.80E-254//1477bp//84%//X69942

- C-Y79AA1000734//"Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds."//0//1594bp//99%//AF093670
- C-Y79AA1000748//"Homo sapiens CGI-05 protein mRNA, complete cds."//1.9E-239//1367bp//91%//AF152097
- 5 C-Y79AA1000752//"PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//4.9E-91//200aa//64%//Q61990
- C-Y79AA1000774
- C-Y79AA1000782//"CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3E-37//469aa//27%//P49902
- 10 C-Y79AA1000784//"Homo sapiens RanBP7/importin 7 mRNA, complete cds."//1.10E-236//1076bp//99%//AF098799
- C-Y79AA1000794//"Homo sapiens actin-associated protein 2E4/kaptn (2E4) mRNA, 2E4-1 allele, complete cds."//0//1610bp//99%//AF105369
- C-Y79AA1000800//"Homo sapiens putative secreted protein (ZS1G1) mRNA, complete cds."//1.6E-284//1288bp//99%//AF072733
- 15 C-Y79AA1000805
- C-Y79AA1000824
- C-Y79AA1000833//"TUBULIN ALPHA-1 CHAIN.//5E-173//220aa//79%//P05209
- C-Y79AA1000850
- C-Y79AA1000962//"MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II)."//4.2E-17//1430aa//27%//Q99323
- 20 C-Y79AA1000968//"Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds."//3.9E-248//1468bp//87%//U38253
- C-Y79AA1000976
- C-Y79AA1001023
- 25 C-Y79AA1001041
- C-Y79AA1001048//"ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD)."//3.1E-138//583aa//47%//P45953
- C-Y79AA1001077
- C-Y79AA1001078
- 30 C-Y79AA1001145
- C-Y79AA1001177
- C-Y79AA1001185
- C-Y79AA1001211//"Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds."//0//1435bp//99%//AF139658
- 35 C-Y79AA1001228
- C-Y79AA1001233//"ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HYDROXYSTEROID DEHYDROGENASE 1).//7.7E-50//228aa//42%//P51657
- C-Y79AA1001236//"Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc1101133Q7 (RZPD Berlin))."//0//1653bp//99%//AJ005892
- 40 C-Y79AA1001281
- C-Y79AA1001312//"ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46).//0.000000023//193aa//30%//Q03309
- C-Y79AA1001323//"Mus musculus mRNA for GSG1, complete cds."//3.3E-172//1171bp//83%//D87325
- 45 C-Y79AA1001391//"HOMEBOX PROTEIN HOX-A13 (HOX-1J).//1.2E-58//178aa//66%//P31271
- C-Y79AA1001394//"CELL DIVISION PROTEIN FTSH HOMOLOG (EC 3.4.24.-).//1.2E-13//230aa//32%//O83746
- C-Y79AA1001402//"Homo sapiens paraneoplastic cancer-testis-brain antigen (MA4) mRNA, partial cds."//8.50E-65//784bp//62%//AF083115
- 50 C-Y79AA1001493//"UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//3.80E-18//151aa//38%//P35132
- C-Y79AA1001533//"Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds."//4.5E-193//1333bp//80%//D14336
- C-Y79AA1001541
- C-Y79AA1001548//"PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//7.5E-76//85aa//90%//P42356
- 55 C-Y79AA1001555
- C-Y79AA1001581//"ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL-AC-TIVATING ENZYME).//1.9E-40//482aa//27%//P27550

C-Y79AA1001585
 C-Y79AA1001603//"POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PRO-
 TEIN- UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALAC-
 TOSAMINYLTRANSFERASE) (GALNAC-T1)."./1.7E-84//313aa//48%//Q07537
 5 C-Y79AA1001613//ZINC FINGER PROTEIN 132./3.8E-91//209aa//41%//P52740
 C-Y79AA1001665
 C-Y79AA1001679//"Homo sapiens lambda-crystallin mRNA, complete cds."./3.4E-310//1430bp//98%//
 AF077049
 10 C-Y79AA1001696//"Homo sapiens mRNA for KIAA1109 protein, partial cds."./0//1669bp//100%//
 AB029032
 C-Y79AA1001705//"Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds.
 "./3.4E-47//626bp//68%//AF033120
 C-Y79AA1001711//"Human 60-kdal ribonucleoprotein (Ro) mRNA, complete cds."./1.2E-258//
 15 1185bp//99%//J04137
 C-Y79AA1001781
 C-Y79AA1001805
 C-Y79AA1001827//"Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA, com-
 plete cds."./0//1689bp//98%//AF177145
 C-Y79AA1001846
 20 C-Y79AA1001923
 C-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE
 SPAC10F6.02C./1E-10//94aa//47%//O42643
 C-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN
 LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42)./9.9E-39//143aa//52%//P42743
 25 C-Y79AA1002083//H.sapiens mRNA for MUF1 protein./5E-163//752bp//99%//X86018
 C-Y79AA1002089
 C-Y79AA1002115
 C-Y79AA1002125
 C-Y79AA1002204
 30 C-Y79AA1002208//ANKYRIN./8.1E-34//188aa//38%//Q02357
 C-Y79AA1002209//"Homo sapiens CGI-04 protein mRNA, complete cds."./0//1617bp//99%//
 AF132939
 C-Y79AA1002229//DNA CROSS-LINK REPAIR PROTEIN PSO2/SNM1./7.10E-17//213aa//31%//P30620
 C-Y79AA1002246//SYNAPTOTAGMIN V./1.6E-28//286aa//32%//000445
 35 C-Y79AA1002298
 C-Y79AA1002307//"Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds."./0//1209bp//99%//
 AF116574
 C-Y79AA1002311//R.norvegicus mRNA for cytosolic reseniferatoxin-binding protein./2.9E-186//1130bp//82%//
 X67877
 40 C-Y79AA1002351
 C-Y79AA1002407
 C-Y79AA1002433//"Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit
 mRNA, complete cds."./0//1545bp//96%//AF152961
 C-Y79AA1002472//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)./1.5E-136//472aa//
 45 49%//Q05481

Homology Search Result Data 13.

[0333] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequenc-
 es. Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology,
 and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.

C-HEMBA1000042
 C-HEMBA1000141//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds./0//1135bp//100%//
 55 AF196304
 C-HEMBA1000150//H.sapiens gene for U5 snRNP-specific 200kD protein./2.50E-153//525bp//91%//Z70200
 C-HEMBA1000213
 C-HEMBA1000243

C-HEMBA1000244
 C-HEMBA1000251
 C-HEMBA1000338
 C-HEMBA1000357
 5 C-HEMBA1000376
 C-HEMBA1000428
 C-HEMBA1000469
 C-HEMBA1000497
 10 C-HEMBA1000561//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF 10) (HPF7).//3.40E-37//674aa//
 25%/Q05481
 C-HEMBA1000569//GPI-ANCHORED PROTEIN P137.//6.50E-19//265aa//32%/Q60865
 C-HEMBA1000575
 C-HEMBA1000591//PTB-ASSOCIATED SPLICING FACTOR (PSF).//2.20E-17//198aa//40%/P23246
 15 C-HEMBA1000673
 C-HEMBA1000702
 C-HEMBA1000722
 C-HEMBA1000726
 C-HEMBA1000876
 C-HEMBA1000942
 20 C-HEMBA1000943
 C-HEMBA1000960
 C-HEMBA1000985
 C-HEMBA1001019//CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.-) (P34 PROTEIN KINASE)
 (CYCLIN-DEPENDENT KINASE 1) (CDK1).//3.10E-10//70aa//58%/P06493
 25 C-HEMBA1001020
 C-HEMBA1001024
 C-HEMBA1001026
 C-HEMBA1001051
 C-HEMBA1001060
 30 C-HEMBA1001071//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSORS.//1.50E-92//82aa//100%/P02461
 C-HEMBA1001077//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.//2.00E-80//
 432bp//94%/AF119043
 C-HEMBA1001099
 C-HEMBA1001121
 35 C-HEMBA1001123
 C-HEMBA1001208
 C-HEMBA1001213
 C-HEMBA1001226
 C-HEMBA1001247
 40 C-HEMBA1001299
 C-HEMBA1001319
 C-HEMBA1001323
 C-HEMBA1001327
 C-HEMBA1001361
 45 C-HEMBA1001375
 C-HEMBA1001377
 C-HEMBA1001383
 C-HEMBA1001391
 C-HEMBA1001411
 50 C-HEMBA1001432
 C-HEMBA1001433
 C-HEMBA1001435
 C-HEMBA1001442
 C-HEMBA1001463
 55 C-HEMBA1001515
 C-HEMBA1001522
 C-HEMBA1001557
 C-HEMBA1001566

C-HEMBA1001589
 C-HEMBA1001608
 C-HEMBA1001636
 C-HEMBA1001647
 5 C-HEMBA1001651
 C-HEMBA1001658
 C-HEMBA1001675//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.//5.40E-09//101aa//35%//
 P54787
 C-HEMBA1001712
 10 C-HEMBA1001734//CADHERIN-11 PRECURSOR (OSTEOBLAST-CADHERIN) (OB-CADHERIN) (OSF-4).//
 1.10E-38//87aa//96%//P55288
 C-HEMBA1001745
 C-HEMBA1001750
 C-HEMBA1001784
 15 C-HEMBA1001791
 C-HEMBA1001803
 C-HEMBA1001820
 C-HEMBA1001835
 C-HEMBA1001888
 20 C-HEMBA1001912
 C-HEMBA1001915
 C-HEMBA1001918
 C-HEMBA1001940
 C-HEMBA1001942
 25 C-HEMBA1001964
 C-HEMBA1002022
 C-HEMBA1002039
 C-HEMBA1002100
 C-HEMBA1002113
 30 C-HEMBA1002119
 C-HEMBA1002139//LIM AND SH3 DOMAIN PROTEIN LASP-1 (MLN 50).//7.10E-05//51aa//49%//Q14847
 C-HEMBA1002160
 C-HEMBA1002162
 C-HEMBA1002166
 35 C-HEMBA1002185
 C-HEMBA1002204
 C-HEMBA1002328
 C-HEMBA1002337
 C-HEMBA1002348
 40 C-HEMBA1002381
 C-HEMBA1002486
 C-HEMBA1002498
 C-HEMBA1002538
 C-HEMBA1002552
 45 C-HEMBA1002555//Homo sapiens mSin3A associated polypeptide p30 mRNA, complete cds.//5.30E-51//768bp//
 68%//AF055993
 C-HEMBA1002558
 C-HEMBA1002621
 C-HEMBA1002629
 50 C-HEMBA1002645
 C-HEMBA1002659
 C-HEMBA1002661
 C-HEMBA1002666
 C-HEMBA1002678
 55 C-HEMBA1002679
 C-HEMBA1002712
 C-HEMBA1002716
 C-HEMBA1002742

C-HEMBA1002746//DNA POLYMERASE BETA (EC 2.7.7.7).//5.00E-37//268aa//34%//P06746
 C-HEMBA1002748
 C-HEMBA1002780
 C-HEMBA1002801
 5 C-HEMBA1002826
 C-HEMBA1002833
 C-HEMBA1002921
 C-HEMBA1002934
 10 C-HEMBA1002944
 C-HEMBA1002968
 C-HEMBA1003034
 C-HEMBA1003037
 C-HEMBA1003071//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN
 15 PRECURSOR (ALS).//1.30E-09//121aa//40%//P35858
 C-HEMBA1003078
 C-HEMBA1003083
 C-HEMBA1003086
 C-HEMBA1003098//Homo sapiens NY-REN-6 antigen mRNA, partial cds.//6.20E-273//1253bp//99%//AF155096
 20 C-HEMBA1003133
 C-HEMBA1003142
 C-HEMBA1003166
 C-HEMBA1003197
 C-HEMBA1003202
 C-HEMBA1003220
 25 C-HEMBA1003229
 C-HEMBA1003276
 C-HEMBA1003278
 C-HEMBA1003328
 C-HEMBA1003373
 30 C-HEMBA1003597
 C-HEMBA1003598
 C-HEMBA1003656
 C-HEMBA1003680//PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-).//2.40E-92//
 423aa//47%//P34629
 35 C-HEMBA1003733
 C-HEMBA1003742
 C-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN)
 (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//3.70E-124//347aa//55%//Q16665
 40 C-HEMBA1003803
 C-HEMBA1003854
 C-HEMBA1003926
 C-HEMBA1003939
 C-HEMBA1003987
 C-HEMBA1004012
 45 C-HEMBA1004015
 C-HEMBA1004193
 C-HEMBA1004225
 C-HEMBA1004241
 C-HEMBA1004267
 50 C-HEMBA1004295//Homo sapiens NY-REN-25 antigen mRNA, partial cds.//9.40E-31//381bp//65%//AF155103
 C-HEMBA1004354//CHL1 PROTEIN.//9.90E-26//130aa//42%//P22516
 C-HEMBA1004356//H. sapiens MSSP-2 mRNA.//3.00E-243//573bp//98%//X77494
 C-HEMBA1004396
 55 C-HEMBA1004405
 C-HEMBA1004433
 C-HEMBA1004538
 C-HEMBA1004542
 C-HEMBA1004573

C-HEMBA1004577
 C-HEMBA1004604//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.//0//1612bp//99%//AF193844
 C-HEMBA1004617
 C-HEMBA1004631
 5 C-HEMBA1004705
 C-HEMBA1004733
 C-HEMBA1004748
 C-HEMBA1004778
 10 C-HEMBA1004803
 C-HEMBA1004807
 C-HEMBA1004820
 C-HEMBA1004865
 C-HEMBA1004880
 C-HEMBA1004900
 15 C-HEMBA1004909
 C-HEMBA1004960
 C-HEMBA1004978
 C-HEMBA1004980
 C-HEMBA1004983
 20 C-HEMBA1004995
 C-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0//2212bp//99%//AB014548
 C-HEMBA1005029//Homo sapiens CGI-13 protein mRNA, complete cds.//0//1487bp//99%//AF132947
 C-HEMBA1005035
 C-HEMBA1005039
 25 C-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16).//3.40E-101//106aa//98%//P35290
 C-HEMBA1005050
 C-HEMBA1005062
 C-HEMBA1005066
 C-HEMBA1005075
 30 C-HEMBA1005079
 C-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//0//2762bp//99%//
 AF080561
 C-HEMBA1005123
 C-HEMBA1005149
 35 C-HEMBA1005152
 C-HEMBA1005201//Homo sapiens CGI-07 protein mRNA, complete cds.//0//1608bp//99%//AF132941
 C-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.90E-179//361aa//95%//
 Q00004
 C-HEMBA1005223
 40 C-HEMBA1005232
 C-HEMBA1005241
 C-HEMBA1005275
 C-HEMBA1005293
 C-HEMBA1005311
 45 C-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial.//3.90E-241//1095bp//99%//AJ007581
 C-HEMBA1005359//ZINC FINGER PROTEIN 137.//3.90E-85//206aa//69%//P52743
 C-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds.//9.00E-77//620bp//74%//
 AF071787
 C-HEMBA1005374
 50 C-HEMBA1005382
 C-HEMBA1005411
 C-HEMBA1005426
 C-HEMBA1005443
 C-HEMBA1005447
 55 C-HEMBA1005497
 C-HEMBA1005500
 C-HEMBA1005506
 C-HEMBA1005508

C-HEMBA1005526
 C-HEMBA1005530//Homo sapiens anaphase-promoting complex subunit 7 (APC7) mRNA, complete cds.//0//
 1578bp//98%//AF191340
 C-HEMBA1005548//Homo sapiens MAFB/Kreisler basic region/leucine zipper transcription factor (MAFB) mRNA,
 5 complete cds.//1.00E-220//1014bp//99%//AF134157
 C-HEMBA1005552
 C-HEMBA1005568
 C-HEMBA1005588
 10 C-HEMBA1005593
 C-HEMBA1005606
 C-HEMBA1005616
 C-HEMBA1005627
 C-HEMBA1005670
 C-HEMBA1005679
 15 C-HEMBA1005699
 C-HEMBA1005705
 C-HEMBA1005732//Human mRNA for KIAA1293 gene, complete cds.//5.50E-102//317bp//98%//D14697
 C-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM ACTIVATED NEU-
 20 TRAL PROTEINASE) (CANP) (MU//M-TYPE).//2.00E-36//342aa//33%//P00789
 C-HEMBA1005852
 C-HEMBA1005894
 C-HEMBA1005921
 C-HEMBA1006035
 C-HEMBA1006036
 25 C-HEMBA1006090
 C-HEMBA1006138
 C-HEMBA1006173
 C-HEMBA1006252
 C-HEMBA1006268//Homo sapiens HQ0024c mRNA, complete cds.//3.50E-157//845bp//92%//AF073836
 30 C-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.60E-130//332aa//62%//I002193
 C-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//3.50E-105//381aa//54%//P28160
 C-HEMBA1006380
 C-HEMBA1006416
 C-HEMBA1006421
 35 C-HEMBA1006424
 C-HEMBA1006426
 C-HEMBA1006446
 C-HEMBA1006485//PUROMYCIN-SENSITIVE AMINOPEPTIDASE (EC 3.4.11.-) (PSA).//1.90E-81//153aa//
 97%//P55786
 40 C-HEMBA1006486
 C-HEMBA1006494
 C-HEMBA1006546
 C-HEMBA1006562
 C-HEMBA1006595
 45 C-HEMBA1006597
 C-HEMBA1006631
 C-HEMBA1006639
 C-HEMBA1006652//60S RIBOSOMAL PROTEIN L7.//2.40E-44//206aa//47%//P14148
 C-HEMBA1006659
 50 C-HEMBA1006665
 C-HEMBA1006676
 C-HEMBA1006695
 C-HEMBA1006709
 C-HEMBA1006758//Homo sapiens protocadherin beta 13 (PCDH-beta13) mRNA, complete cds.//0//1832bp//
 91%//AF152492
 55 C-HEMBA1006780
 C-HEMBA1006807//Homo sapiens mRNA for SPON.//5.70E-125//1109bp//75%//AJ000644
 C-HEMBA1006824

C-HEMBA1006865
 C-HEMBA1006921
 C-HEMBA1006949
 5 C-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2,3-sialyltransferase.//1.90E-80//
 447bp//89%//X74570
 C-HEMBA1007051
 C-HEMBA1007052
 C-HEMBA1007066
 10 C-HEMBA1007073
 C-HEMBA1007078
 C-HEMBA1007085
 C-HEMBA1007113
 C-HEMBA1007121//Homo sapiens bisphosphate 3'-nucleotidase mRNA, complete cds.//1.70E-252//1118bp//
 92%//AF125042
 15 C-HEMBA1007129
 C-HEMBA1007147
 C-HEMBA1007151//Homo sapiens synphilin 1 mRNA, complete cds.//0//1900bp//99%//AF076929
 C-HEMBA1007178
 C-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds.//0//1212bp//98%//D86987
 20 C-HEMBA1007224//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1590bp//99%//
 AF196304
 C-HEMBA1007243//Chinese hamster hpert mRNA, complete cds.//2.00E-58//650bp//70%//J00060
 C-HEMBA1007251
 C-HEMBA1007288
 25 C-HEMBA1007322
 C-HEMBA1007341
 C-HEMBA1000050
 C-HEMBA1000054
 C-HEMBA1000059
 30 C-HEMBA1000089
 C-HEMBA1000113
 C-HEMBA1000144//GUANYLATE CYCLASE ACTIVATING PROTEIN 2 (GCAP 2) (RETINAL GUANYLYL CYCLA-
 SE ACTIVATOR PROTEIN P24).//1.40E-24//71aa//77%//P51177
 C-HEMBA1000173
 35 C-HEMBA1000175
 C-HEMBA1000272
 C-HEMBA1000317//FIBULIN-1, ISOFORM D PRECURSOR.//7.10E-62//458aa//35%//P37888
 C-HEMBA1000318
 C-HEMBA1000336
 40 C-HEMBA1000341
 C-HEMBA1000343
 C-HEMBA1000354
 C-HEMBA1000374
 C-HEMBA1000434
 45 C-HEMBA1000441
 C-HEMBA1000491
 C-HEMBA1000493
 C-HEMBA1000510
 C-HEMBA1000652
 50 C-HEMBA1000672
 C-HEMBA1000684
 C-HEMBA1000709
 C-HEMBA1000726
 C-HEMBA1000770
 55 C-HEMBA1000827
 C-HEMBA1000831
 C-HEMBA1000883
 C-HEMBA1000888

C-HEMBB1000893
 C-HEMBB1000913
 C-HEMBB1000996
 C-HEMBB1001004
 5 C-HEMBB1001047
 C-HEMBB1001060
 C-HEMBB1001114
 C-HEMBB1001119
 C-HEMBB1001133
 10 C-HEMBB1001142
 C-HEMBB1001177
 C-HEMBB1001208
 C-HEMBB1001209
 C-HEMBB1001249
 15 C-HEMBB1001253
 C-HEMBB1001254
 C-HEMBB1001271
 C-HEMBB1001304
 C-HEMBB1001317
 20 C-HEMBB1001348
 C-HEMBB1001394
 C-HEMBB1001410
 C-HEMBB1001424
 C-HEMBB1001426
 25 C-HEMBB1001429//Homo sapiens leucine aminopeptidase mRNA, complete cds.//0//1933bp//99%//AF061738
 C-HEMBB1001436
 C-HEMBB10014437//Rattus norvegicus pyruvate dehydrogenase phosphatase isoenzyme 1 mRNA, complete
 cds.//3.00E-130//553bp//86%//AF062740
 30 C-HEMBB1001449
 C-HEMBB1001458
 C-HEMBB1001521
 C-HEMBB1001531
 C-HEMBB1001535
 C-HEMBB1001536
 35 C-HEMBB1001564
 C-HEMBB1001565
 C-HEMBB1001585
 C-HEMBB1001588
 C-HEMBB1001603
 40 C-HEMBB1001618
 C-HEMBB1001635
 C-HEMBB1001653
 C-HEMBB1001668
 C-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//0//2035bp//99%//AB014546
 45 C-HEMBB1001685
 C-HEMBB1001695
 C-HEMBB1001707
 C-HEMBB1001735
 50 C-HEMBB1001736//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 (EIF3 P116) (EIF3
 P110).//4.60E-15//391aa//25%//P55884
 C-HEMBB1001747
 C-HEMBB1001749//TRANSCRIPTIONAL ACTIVATOR GCN5.//1.70E-16//84aa//47%//Q03330
 C-HEMBB1001753
 C-HEMBB1001756
 55 C-HEMBB1001760
 C-HEMBB1001785
 C-HEMBB1001797
 C-HEMBB1001802//Human desmin mRNA, complete cds.//0//1523bp//98%//U59167

C-HEMBB1001816
 C-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA complete cds.//0//
 1514bp//99%//AF056209
 C-HEMBB1001839//GASTRULA ZINC FINGER PROTEIN XLCGF42.1 (FRAGMENT).//6.90E-11//87aa//35%//
 5 P18720
 C-HEMBB1001850
 C-HEMBB1001863
 C-HEMBB1001868
 C-HEMBB1001874
 10 C-HEMBB1001880
 C-HEMBB1001899
 C-HEMBB1001906
 C-HEMBB1001910
 C-HEMBB1001911
 15 C-HEMBB1001921
 C-HEMBB1001922
 C-HEMBB1001930
 C-HEMBB1001944
 C-HEMBB1001945
 20 C-HEMBB1001947
 C-HEMBB1001950//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.)
 (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1.60E-41//370aa//31%//P54304
 C-HEMBB1001952
 C-HEMBB1001957
 25 C-HEMBB1001962
 C-HEMBB1001983
 C-HEMBB1001990
 C-HEMBB1001996
 C-HEMBB1002002
 30 C-HEMBB1002005
 C-HEMBB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYP1VC1).//2.70E-49//139aa//55%//P29981
 C-HEMBB1002043
 C-HEMBB1002045
 C-HEMBB1002049
 35 C-HEMBB1002050
 C-HEMBB1002068
 C-HEMBB1002092
 C-HEMBB1002139
 C-HEMBB1002142
 40 C-HEMBB1002190
 C-HEMBB1002193
 C-HEMBB1002217//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-132//399aa//
 44%//Q05481
 C-HEMBB1002218
 45 C-HEMBB1002232
 C-HEMBB1002247
 C-HEMBB1002249
 C-HEMBB1002266//NEURONAL PROTEIN.//2.10E-46//121aa//76%//P41737
 C-HEMBB1002327
 50 C-HEMBB1002329
 C-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.//1.10E-274//1249bp//99%//
 AJ010841
 C-HEMBB1002358
 C-HEMBB1002371
 55 C-HEMBB1002387
 C-HEMBB1002409
 C-HEMBB1002425
 C-HEMBB1002442//ILIN-10 PROTEIN.//9.70E-14//121aa//31%//P34692

C-HEMBB1002453
 C-HEMBB1002458
 C-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds.//7.70E-258//774bp//99%/U43885
 C-HEMBB1002489
 5 C-HEMBB1002510//GYP7 PROTEIN.//3.10E-50//192aa//42%/P48365
 C-HEMBB1002520
 C-HEMBB1002522
 C-HEMBB1002545
 10 C-HEMBB1002579
 C-HEMBB1002582
 C-HEMBB1002596
 C-HEMBB1002603
 C-HEMBB1002610
 C-HEMBB1002613
 15 C-HEMBB1002617
 C-HEMBB1002623
 C-HEMBB1002635
 C-HEMBB1002677
 C-HEMBB1002683
 20 C-HEMBB1002689
 C-HEMBB1002702
 C-MAMMA1000009
 C-MAMMA1000043
 25 C-MAMMA1000045//ENV POLYPROTEIN [CONTAINS: SURFACE PROTEIN GP85; MEMBRANE PROTEIN
 GP37].//1.90E-07//249aa//27%/P03396
 C-MAMMA1000057
 C-MAMMA1000085//PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.16) (CYSTEINE--
 TRNA LIGASE) (CYRSR).//2.10E-90//427aa//39%/Q09860
 C-MAMMA1000092
 30 C-MAMMA1000103
 C-MAMMA1000117
 C-MAMMA1000129
 C-MAMMA1000133
 C-MAMMA1000155
 35 C-MAMMA1000175
 C-MAMMA1000198
 C-MAMMA1000241
 C-MAMMA1000251
 C-MAMMA1000254
 40 C-MAMMA1000287
 C-MAMMA1000307
 C-MAMMA1000331
 C-MAMMA1000339
 C-MAMMA1000340
 45 C-MAMMA1000348
 C-MAMMA1000356
 C-MAMMA1000360
 C-MAMMA1000402
 C-MAMMA1000414
 50 C-MAMMA1000431
 C-MAMMA1000444
 C-MAMMA1000458
 C-MAMMA1000500
 C-MAMMA1000522
 55 C-MAMMA1000576
 C-MAMMA1000583
 C-MAMMA1000594
 C-MAMMA1000605

C-MAMMA1000616
 C-MAMMA1000643
 C-MAMMA1000684//Homo sapiens 7-60 mRNA, complete cds./0//2402bp//99%//AF109134
 C-MAMMA1000696
 5 C-MAMMA1000707
 C-MAMMA1000714
 C-MAMMA1000720
 C-MAMMA1000744
 10 C-MAMMA1000761
 C-MAMMA1000776
 C-MAMMA1000798
 C-MAMMA1000839
 C-MAMMA1000851
 15 C-MAMMA1000863
 C-MAMMA1000867
 C-MAMMA1000876
 C-MAMMA1000880
 C-MAMMA1000883
 C-MAMMA1000921
 20 C-MAMMA1000931
 C-MAMMA1000941
 C-MAMMA1000957
 C-MAMMA1000962
 C-MAMMA1000975
 25 C-MAMMA1000987
 C-MAMMA1001003
 C-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CG-R) (LSH-R)
 (LUTEINIZING HORMONE RECEPTOR) (FRAGMENT)/1.20E-26//276aa//28%//Q90674
 30 C-MAMMA1001038//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC
 2.7.1.117) (MLCK) [CONTAINS: TELOKIN]/2.60E-107//190aa//95%//Q15746
 C-MAMMA1001082
 C-MAMMA1001162
 C-MAMMA1001186
 C-MAMMA1001191
 35 C-MAMMA1001206
 C-MAMMA1001220
 C-MAMMA1001243
 C-MAMMA1001249
 C-MAMMA1001256
 40 C-MAMMA1001268
 C-MAMMA1001271
 C-MAMMA1001274
 C-MAMMA1001292
 C-MAMMA1001305//RHO-GTPASE-ACTIVATING PROTEIN 1 (GTPASE-ACTIVATING PROTEIN RHOGAP)
 (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN)
 (P50-RHOGAP)/2.20E-98//283aa//63%//Q07960
 45 C-MAMMA1001324
 C-MAMMA1001341
 C-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG)/1.40E-165//312aa//99%//P02750
 50 C-MAMMA1001397
 C-MAMMA1001408
 C-MAMMA1001420
 C-MAMMA1001442
 C-MAMMA1001452
 55 C-MAMMA1001465
 C-MAMMA1001487
 C-MAMMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-
 TRAL PROTEINASE) (CANP) (MU-TYPE)/5.70E-55//86aa//97%//P07384

C-MAMMA1001547
 C-MAMMA1001551
 C-MAMMA1001575
 C-MAMMA1001590
 5 C-MAMMA1001600
 C-MAMMA1001606
 C-MAMMA1001627//Homo sapiens mRNA for transcription factor TBX6.//5.20E-189//871bp//99%//AJ007989
 C-MAMMA1001663
 10 C-MAMMA1001670
 C-MAMMA1001671
 C-MAMMA1001679//F-ACTIN CAPPING PROTEIN BETA SUBUNIT (CAPZ).//0.00000058//29aa//100%//P47756
 C-MAMMA1001711
 C-MAMMA1001735//TUBULIN BETA-5 CHAIN (BETA-TUBULIN CLASS-V).//5.90E-240//445aa//97%//P09653
 15 C-MAMMA1001744
 C-MAMMA1001745
 C-MAMMA1001751//Homo sapiens tandem pore domain potassium channel TWIK-2 (KCNK6) mRNA, complete
 cds.//0//2332bp//99%//AF117708
 C-MAMMA1001783
 C-MAMMA1001788
 20 C-MAMMA1001806
 C-MAMMA1001812
 C-MAMMA1001815
 C-MAMMA1001817
 C-MAMMA1001818
 25 C-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene.//1.30E-198//1157bp//80%//Y13148
 C-MAMMA1001824
 C-MAMMA1001851
 C-MAMMA1001854
 C-MAMMA1001864
 30 C-MAMMA1001878
 C-MAMMA1001890
 C-MAMMA1001907
 C-MAMMA1001908
 C-MAMMA1001931
 35 C-MAMMA1001969
 C-MAMMA1002011
 C-MAMMA1002032
 C-MAMMA1002041
 C-MAMMA1002047
 40 C-MAMMA1002056
 C-MAMMA1002058
 C-MAMMA1002078
 C-MAMMA1002082
 C-MAMMA1002084
 45 C-MAMMA1002093
 C-MAMMA1002094
 C-MAMMA1002118
 C-MAMMA1002125
 C-MAMMA1002132
 50 C-MAMMA1002140
 C-MAMMA1002143//Homo sapiens Cdc42 effector protein 4 mRNA, complete cds7//1.70E-252//1170bp//99%//
 AF099664
 C-MAMMA1002145
 C-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE
 55 1) (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) (TSA) (PRP) (NATURAL KILLER CELL ENHANCING FACTOR
 B) (NKEF-B).//5.20E-61//60aa//90%//P32119
 C-MAMMA1002230
 C-MAMMA1002250

C-MAMMA1002282
 C-MAMMA1002293
 C-MAMMA1002298
 C-MAMMA1002299
 5 C-MAMMA1002308
 C-MAMMA1002310
 C-MAMMA1002311
 C-MAMMA1002322
 10 C-MAMMA1002339
 C-MAMMA1002352
 C-MAMMA1002359
 C-MAMMA1002360
 C-MAMMA1002392
 15 C-MAMMA1002411
 C-MAMMA1002413
 C-MAMMA1002417
 C-MAMMA1002428//LYSOSOME MEMBRANE PROTEIN II (LIMP II) (85 KD LYSOSOMAL MEMBRANE
 SIALOGLYCOPROTEIN) (LGP85) (CD36 ANTIGEN-LIKE 2) //1.10E-24//96aa//68%/Q14108
 C-MAMMA1002434
 20 C-MAMMA1002446
 C-MAMMA1002454
 C-MAMMA1002461
 C-MAMMA1002475
 C-MAMMA1002556
 25 C-MAMMA1002566
 C-MAMMA1002612
 C-MAMMA1002622//VILLIN.//7.20E-35//53aa//64%/P02640
 C-MAMMA1002637//KINESIN LIGHT CHAIN (KLC).//1.30E-198//550aa//70%/Q07866
 C-MAMMA1002650//Mus musculus ODA-8S protein mRNA, complete cds.//5.40E-57//480bp//68%/AF194030
 30 C-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//4.3E-317//
 1942bp//85%/AF018261
 C-MAMMA1002727
 C-MAMMA1002748
 C-MAMMA1002758
 35 C-MAMMA1002780
 C-MAMMA1002820
 C-MAMMA1002833
 C-MAMMA1002843
 C-MAMMA1002895
 40 C-MAMMA1002937//ZINC FINGER PROTEIN 135.//8.30E-99//393aa//43%/P52742
 C-MAMMA1003004
 C-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds.//0//
 1533bp//99%/AF077952
 C-NT2RM1000001//D.melanogaster sap47-2 mRNA.//1.50E-10//417bp//62%/X80110
 45 C-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds.//0//3376bp//99%/D31886
 C-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds.//0//3551bp//99%/AB014590
 C-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds.//0//3035bp//96%/AB014561
 C-NT2RM1000421//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%/P10775 C-NT2RM1000499
 C-NT2RM1001059//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB4.//3.60E-11//180aa//28%///
 50 Q99383
 C-NT2RM1001092//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.60E-115//332aa//
 52%/Q05481
 C-NT2RM2001592//Homo sapiens mRNA for KIAA1067 protein, partial cds.//0//3471bp//99%/AB028990
 C-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds.//0//1632bp//99%/AB014518
 55 C-NT2RM2001637
 C-NT2RM2001641
 C-NT2RM2001670//ZINC FINGER PROTEIN 29 (ZFP-29).//6.50E-104//407aa//43%/Q07230
 C-NT2RM2001699

- C-NT2RM2001706
C-NT2RM2001718
C-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds.//01/2892bp//99%/AB007931
C-NT2RM2001805
5 C-NT2RM4000086
C-NT2RM4000215//MAK16 PROTEIN.//1.30E-68//295aa//49%/P10962
C-NT2RM4000414
C-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).//1.00E-59//595aa//28%/Q04652
C-NT2RM4000634
10 C-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//01/1412bp//100%/AB028992
C-NT2RM4000783
C-NT2RM4000857//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//6.70E-22//250aa//29%/P02750
C-NT2RM4000971
C-NT2RM4000996//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//8.00E-211//738aa//
15 50%/Q05481
C-NT2RM4001092//ZINC FINGER PROTEIN GLO3.//3.10E-24//265aa//33%/P38682
C-NT2RM4001178//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//1.10E-48//218aa//43%/Q03532
C-NT2RM4001569
C-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds.//
20 8.10E-300//1395bp//98%/M37712
C-NT2RM4001905
C-NT2RM4001938//Homo sapiens mRNA for KIAA0898 protein, partial cds.//01/2234bp//99%/AB020705
C-NT2RM4002062//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//
1.90E-31//80aa//52%/P36419
25 C-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//9.30E-293//1751bp//83%/AF072758
C-NT2RM4002093//Homo sapiens neural polypyrimidine tract binding protein (PTB) mRNA, complete cds.//01/
2550bp//99%/AF176085
C-NT2RM4002109//Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.//01/2572bp//99%/AF071592
30 C-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.90E-70//454bp//85%/AF035940
C-NT2RM4002194//Mus musculus semaphorin VIa mRNA, complete cds.//5.20E-297//1753bp//87%/AF030430
C-NT2RM4002390
C-NT2RM4002398
35 C-NT2RM4002420
C-NT2RM4002534
C-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//01/1915bp//87%/AF022962
C-NT2RM4002571//H. sapiens mRNA for UDP-GalNAc:polypeptide N-acetyl-galactosaminyltransferase (T2).//
4.60E-78//921bp//69%/X85019
40 C-NT2RP1000358//Homo sapiens mRNA; cDNA DKFZp564C186 (from clone DKFZp564C186).//01/1938bp//88%/AL050019
C-NT2RP1000522//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-
OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-
ZYME 1).//8.20E-83//345aa//47%/Q61068
45 C-NT2RP1000609//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//01/2165bp//99%/AL050118
C-NT2RP1000677//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER (ORGANIC ANION TRANS-
PORTING POLYPEPTIDE).//1.20E-78//483aa//31%/P46721
C-NT2RP1000701//Homo sapiens phospholipase A2 activating protein (PLA2P) mRNA, complete cds.//01/
50 1687bp//99%/AF145020
C-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.80E-176//829bp//98%/AF047020
C-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds.//01/1555bp//99%/AF064094
C-NT2RP1000916
C-NT2RP1000944
55 C-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//01/2085bp//99%/U82267
C-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9.//2.30E-116//319aa//46%/Q06218

- C-NT2RP1001113
C-NT2RP1001173//Homo sapiens mRNA; cDNA DKFZp566D1146 (from clone DKFZp566D1146).//0//2333bp//99%//AL080222
- 5 C-NT2RP1001177//Rattus norvegicus histone macroH2A.1 mRNA, complete cds.//5.20E-108//1278bp//69%//U79139
C-NT2RP1001185//Human isovaleryl-coA dehydrogenase (IVD) mRNA, complete cds.//1.90E-158//728bp//99%//M34192
C-NT2RP1001247//Homo sapiens TGF-beta type secreted signaling protein LEFTYA mRNA, complete cds.//0//2006bp//100%//AF081513
- 10 C-NT2RP1001311
C-NT2RP1001313//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//7.50E-121//1394bp//69%//AF126799
C-NT2RP2000001//Homo sapiens mRNA for KIAA1111 protein, partial cds.//0//3188bp//99%//AB029034
C-NT2RP2000027
- 15 C-NT2RP2000183//DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL SPECIFIC PROTEIN NSP60).//3.30E-16//114aa//44%//002675
C-NT2RP2000198
C-NT2RP2000523//APOLOPROTEIN B MRNA EDITING PROTEIN (HEPR) (APOBEC-1).//6.00E-16//124aa//34%//P41238
- 20 C-NT2RP2000551
C-NT2RP2000644
C-NT2RP2000660//SAP1 PROTEIN.//5.20E-68//474aa//32%//P39955
C-NT2RP2000678
C-NT2RP2000715
- 25 C-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds.//0//1562bp//99%//U80811
C-NT2RP2000970
C-NT2RP2001347
C-NT2RP2001460//TRICHOHYALIN.//1.00E-14//521aa//24%//P37709
- 30 C-NT2RP2001613//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT).//6.10E-12//184aa//31%//P24391
C-NT2RP2001634//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//0//2445bp//99%//U97067
C-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds.//0//1287bp//99%//AF058718
- 35 C-NT2RP2001677
C-NT2RP2001678
C-NT2RP2001720
C-NT2RP2001740//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//7.90E-52//220aa//44%//O61068
- 40 C-NT2RP2001756//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.70E-49//411aa//32%//P51523
C-NT2RP2001839//SCY1 PROTEIN.//5.40E-32//621aa//24%//P53009
C-NT2RP2001861
- 45 C-NT2RP2001869//ZINC FINGER PROTEIN 191.//7.10E-26//126aa//52%//O14754
C-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AlF-1) (IONIZED CALCIUM BINDING ADAPTER MOLECULE 1).//1.20E-45//141aa//65%//P55008
C-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end.//0//2518bp//98%//M74161
- 50 C-NT2RP2001936
C-NT2RP2001943
C-NT2RP2001946
C-NT2RP2002032
C-NT2RP2002033
- 55 C-NT2RP2002041
C-NT2RP2002047
C-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//1.60E-226//1301bp//88%//U87306

- C-NT2RP2002124//Homo sapiens mRNA for KIAA1097 protein, partial cds.//0//1772bp//95%//AB029020
 C-NT2RP2002172
 C-NT2RP2002219
 C-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//0//1528bp//98%//AF005418
 5 C-NT2RP2002316
 C-NT2RP2002373
 C-NT2RP2002439
 C-NT2RP2002475
 C-NT2RP2002546
 10 C-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-155//562aa//50%//P51523
 C-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds.//9.20E-147//874bp//87%//U19181
 C-NT2RP2002643
 C-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.//3.50E-74//727bp//72%//AF041107
 15 C-NT2RP2002736
 C-NT2RP2002740
 C-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.//9.90E-54//964bp//64%//D89016
 C-NT2RP2002752
 C-NT2RP2002753
 20 C-NT2RP2002857
 C-NT2RP2003000//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//1.90E-11//132aa//38%//Q13829
 C-NT2RP2003073
 C-NT2RP2003164//Homo sapiens mRNA for protein kinase.//0//2313bp//99%//AJ132545
 25 C-NT2RP2003206
 C-NT2RP2003228//H.sapiens P1-Cdc21 mRNA.//0//2870bp//98%//X74794
 C-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.60E-186//1551bp//77%//AF023657
 C-NT2RP2003237
 30 C-NT2RP2003272//Homo sapiens ubiquitin mRNA, complete cds.//0//1789bp//99%//AF176069
 C-NT2RP2003280
 C-NT2RP2003293
 C-NT2RP2003394//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//5.50E-13//302aa//26%//P25386
 35 C-NT2RP2003401//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//9.60E-78//346aa//43%//061068
 C-NT2RP2003456
 C-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/PDGF2) mRNA, complete cds.//0//1746bp//95%//M12783
 40 C-NT2RP2003522//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//1764bp//99%//AF125158
 C-NT2RP2003559
 C-NT2RP2003564//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//2.10E-59//270aa//46%//P19474
 45 C-NT2RP2003581
 C-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.//9.40E-243//1624bp//82%//AJ006215
 C-NT2RP2003702//Homo sapiens 17 beta-hydroxysteroid dehydrogenase type VII (HSD17B7) mRNA, complete cds.//2.1e-313//978bp//99%//AF098786
 50 C-NT2RP2003704//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//1.80E-72//350bp//100%//AJ132637
 C-NT2RP2003727
 C-NT2RP2003751
 55 C-NT2RP2003781//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.//5.50E-63//253aa//50%//Q09201
 C-NT2RP2003825
 C-NT2RP2003871

C-NT2RP2003885
 C-NT2RP2003912//SERINE/THREONINE-PROTEIN KINASE NEK1 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 1)/J6.10E-183//387aa//87%//P51954
 C-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds./0//2866bp//98%//AB007916
 5 C-NT2RP2003988
 C-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3)/J2.30E-53//141aa//78%//P20290
 C-NT2RP2004098//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE)/J5.40E-30//319aa//31%//Q01513
 10 C-NT2RP2004142
 C-NT2RP2004170//Homo sapiens mRNA for transducin (beta) like 1 protein./J1.10E-138//1236bp//74%//Y12781
 C-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds./J3.80E-52//397bp//82%//AF003998
 C-NT2RP2004207
 15 C-NT2RP2004226
 C-NT2RP2004232//Homo sapiens EPK2 mRNA for serine/threonine kinase, complete cds./0//2272bp//99%//AB015982
 C-NT2RP2004242//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)/J9.90E-12//427aa//26%//P19246
 20 C-NT2RP2004270//PROTEIN PTM1 PRECURSOR./J1.40E-16//334aa//24%//P32857
 C-NT2RP2004321
 C-NT2RP2004339
 C-NT2RP2004347
 C-NT2RP2004396//Homo sapiens mRNA for activator of S phase Kinase, complete cds./J5.40E-243//1108bp//99%//AB028069
 25 C-NT2RP2004399
 C-NT2RP2004400
 C-NT2RP2004412
 C-NT2RP2004425//Mus musculus axotrophin mRNA, complete cds./0//2321bp//86%//AF155739
 30 C-NT2RP2004490
 C-NT2RP2004523
 C-NT2RP2004538//Mus musculus kinesin-like protein KIF1B (Kif1b) mRNA, complete cds./0//1387bp//86%//AF090190
 C-NT2RP2004580
 35 C-NT2RP2004587//Homo sapiens mRNA for KIAA0888 protein, partial cds./0//2886bp//100%//AB020695
 C-NT2RP2004594
 C-NT2RP2004681
 C-NT2RP2004709
 C-NT2RP2004710//Homo sapiens mRNA for KIAA1014 protein, partial cds./0//2587bp//100%//AB023231
 40 C-NT2RP2004732//Homo sapiens mRNA for KIAA0884 protein, partial cds./0//1774bp//99%//AB020691
 C-NT2RP2004767
 C-NT2RP2004775
 C-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1 (KS1) mRNA, complete cds./J1.00E-228//1666bp//75%//U56732
 45 C-NT2RP2004962
 C-NT2RP2004982
 C-NT2RP2005003//52 KD RO PROTEIN (SJOEGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))/J1.80E-99//376aa//43%//P19474
 C-NT2RP2005018
 50 C-NT2RP2005020
 C-NT2RP2005022
 C-NT2RP2005031
 C-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds./0//4069bp//99%//AB014564
 C-NT2RP2005139//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT)/J0.000000022//139aa//35%//Q05921
 55 C-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein./0//2769bp//98%//AJ007509
 C-NT2RP2005254
 C-NT2RP2005325//Homo sapiens LIM-homeodomain protein HLHX2 (LHX2) mRNA, complete cds./0//1643bp//

- 99%//AF124735
 C-NT2RP2005336//TRICHOHYALIN //5.40E-10//545aa//22%//P37709
 C-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPASE 5 (EC 3.6.1.38) //2.10E-124//636aa//38%//P32660
- 5 C-NT2RP2005360
 C-NT2RP2005407//OXISTEROL-BINDING PROTEIN //5.30E-63//410aa//40%//P22059
 C-NT2RP2005454
 C-NT2RP2005457//Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA, complete cds.//1.20E-130//608bp//99%//AF070652
- 10 C-NT2RP2005476//Human p190-B (p190-B) mRNA, complete cds.//3.40E-108//668bp//88%//U17032
 C-NT2RP2005491//PARAMYOSIN (PMY) (ANTIGEN B) //0.00000015//279aa//26%//P35418
 C-NT2RP2005496//ZINC FINGER PROTEIN 135 //2.90E-146//398aa//59%//P52742
 C-NT2RP2005501
- 15 C-NT2RP2005531//PROTEIN 4.1 (BAND 4.1) (P4.1) //5.50E-70//393aa//39%//P11171
 C-NT2RP2005600//Homo sapiens mRNA for KIAA1020 protein, partial cds.//0//2554bp//99%//AB028943
 C-NT2RP2005645
 C-NT2RP2005694//X-LINKED RETINITIS PIGMENTOSA GTPASE REGULATOR //2.60E-10//175aa//27%//Q92834
- 20 C-NT2RP2005701//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN) //3.00E-63//323aa//39%//Q62158
 C-NT2RP2005741
 C-NT2RP2005806
 C-NT2RP2005815
 C-NT2RP2005841
 C-NT2RP2005882
- 25 C-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE) //1.50E-67//388aa//44%//P25500
 C-NT2RP2006103
 C-NT2RP2006166
 C-NT2RP2006258
 C-NT2RP2006261
- 30 C-NT2RP2006321
 C-NT2RP2006454
 C-NT2RP2006598//Homo sapiens retinoid x receptor interacting protein mRNA, complete cds.//3.10E-295//1193bp//99%//AF113538
- 35 C-NT2RP3000046//MITOCHONDRIAL GTPASE MSS1 PRECURSOR //4.60E-78//421aa//37%//P32559
 C-NT2RP3000047//NPL4 PROTEIN //1.10E-85//526aa//36%//P33755
 C-NT2RP3000418
 C-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION //2.90E-1511319aa//26%//P37908
- 40 C-NT2RP3000487
 C-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus //0//1934bp//99%//X16667
 C-NT2RP3000526
 C-NT2RP3000603//NEUROGENIC DIFFERENTIATION FACTOR 1 //3.70E-11//90aa//42%//Q13562
 C-NT2RP3000605//Mus musculus mRNA for w1ZL, complete cds.//0//2232bp//82%//AB012265
- 45 C-NT2RP3000628
 C-NT2RP3000739//DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN //1.40E-24//155aa//37%//Q10149
 C-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.) //8.30E-108//331aa//50%//P27448
- 50 C-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A //1.90E-46//73aa//98%//P39027
 C-NT2RP3001057//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7) //9.00E-201//584aa//54%//Q05481
 C-NT2RP3001113//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1 //2.90E-11//631aa//23%//P25386
- 55 C-NT2RP3001245//Homo sapiens mRNA for KIAA0923 protein, complete cds.//0//2659bp//99%//AB023140
 C-NT2RP3001253//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110) //1.70E-10//540aa//23%//P32380
 C-NT2RP3001356

- C-NT2RP3001383
C-NT2RP3001399//SSU72 PROTEIN.//1.30E-16//84aa//52%//P53538
C-NT2RP3001554//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//1.40E-76//388aa//32%//P46821
- 5 C-NT2RP3001712//Homo sapiens HP1-BP74 protein mRNA, complete cds.//0//1788bp//99%//AF113534
C-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//1.10E-240//902bp//99%//AF054177
C-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds.//6.90E-132//774bp//88%//AF008554
- 10 C-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT).//7.10E-132//294aa//84%//Q14141
C-NT2RP3001739
C-NT2RP3001777
C-NT2RP3001857//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.20E-14//242aa//24%//Q00808
C-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds.//0//3747bp//99%//AB014575
- 15 C-NT2RP3001944
C-NT2RP3002033
C-NT2RP3002054
C-NT2RP3002063//Homo sapiens mRNA for KIAA1033 protein, partial cds.//0//2830bp//99%//AB028956
C-NT2RP3002099
C-NT2RP3002102
C-NT2RP3002147
C-NT2RP3002163
C-NT2RP3002173
C-NT2RP3002255
- 25 C-NT2RP3002303//PROBABLE UNDECAPRENYL PYROPHOSPHATE SYNTHETASE (EC 2.5.1.31) (UPP SYNTHETASE) (DI-TRANS-POLY-CIS-DECAPRENYLCISTRANSFERASE).//8.60E-49//243aa//43%//Q58767
C-NT2RP3002343
C-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15).//4.20E-70//590bp//76%//X16396
- 30 C-NT2RP3002399//DNA REPLICATION LICENSING FACTOR MCM4 (CDC21 HOMOLOG)(P1-CDC21).//8.60E-79//416aa//34%//P33991
C-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds.//0//3811bp//99%//AB014578
C-NT2RP3002545//Homo sapiens mRNA; cDNA DKFZp586G0518 (from clone DKFZp586G0518).//0//2499bp//99%//AL050092
- 35 C-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III.//5.80E-40//161aa//52%//Q10010
C-NT2RP3002602//PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (EC 5.3.4.1) (ERP60) (58 KD MICROSOMAL PROTEIN) (P58) (HIP-70) (Q-2).//2.90E-19//173aa//28%//P11598
C-NT2RP3002603
C-NT2RP3002628//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//2.50E-26//90aa//42%//P38660
C-NT2RP3002659
C-NT2RP3002660
C-NT2RP3002682//Homo sapiens CGI-145 protein mRNA, complete cds.//0//1596bp//98%//AF151903
- 45 C-NT2RP3002687
C-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kifib), complete cds.//1.10E-93//1205bp//69%//D17577
C-NT2RP3002701
C-NT2RP3002785//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//2.50E-55//187aa//39%//Q24371
C-NT2RP3002869//Mus musculus semaphorin VIa mRNA, complete cds.//2.50E-232//1282bp//85%//AF030430
- 50 C-NT2RP3002876
C-NT2RP3002877
C-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//0//2085bp//94%//AB018314
C-NT2RP3002969//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2722bp//99%//D89053
C-NT2RP3002972//Halocynthia roretzi mRNA for HrPET-1, complete cds.//3.90E-52//899bp//64%//AB029333
C-NT2RP3003032//Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds.//0//2656bp//99%//AF084555
- 55 C-NT2RP3003061//ANKYRIN.//1.40E-20//200aa//37%//Q02357
C-NT2RP3003071//NEUROGENIC PROTEIN BIG BRAIN.//1.10E-05//258aa//24%//P23645

- C-NT2RP3003078
C-NT2RP3003139
C-NT2RP3003145//Mus musculus metalcarboxypeptidase CPX-1 mRNA, complete cds.//0//2251bp//81%//AF07773 8
- 5 C-NT2RP3003150
C-NT2RP3003197//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME 1.//5.70E-09//169aa//31%//Q09674
C-NT2RP3003203//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//2.00E-210//1851bp//76%//AF110267
- 10 C-NT2RP3003210
C-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//4.30E-187//1750bp//75%//U20286
C-NT2RP3003230//Homo sapiens mRNA for hCRNN4, complete cds.//0//2350bp//99%//AB030656
C-NT2RP3003242//Homo sapiens stanniocalcin-related protein mRNA, complete cds.//0//2366bp//99%//AF098462
- 15 C-NT2RP3003251//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//4.20E-86//366aa//48%//P19474
C-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//1.10E-170//585aa//54%//O64948
- 20 C-NT2RP3003311
C-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds.//9.20E-45//782bp//65%//U90653
C-NT2RP3003427
C-NT2RP3003543
- 25 C-NT2RP3003552
C-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC REGION.//4.50E-30//191aa//40%//P40529
C-NT2RP3003564
C-NT2RP3003569//Homo sapiens ras-related GTP-binding protein mRNA, complete cds.//0//3131bp//94%//AF106681
- 30 C-NT2RP3003621
C-NT2RP3003625
C-NT2RP3003656
C-NT2RP3003659//HES1 PROTEIN.//5.90E-22//229aa//27%//P35843
- 35 C-NT2RP3003686
C-NT2RP3003701//F-SPONDIN PRECURSOR.//1.80E-17//324aa//26%//P35446
C-NT2RP3003716//SLIT PROTEIN PRECURSOR.//6.60E-10//150aa//34%//P24014
C-NT2RP3003726//Homo sapiens spermatogenesis associated PD1 mRNA, complete cds.//0//2568bp//99%//U28164
- 40 C-NT2RP3003795
C-NT2RP3003805
C-NT2RP3003809//SAV PROTEIN.//1.10E-131//576aa//41%//Q07590
C-NT2RP3003819
C-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP).//9.60E-19//174aa//31%//P02720
- 45 C-NT2RP3003831//Homo sapiens ENDOGL-1 (alias ENGL-a) mRNA for endonuclease G-like protein-1, complete cds.//2.2e-316//1436bp//99%//AB020523
C-NT2RP3003833
C-NT2RP3003842
- 50 C-NT2RP3003846//Homo sapiens mRNA for putative phospholipase, complete cds.//4.80E-277//1255bp//99%//AB019435
C-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds.//0//2557bp//99%//AB018343
C-NT2RP3003876
C-NT2RP3003914//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//2.20E-20//76aa//64%//Q09332
- 55 C-NT2RP3003918//Homo sapiens VAMP-associated protein B (VAP-B) mRNA, complete cds.//0//2191bp//99%//AF086628
C-NT2RP3003989

C-NT2RP3004016//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1)
 (KRAB-ASSOCIATED PROTEIN 1).//1.50E-17//226aa//26%//Q13263
 C-NT2RP3004070
 C-NT2RP3004145
 5 C-NT2RP3004215
 C-NT2RP3004253
 C-NT2RP3004282//Homo sapiens IrsinA (DYT1) mRNA, complete cds.//5.10E-24//597bp//61 %//AF007871
 C-NT2RP3004348//R. norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.10E-185//1130bp//82%//
 X67877
 10 C-NT2RP3004490//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//0//1778bp//99%//AC003982
 C-NT2RP3004503
 C-NT2RP3004566//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-95//434aa//43%//
 P51523
 15 C-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acetylglucosamine-6-O-sulfotransferase e (GlcNAc6ST),
 complete cds.//0//2393bp//99%//AB014679
 C-NT2RP4000023
 C-NT2RP4000218
 C-NT2RP4000424
 C-NT2RP4001213//ZINC FINGER PROTEIN 184 (FRAGMENT).//5.70E-141//511aa//43%//Q99676
 20 C-NT2RP4001447
 C-NT2RP4001841
 C-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1.//1.40E-85//489aa//43%//P55194
 C-NT2RP4002047//GTP-BINDING PROTEIN LEPA.//1.50E-168//601aa//52%//0067618
 C-NT2RP4002075
 25 C-NT2RP4002083
 C-OVARC1000001//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//7.00E-217//683bp//
 99%//AB029290
 C-OVARC1000008
 C-OVARC1000017
 30 C-OVARC1000058
 C-OVARC1000068
 C-OVARC1000071//Homo sapiens NTF2-related export protein NXT1 (NXT1) mRNA, complete cds.//1.50E-47//
 727bp//67%//AF156957
 C-OVARC1000085//Human mRNA for proteasome subunit HC5.//1.00E-151//699bp//100%//D00761
 35 C-OVARC1000109
 C-OVARC1000114
 C-OVARC1000145
 C-OVARC1000240
 C-OVARC1000302
 40 C-OVARC1000408
 C-OVARC1000414
 C-OVARC1000440
 C-OVARC1000442
 C-OVARC1000496
 45 C-OVARC1000556//RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1.-) (S6KII-ALPHA 2) (P90-RSK 2)
 (RIBOSOMAL S6 KINASE 3) (RSK3) (PP90RSK3).//3.30E-67//132aa//95%//015349
 C-OVARC1000557
 C-OVARC1000578
 C-OVARC1000622
 50 C-OVARC1000679//Homo sapiens myosin-IXa mRNA, complete cds.//0//808bp//99%//AF117888
 C-OVARC1000681
 C-OVARC1000700
 C-OVARC1000724
 C-OVARC1000751//PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16) (PP2C).//5.60E-11//
 74aa//37%//P49596
 55 C-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR (75 KD GLUCOSE REGULATED
 PROTEIN) (GRP 75).//3.90E-46//78aa//98%//035501
 C-OVARC1000885//OXIDOREDUCTASE UCPA (EC 1.-.-.-).//1.30E-32//170aa//34%//P37440

C-OVARC1000936//COAT PROTEIN GP37 (ENV PROTEIN GP37).//0.000054//135aa//28%//P03398
 C-OVARC1000937//S-PHASE ENTRY CYCLIN 6.//4.90E-10//61aaaa//49%//P32943
 C-OVARC1000960
 C-OVARC1000971
 5 C-OVARC1000999//ANKYRIN HOMOLOG PRECURSOR.//4.10E-11//189aa//32%//Q06527
 C-OVARC1001000
 C-OVARC1001029
 C-OVARC1001040
 C-OVARC1001051//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN
 10 EPS15) (AF-1P PROTEIN).//1.10E-08//216aa//23%//P42566
 C-OVARC1001113//Homo sapiens diaphanous 1 (HDI/A1) mRNA, complete cds.//5.1e-310//1588bp//93%//
 AF051782
 C-OVARC1001118
 C-OVARC1001129
 15 C-OVARC1001169
 C-OVARC1001240
 C-OVARC1001261
 C-OVARC1001339
 C-OVARC1001342//40S RIBOSOMAL PROTEIN S8.//1.40E-110//207aa//99%//P09058
 20 C-OVARC1001357
 C-OVARC1001442
 C-OVARC1001611
 C-OVARC1001813
 C-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//0//1760bp//99%//AF054174
 25 C-OVARC1002143
 C-OVARC1002165//3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 2 (EC 1.3.99.5) (STEROID 5-ALPHA-
 REDUCTASE 2) (SR TYPE 2) //7.60E-08//114aa//37%//P31213
 C-OVARC1002182//BETA-TRCP (BETA-TRANSDUCIN REPEAT-CONTAINING PROTEIN) (BTRCP).//1.70E-
 09//207aa//30%//Q91854
 30 C-PLACE1000014
 C-PLACE1000078
 C-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//0//2041bp//87%//
 U35245
 C-PLACE1000793//NEUROGENIC PROTEIN BIG BRAIN.//1.70E-07//251aa//24%//P23645
 35 C-PLACE1000814
 C-PLACE1000979//ZINC FINGER PROTEIN 135.//2.50E-153//326aa//64%//P52742
 C-PLACE1001007
 C-PLACE1001054//Homo sapiens mRNA for RuvB-like DNA helicase TIP49b, complete cds.//4.00E-300//
 1355bp//100%//AB024301
 40 C-PLACE1001088
 C-PLACE1001136
 C-PLACE1001241
 C-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds.//5.90E-228//827bp//99%//
 AF009815
 45 C-PLACE1001395
 C-PLACE1001740
 C-PLACE1001746
 C-PLACE1001983//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//7.50E-16//
 319aa//26%//P37908
 50 C-PLACE1002066
 C-PLACE1002115
 C-PLACE1002213
 C-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds.//0//1657bp//98%//AB018271
 C-PLACE1002450//Human zinc finger protein mRNA, complete cds.//0//2565bp//99%//U69274
 55 C-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//0//2092bp//84%//U69262
 C-PLACE1002499
 C-PLACE1002578
 C-PLACE1002714

C-PLACE1002772
 C-PLACE1002775//PEREGRIN (BR140 PROTEIN).//3.80E-13//272aa//28%//P55201
 C-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//5.50E-203//396aa//86%//
 P51522
 5 C-PLACE1002993
 C-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete
 cds.//8.50E-44//225bp//100%//AF032387
 C-PLACE1003205
 C-PLACE1003249
 10 C-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSORS.//1.70E-23//594aa//33%//P28481
 C-PLACE1003553
 C-PLACE1003592
 C-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.//2.60E-93//270aa//66%//
 P46975
 15 C-PLACE1003669//TRICHOHYALIN.//5.60E-09//219aa//30%//P22793
 C-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA, complete cds.//6.20E-282//
 1316bp//98%//AF053305
 C-PLACE1003870
 20 C-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANS-
 FERASE).//3.70E-22//651aa//66%//P25500
 C-PLACE1003892
 C-PLACE1003900
 C-PLACE1004336
 C-PLACE1004384
 25 C-PLACE1004425
 C-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//2.90E-56//276aa//41%//
 P51522
 C-PLACE1004506//Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds.//2.10E-
 16//402bp//62%//U90878
 30 C-PLACE1004518
 C-PLACE1004550//Homo sapiens CGI-20 protein mRNA, complete cds.//3.50E-274//1305bp//97%//AF132954
 C-PLACE1004681
 C-PLACE1004693
 35 C-PLACE1004716//Homo sapiens HSPC038 protein mRNA, complete cds.//2.70E-103//586bp//91%//AF125099
 C-PLACE1004815
 C-PLACE1004836
 C-PLACE1004838
 C-PLACE1004840
 C-PLACE1004900
 40 C-PLACE1004985
 C-PLACE1005085
 C-PLACE1005086
 C-PLACE1005108
 C-PLACE1005146
 45 C-PLACE1005409
 C-PLACE1005453
 C-PLACE1005477
 C-PLACE1005557//60S RIBOSOMAL PROTEIN L27.//1.90E-11//60aa//48%//P46288
 50 C-PLACE1005595
 C-PLACE1005603
 C-PLACE1005639
 C-PLACE1005727//Homo sapiens STRIN protein (STRIN) mRNA, complete cds.//2.00E-118//378bp//98%//
 AF162680
 C-PLACE1005799
 55 C-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2040bp//99%//AF065482
 C-PLACE1005884
 C-PLACE1005968
 C-PLACE1006002

- C-PLACE1006003//Homo sapiens CGI-94 protein mRNA, complete cds.//2.40E-177//829bp//99%//AF151852
 C-PLACE1006017
 C-PLACE1006037
 C-PLACE1006076
 5 C-PLACE1006143
 C-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0//1489bp//100%//AB014548
 C-PLACE1006288//VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 1 (VDAC1) (PLASMA-
 LEMMAL PORIN) (OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN) (PORIN 31HL) (PORIN 31HM).//
 4.60E-117//147aa//80%//P21796
 10 C-PLACE1006318//Mus musculus skm-BOP2 (Bop) mRNA, complete cds.//3.00E-07//376bp//59%//U76374
 C-PLACE1006368//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//
 1.30E-18//460aa//24%//Q00547
 C-PLACE1006371
 15 C-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-
 TIVATING ENZYME).//1.20E-83//313aa//49%//P27550
 C-PLACE1006506//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.//0//
 2170bp//99%//AF191338
 C-PLACE1006521
 20 C-PLACE1006534//Homo sapiens mRNA; cDNA DKFZp564G1964 (from clone DKFZp564G1964).//1.70E-192//
 883bp//99%//AL110144
 C-PLACE1006617
 C-PLACE1006640
 C-PLACE1006754//BILIARY GLYCOPROTEIN 1 PRECURSOR (BGP-1) (ANTIGEN CD66) (CD66A ANTIGEN).//
 6.20E-63//191aa//43%//P13688
 25 C-PLACE1006760
 C-PLACE1006779
 C-PLACE1006805
 C-PLACE1006815
 C-PLACE1006867
 30 C-PLACE1007045
 C-PLACE1007097
 C-PLACE1007111
 C-PLACE1007112
 C-PLACE1007140//Homo sapiens mRNA for KIAA1009 protein, complete cds.//0//3492bp//99%//AB023226
 35 C-PLACE1007218
 C-PLACE1007454
 C-PLACE1007478
 C-PLACE1007677
 40 C-PLACE10077057//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.//1.10E-184//1096bp//
 82%//AB033922
 C-PLACE1007737
 C-PLACE1007743
 C-PLACE1007852//Homo sapiens mRNA for KIAA0878 protein, complete cds.//1.00E-232//1174bp//94%//
 AB020885
 45 C-PLACE1007877
 C-PLACE1008045
 C-PLACE1008080//Homo sapiens mRNA for HEXIM1 protein, complete cds.//0//2152bp//99%//AB021179
 C-PLACE1008111//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).//3.00E-25//208aa//37%//Q03326
 C-PLACE1008201//Rattus rattus zinc finger protein, complete cds.//0//2265bp//83%//L23077
 50 C-PLACE1008231
 C-PLACE1008244//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//9.50E-21//148aa//38%//Q00808
 C-PLACE1008330//EOSINOPHIL LYSOPHOSPHOLIPASE (EC 3.1.1.5) (CHARCOT-LEYDEN CRYSTAL PRO-
 TEIN) (LYSOLECITHIN ACYLHYDROLASE) (CLC) (GALACTIN- 10) //2.20E-23//94aa//47%//Q05315
 C-PLACE1008331
 55 C-PLACE1008369
 C-PLACE1008392
 C-PLACE1008405
 C-PLACE1008424

C-PLACE1008584
 C-PLACE1008625
 C-PLACE1008630
 5 C-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2).//5.20E-90//483aa//38%//002668
 C-PLACE1008715
 C-PLACE1008748
 C-PLACE1008757
 10 C-PLACE1008798
 C-PLACE1008851
 C-PLACE1008947
 C-PLACE1009039
 C-PLACE1009048
 C-PLACE1009050
 15 C-PLACE10091137//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//0//2529bp//99%//AF035586
 C-PLACE1009150
 C-PLACE1009200
 C-PLACE1009246//POLLEN SPECIFIC PROTEIN SF3.//4.40E-16//82aa//43%//P29675
 20 C-PLACE1009298//Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds.//0//2262bp//99%//AF191298
 C-PLACE1009308//GLUCOSE REPRESSION MEDIATOR PROTEIN.//4.00E-06//439aa//23%//P14922
 C-PLACE1009398//ZINC FINGER PROTEIN 135.//6.20E-97//361aa//51%//P52742
 C-PLACE1009410
 25 C-PLACE1009477//Homo sapiens mRNA for KIAA0684 protein, partial cds.//6.50E-148//592bp//99%//AB014584
 C-PLACE1009493
 C-PLACE1009539
 C-PLACE1009595
 C-PLACE1009637
 30 C-PLACE1009639
 C-PLACE1009798//RLR1 PROTEIN.//1.60E-18//270aa//23%//P53552
 C-PLACE1009861//CATHEPSIN B-LIKE CYSTEINE PROTEINASE 6 PRECURSOR (EC 3.4.22.-).//6.50E-28//209aa//38%//P43510
 C-PLACE1009888
 35 C-PLACE1009925//Homo sapiens RNA helicase (RIG-I) mRNA, complete cds.//0//1730bp//99%//AF038963
 C-PLACE1009947
 C-PLACE1010069
 C-PLACE1010089//Homo sapiens mRNA for KIAA1097 protein, partial cds.//0//1554bp//100%//AB029020
 C-PLACE1010231//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR).//5.10E-27//371aa//28%//Q14246
 40 C-PLACE1010270
 C-PLACE1010562
 C-PLACE1010579//Homo sapiens PTB domain adaptor protein CED-6 mRNA, complete cds.//9.30E-299//1362bp//99%//AF200715
 45 C-PLACE1010624
 C-PLACE1010628//Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds.//7.50E-08//324bp//64%//AF109907
 C-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//1.80E-22//808aa//52%//Q09332
 50 C-PLACE1010702//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//5.20E-151//427aa//55%//P28160
 C-PLACE1010761
 C-PLACE1010802 C-PLACE1010833//CALTRACTIN (CENTRIN).//0.0000001//154aa//28%//P41209
 C-PLACE1010896//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//1.50E-25//583aa//23%//P35580
 55 C-PLACE1010916
 C-PLACE1010947
 C-PLACE1010965
 C-PLACE1011032

- C-PLACE1011041//Homo sapiens mRNA for BAP2-alpha protein, complete cds.//0//1701bp//97%//AB015019
 C-PLACE1011056//HISTONE H1, GONADAL.//6.80E-13//154aa//37%//P02256
 C-PLACE1011090//Homo sapiens mRNA; cDNA DKFZp586A0522 (from clone DKFZp586A0522).//0//880bp//99%//AL050159
- 5 C-PLACE1011160//Homo sapiens HFB30 mRNA, complete cds.//0//1691bp//99%//AB022663
 C-PLACE1011214
 C-PLACE1011229//Homo sapiens ubiquitin-specific protease homolog (UPH) mRNA, complete cds.//2.30E-152//701bp//99%//AF153604
 C-PLACE1011273
- 10 C-PLACE1011291
 C-PLACE1011310//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE.//3.50E-20//496aa//25%//P10587
 C-PLACE1011371//INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2).//1.70E-78//383aa//39%//Q61703
 C-PLACE1011503
- 15 C-PLACE1011635//Homo sapiens heparan sulfate D-glucosaminyl 3-O-sulfotransferase-3B (30ST3B1) mRNA, complete cds.//0//1559bp//99%//AF105377
 C-PLACE1011646//Homo sapiens clone 25059 mRNA sequence.//5.00E-223//1035bp//99%//AF131752
 C-PLACE1011650
 C-PLACE1011675
- 20 C-PLACE1011725
 C-PLACE1011749
 C-PLACE1011922//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMHC-B).//1.30E-15//409aa//27%//P35580
 C-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//0//1163bp//100%//AB018256
- 25 C-PLACE2000006
 C-PLACE2000007//Homo sapiens mRNA for KIAA0913 protein, partial cds.//0//1968bp//97%//AB020720
 C-PLACE2000034//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//2.20E-29//212aa//35%//P10586
 C-PLACE2000039//Rattus norvegicus cytoplasmic dynein heavy chain (MAP 1C), mRNA, complete cds.//4.60E-291//1167bp//89%//L08505
- 30 C-PLACE2000061
 C-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0//3174bp//99%//AF027219
 C-PLACE2000097
 C-PLACE2000103
- 35 C-PLACE2000115
 C-PLACE2000124
 C-PLACE2000140
 C-PLACE2000164//TIPD PROTEIN.//2.10E-59//481aa//33%//O15736
 C-PLACE2000176
- 40 C-PLACE2000223
 C-PLACE2000235
 C-PLACE2000274//DYNEIN BETA CHAIN, CILIARY.//2.20E-167//880aa//37%//P23098
 C-PLACE2000302
 C-PLACE2000347
- 45 C-PLACE2000359
 C-PLACE2000371//TENSIN.//2.90E-78//561aa//37%//Q04205
 C-PLACE2000379
 C-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//1.60E-14//180aa//39%//P14209
- 50 C-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//9.90E-229//821aa//54%//Q09996
 C-PLACE2000450
 C-PLACE2000455
- 55 C-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//0//1979bp//90%//Y17267
 C-PLACE3000070
 C-PLACE3000119
 C-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC15.//1.90E-08//281 aa//22%//P22224
 C-PLACE3000136

- C-PLACE3000147//Homo sapiens metalloproteinase with thrombospondin type 1 motifs ADAMTS1 (ADAMTS1) mRNA, complete cds.//0//2043bp//99%//AF170084
- C-PLACE3000148
- 5 C-PLACE3000155//Homo sapiens mRNA for KIAA0672 protein, complete cds.//2.10E-75//382bp//99%//AB014572
- C-PLACE3000160
- C-PLACE3000169//ZINC FINGER PROTEIN 135.//2.50E-90//358aa//47%//P52742
- C-PLACE3000194
- C-PLACE3000199
- 10 C-PLACE3000218//Homo sapiens putative protein O-mannosyltransferase (POMT2) mRNA, complete cds.//0//1862bp//98%//AF105020
- C-PLACE3000230
- C-PLACE3000244//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//0//1435aa//92%//P53995
- C-PLACE3000254//Homo sapiens transcriptional activator SRCAP (SRCAP) mRNA, complete cds.//0//4583bp//83%//AF143946
- 15 C-PLACE3000276
- C-PLACE3000310
- C-PLACE3000320
- C-PLACE3000331
- 20 C-PLACE3000339//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.60E-08//359aa//23 %//P08640
- C-PLACE3000352
- C-PLACE3000353//Homo sapiens mRNA; cDNA DKFZp586H0623 (from clone DKFZp586H0623).//0//2456bp//99%//AL096739
- 25 C-PLACE3000362
- C-PLACE3000365
- C-PLACE3000388
- C-PLACE3000413
- C-PLACE3000425
- 30 C-PLACE4000009//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMHC-B).//2.90E-54//626aa//29%//P35580
- C-PLACE4000014//X-LINKED HELICASE II (X-LINKED NUCLEAR PROTEIN) (XNP).//3.10E-111//348aa//41%//P46100
- C-PLACE4000052//Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA, complete cds.//0//4661bp//99%//AF165281
- 35 C-PLACE4000089
- C-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds.//1.60E-86//190aa//88%//AF091234
- C-PLACE4000129
- 40 C-PLACE4000147
- C-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//7.00E-22//369aa//25%//P52746
- C-PLACE4000211//Homo sapiens TTF-I interacting peptide 5 mRNA, partial cds.//1.70E-262//1217bp//98%//AF000422
- C-PLACE4000222
- 45 C-PLACE4000269//Homo sapiens mRNA for KIAA1067 protein, partial cds.//0//3787bp//99%//AB028990
- C-PLACE4000270
- C-PLACE4000300
- C-PLACE4000387
- C-PLACE4000392
- 50 C-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//0//5142bp//90%//Z70200
- C-PLACE4000450//Homo sapiens TTF-I interacting peptide 5 mRNA, partial cds.//2.70E-261//1217bp//98%//AF000422
- C-PLACE4000465
- 55 C-PLACE4000489//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//5.70E-60//254aa//44%//P13002
- C-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//0//6340bp//87%//Y17267
- C-SKNC100011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//5.50E-35//431aa//29%//O60100

C-SKNMC1000046//Homo sapiens liprin-alpha3 mRNA, partial cds.//1.90E-162//1749bp//99%//AF034800
 C-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (M-TYPE).//3.20E-41//87aa//98%//P17655
 C-THYRO1000034//TRICHOHYALIN.//9.40E-10//176aa//30%//P37709
 5 C-THYRO1000070
 C-THYRO1000072//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//3.40E-16//201aa//29%//P11799
 C-THYRO1000092
 10 C-THYRO1000121//Homo sapiens mRNA for KIAA1116 protein, complete cds.//0//2159bp//99%//AB029039
 C-THYRO1000124
 C-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//0//2362bp//99%//AJ005698
 C-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//0//1409bp//98%//AB014552
 C-THYRO1000206
 15 C-THYRO1000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.00E-118//239aa//66%//P51523
 C-THYRO1000253
 C-THYRO1000270
 C-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//0//2161bp//99%//AB016068
 C-THYRO1000320
 20 C-THYRO1000358//SELENIUM-BINDING LIVER PROTEIN.//2.30E-229//237aa//79%//P17563
 C-THYRO1000368
 C-THYRO1000381
 C-THYRO1000387
 C-THYRO1000394//Homo sapiens peroxisomal membrane protein PMP 24 mRNA, complete cds.//1.20E-299//1325bp//99%//AF072864
 25 C-THYRO10003957//Homo sapiens actin-binding protein (IPP) mRNA, complete cds.//0//2092bp//99%//AF156857
 C-THYRO1000401
 C-THYRO1000488//Homo sapiens HFB30 mRNA, complete cds.//0//2254bp//100%//AB022663
 C-THYRO1000501//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//4.20E-98//408aa//42%//P19474
 30 C-THYRO1000558
 C-THYRO1000570
 C-THYRO1000605//Homo sapiens histone acetyltransferase (HBOa) mRNA, complete cds.//0//3080bp//99%//AF140360
 35 C-THYRO1000625
 C-THYRO1000637
 C-THYRO1000676
 C-THYRO1000684//Homo sapiens mRNA for KIAA0872 protein, complete cds.//0//2131bp//99%//AB020679
 40 C-THYRO1000712
 C-THYRO1000805
 C-THYRO1000815
 C-THYRO1000855
 C-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//7.50E-57//315aa//43%//P32322
 45 C-THYRO1000988
 C-THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//8.40E-12//167aa//29%//P31948
 C-THYRO1001120//Mus musculus FX-induced thymoma transcript (FXI-T1) mRNA, complete cds.//1.90E-92//1479bp//66%//U38252
 50 C-THYRO1001204//Homo sapiens cathepsin Z precursor (CTS2) gene, exons 4, 5, and 6 and complete cds; and TH1 gene partial sequence.//3.80E-100//478bp//99%//AF136276
 C-THYRO1001262
 C-THYRO1001271
 C-THYRO1001287//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE) (FRAGMENT).//3.40E-51//429aa//33%//P45701
 55 C-THYRO1001313//Homo sapiens sorting nexin 11 (SNX11) mRNA, complete cds.//0//2330bp//94%//AF121861
 C-THYRO1001347
 C-THYRO1001363//Homo sapiens mRNA; cDNA DKFp56400423 (from clone DKFp56400423).//0//2173bp//99%//AL080120

- C-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds.//01/1700bp//99%//AB014607
C-THYRO1001403
C-THYRO1001405//PLECTIN.//6.90E-19//450aa//27%//P30427
5 C-THYRO1001406//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//01/1676bp//98%//AF078850
C-THYRO1001426
C-THYRO1001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMHC-B).//2.70E-17//559aa//59%//P35580
10 C-THYRO1001480
C-THYRO1001487
C-THYRO1001584
C-THYRO1001661
C-THYRO1001746
C-THYRO1001772
15 C-THYRO1001854
C-Y79AA1000013//Mus musculus RING finger protein A07 mRNA, complete cds.//8.90E-205//1435bp//81 %//AF171060
C-Y79AA1000033//Homo sapiens CARD4 mRNA, complete cds.//01/2929bp//96%//AF126484
C-Y79AA1000231//Homo sapiens nucleolar protein NOP5/NOP58 mRNA, complete cds.//01/1515bp//99%//AF123534
20 C-Y79AA1000342//Homo sapiens Ciz1 mRNA, complete cds.//01/2644bp//81%//AB030835
C-Y79AA1000349//M.musculus Sprn mRNA for RNA binding protein.//01/2048bp//93%//X84692
C-Y79AA1000410
C-Y79AA1000539
25 C-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence.//1.00E-302//1375bp//99%//AF091080
C-Y79AA1000802
C-Y79AA1000827
C-Y79AA1000968//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//01/1586bp//99%//AF100757
30 C-Y79AA1000969
C-Y79AA1000985//Human centrosomal protein kendrin mRNA, complete cds.//4.70E-151//985bp//87%//U52962
C-Y79AA1001061
C-Y79AA1001068
C-Y79AA1001216
35 C-Y79AA1001299//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//01/996bp//99%//AJ011738
C-Y79AA1001511
C-Y79AA1001594//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//2.50E-14//410aa//24%//Q00547
C-Y79AA1001692//Mus musculus strain C57BL/J germ cell-less protein (Gd) mRNA, complete cds.//1.140E-78//227aa//40%//Q01820
40 C-Y79AA1001868//Homo sapiens zinc finger protein ZNF180 (ZNF180) mRNA, complete cds.//01/2927bp//97%//AF192913
C-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//4.50E-08//135aa//31%//P43489
45 C-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1).//9.00E-17//120aa//45%//Q24133
C-Y79AA1002210//YTUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//0.0000018//140aa//25%//Q13829
C-Y79AA1002211//PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN HOMOLOG F40A3.3.//1.70E-17//146aa//35%//U16264
50 C-Y79AA1002220
C-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//01/3168bp//99%//AB014592
C-Y79AA1002258//Homo sapiens mRNA for HIP1R, complete cds.//01/2106bp//99%//AB013384
C-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//6.90E-140//966bp//82%//Y18208
55 C-Y79AA1002399//Homo sapiens mRNA for sperm protein.//01/1163bp//95%//X91879
C-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds.//3.9e-317//1902bp//86%//U49385
C-Y79AA1002431//TRANSDUCIN-LIKE ENHANCER PROTEIN 2 (ESG2).//9.80E-62//318aa//35%//Q04725

- C-Y79AA1002482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.70E-137//340aa//51%//Q05481
- C-Y79AA1002487//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.//7.3e-310//1444bp//98%//AF129534
- 5 C-HEMBA1000290
- C-HEMBA1000459
- C-HEMBA1000505
- C-HEMBA1001196//Human DNA topoisomerase II (top2) mRNA, complete cds.//1.60E-268//1213bp//100%//J04088
- 10 C-HEMBA1002503
- C-HEMBA1002508
- C-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//0//2432bp//99%//AJ011972
- C-HEMBA1003480
- 15 C-HEMBA1003538//COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41).//2.40E-110//242aa//58%//P00736
- C-HEMBA1003645//TTPD PROTEIN.//2.40E-10//289aa//23%//I015736
- C-HEMBA1003646//Homo sapiens mRNA for KIAA1013 protein, partial cds.//0//3049bp//99%//AB023230
- C-HEMBA1003667
- 20 C-HEMBA1003679//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN).//1.00E-09//611aa//22%//P23253
- C-HEMBA1003827
- C-HEMBA1003838
- C-HEMBA1004055
- 25 C-HEMBA1004056
- C-HEMBA1004086
- C-HEMBA1004335
- C-HEMBA1004353//C-MYC BINDING PROTEIN MM-1.//3.00E-71//89aa//96%//Q99471
- C-HEMBA1004479//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//3.10E-51//152aa//40%//Q61221
- 30 C-HEMBA1004499//Homo sapiens delta-tubulin mRNA, complete cds.//3.40E-92//483bp//95%//AF201333
- C-HEMBA1004507
- C-HEMBA1004638
- C-HEMBA1004669//SON PROTEIN (SON3).//7.30E-17//288aa//36%//P18583
- 35 C-HEMBA1004709
- C-HEMBA1004860
- C-HEMBA1005206//Drosophila simulans anon73B1 gene and Su(P) gene.//1.90E-11//376bp//63%//AJ250308
- C-HEMBA1005472
- C-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.90E-129//332aa//61%//I002193
- 40 C-HEMBA1005572
- C-HEMBA1005780
- C-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//2371bp//100%//AF082516
- C-HEMBA1006038//LAMININ ALPHA-5 CHAIN (FRAGMENT).//3.10E-33//81aa//64%//Q61001
- 45 C-HEMBA1006124
- C-HEMBA1006461
- C-HEMBA1006521//3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE).//4.00E-33//177aa//42%//P25716
- C-HEMBA1006617
- 50 C-HEMBA1006650//ARP2/3 COMPLEX 20 KD SUBUNIT (P20-ARC).//9.00E-40//113aa//82%//I015509
- C-HEMBA1006779
- C-HEMBA1006796
- C-HEMBA1006812
- C-HEMBA1006914//Human anthracycline-associated resistance ARX mRNA, complete cds.//0//1837bp//99%//U35832
- 55 C-HEMBA1007174//Homo sapiens mRNA for KIAA1065 protein, complete cds.//0//1079bp//97%//AB028988
- C-HEMBA1000240
- C-HEMBA1000264//CHL1 PROTEIN.//9.50E-19//104aa//45%//P22516

C-HEMBB1000335
 C-HEMBB1000337
 C-HEMBB1000554
 C-HEMBB1000573
 5 C-HEMBB1000749
 C-HEMBB1000774
 C-HEMBB1000835
 C-HEMBB1001197
 C-HEMBB1001315
 10 C-HEMBB1001482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-57//941aa//
 27%/Q05481
 C-HEMBB1001500
 C-HEMBB1001562//CYLICIN II (MULTIPLE-BAND POLYPEPTIDE II).//1.40E-06//373aa//21%/Q28092
 C-HEMBB1001619
 15 C-HEMBB1001630
 C-HEMBB1001665
 C-HEMBB1001684//Homo sapiens mRNA for KIAA1108 protein, partial cds.//0//2348bp//99%/AB029031
 C-HEMBB1001812
 C-HEMBB1001834
 20 C-HEMBB1001869
 C-HEMBB1001871//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S 1).//5.40E-75//
 241aa//48%/P47853
 C-HEMBB1001872//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR)
 (CELL SURFACE GLYCOPROTEIN F4/80).//1.90E-22//210aa//27%/Q61549
 25 C-HEMBB1001905//TRICHOHYALIN.//2.10E-10//268aa//27%/P37709
 C-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds.//1.60E-131//
 874bp//86%/U47742
 C-HEMBB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THI-
 OLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME
 30 64E).//6.90E-132//561aa//50%/Q24574
 C-HEMBB1001925
 C-HEMBB1002044//Mus musculus mRNA for vascular cadherin-2.//0//3562bp//81%/Y08715
 C-HEMBB1002134//ZINC-FINGER PROTEIN NEURO-D4.//8.10E-56//176aa//67%/P56163
 C-HEMBB1002152
 35 C-HEMBB1002300
 C-HEMBB1002381
 C-HEMBB1002383
 C-HEMBB1002534
 C-MAMMA1000143
 40 C-MAMMA1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.40E-134//359aa//63%/P51523
 C-MAMMA1000227
 C-MAMMA1000257
 C-MAMMA1000264
 45 C-MAMMA1000270
 C-MAMMA1000279
 C-MAMMA1000372
 C-MAMMA1000559
 C-MAMMA1000752
 50 C-MAMMA1000760
 C-MAMMA1000778
 C-MAMMA1000855
 C-MAMMA1000859
 C-MAMMA1000897//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN
 55 H3) (SERUM-DERIVED HYALURONAN-ASSOCIATED PROTEIN) (SHAP).//1.00E-141//576aa//37%/Q06033
 C-MAMMA1000940
 C-MAMMA1001073
 C-MAMMA1001080//Homo sapiens SNC73 protein (SNC73) mRNA, complete cds.//1.6e-312//1596bp//94%/

AF067420
 C-MAMMA10011987/Homo sapiens eps15RmRNA, partial cds.//0//2253bp//99%//AB015346
 C-MAMMA1001202
 C-MAMMA1001222/EBNA-2 NUCLEAR PROTEIN.//6.60E-09//255aa//29%//P12978
 5 C-MAMMA1001252
 C-MAMMA1001296
 C-MAMMA1001502
 C-MAMMA1001630
 C-MAMMA1001633/ZINC FINGER PROTEIN 165.//6.30E-39//160aa//55%//P49910
 10 C-MAMMA1001683
 C-MAMMA1001715
 C-MAMMA1001730/Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.//0//1603bp//99%//AF095687
 15 C-MAMMA1001760
 C-MAMMA1001769
 C-MAMMA1001785
 C-MAMMA1001848
 C-MAMMA1001874
 C-MAMMA1001956
 20 C-MAMMA1002009
 C-MAMMA1002033
 C-MAMMA1002155
 C-MAMMA1002498
 C-MAMMA1002545
 25 C-MAMMA1002571
 C-MAMMA1002573//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3)(GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//2.60E-19//666aa//23%//P08640
 C-MAMMA1002590
 C-MAMMA1002617/ZINC FINGER PROTEIN 135.//7.60E-89//252aa//57%//P52742
 30 C-MAMMA1002618
 C-MAMMA1002636
 C-MAMMA1002646
 C-MAMMA1002665
 C-MAMMA1002708
 35 C-MAMMA1002728
 C-MAMMA1002744
 C-MAMMA1002764
 C-MAMMA1002765
 C-MAMMA1002830
 40 C-MAMMA1002844//TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT).//4.90E-10//334aa//22%//P52178
 C-MAMMA100285 8//Rat cMG1 mRNA.//3.70E-238//1147bp//92%//X52590
 C-MAMMA1002880
 C-MAMMA1002892
 45 C-MAMMA1002909
 C-MAMMA1002941
 C-MAMMA1002947
 C-MAMMA1002972/VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27.//1.10E-05//69aa//42%//P40343
 50 C-MAMMA1002973
 C-MAMMA1002987
 C-MAMMA1003003
 C-MAMMA1003026/Homo sapiens HSPC057 mRNA, complete cds.//0//1773bp//98%//AF161542
 C-MAMMA1003031
 55 C-MAMMA1003089
 C-NT2RM1000092//MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2).//1.00E-07//362aa//23%//P39843
 C-NT2RM1000272

- C-NT2RM1000341
C-NT2RM1000539//Homo sapiens mRNA for Lsm5 protein.//3.00E-158//733bp//99%//AJ238097
C-NT2RM1000553//Homo sapiens putative glycolipid transfer protein mRNA, complete cds.//3.40E-177//814bp//99%//AF103731
- 5 C-NT2RM1000623//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775
C-NT2RM1000702//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//5.60E-08//187aa//27%//P49695
C-NT2RM1000833//Homo sapiens sec61 homolog mRNA, complete cds.//0//3541bp//99%//AF084458
C-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//5107bp//99%//AF082516
- 10 C-NT2RM1001082
C-NT2RM1001112
C-NT2RM2001105//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//1.20E-28//805bp//61%//AF053091
- 15 C-NT2RM2001360//Homo sapiens clone C40 unknown mRNA.//1.00E-250//1136bp//100%//AF103798
C-NT2RM2001797//Homo sapiens mRNA; cDNA DKFZp572C163 (from clone DKFZp572C163); partial cds.//0//2300bp//100%//AL110217
C-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//0//2249bp//99%//AF044195
- 20 C-NT2RM4002504
C-NT2RP1000409
C-NT2RP1000460//Homo sapiens mRNA for KIAA1068 protein, partial cds.//0//3199bp//99%//AB028991
C-NT2RP1000746//Homo sapiens 60S acidic ribosomal protein PO mRNA, complete cds.//9.70E-196//901bp//99%//AF173378
- 25 C-NT2RP1000796
C-NT2RP1001013//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.70E-253//425aa//98%//P51522
C-NT2RP2001214
C-NT2RP2001233//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.00E-128//409aa//45%//Q05481
- 30 C-NT2RP2001440//Homo sapiens mRNA for 14-3-3gamma, complete cds.//0//3712bp//99%//AB024334
C-NT2RP2002056
C-NT2RP2002105//H.sapiens MSH-R gene for melanocyte stimulating hormone receptor.//0//1644bp//98%//X65634
- 35 C-NT2RP2002333
C-NT2RP2002677
C-NT2RP2002755
C-NT2RP2002843
C-NT2RP2003101
- 40 C-NT2RP2003668
C-NT2RP2003799
C-NT2RP2004095
C-NT2RP2004300
C-NT2RP2004675
- 45 C-NT2RP2004920//TRANSCRIPTIONAL REGULATOR ATRX (X-LINKED NUCLEAR PROTEIN) (HETERO-CHROMATIN PROTEIN 2) (HP1 ALPHA-INTERACTING PROTEIN) (HP1-BP38 PROTEIN).//4.20E-09//804aa//22%//Q61687
C-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//2.10E-308//1437bp//98%//AF045583
- 50 C-NT2RP2005719//GPI-ANCHORED PROTEIN P137.//4.00E-14//99aa//43%//Q14444
C-NT2RP2005726
C-NT2RP2005776//POLY(A) POLYMERASE TYPE 2 (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYL-TRANSFERASE).//4.40E-55//358aa//42%//P51005
C-NT2RP2005980
- 55 C-NT2RP2006184//Homo sapiens mRNA for KIAA0918 protein, partial cds.//0//4235bp//99%//AB020725
C-NT2RP2006534//5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-1 CHAIN (EC 2.7.1.-) (AMPK ALPHA-1 CHAIN) (FRAGMENT).//3.20E-11//32aa//96%//Q13131
C-NT2RP2006554

C-NT2RP3000584
 C-NT2RP3001115
 C-NT2RP3001723//Homo sapiens cell recognition molecule Caspr2 (CASPR2) mRNA, complete cds.//1.40E-58//
 1138bp//63%//AF193613
 5 C-NT2RP3001938//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//1.30E-22//2272aa//33%//P08458
 C-NT2RP3002330//Homo sapiens eRF5 mRNA, complete cds.//0//2443bp//99%//U87791
 C-NT2RP3002402
 C-NT2RP3002484//Homo sapiens mRNA for KIAA0998 protein, partial cds.//1.20E-124//597bp//98%//AB023215
 10 C-NT2RP3002512
 C-NT2RP3002713
 C-NT2RP3002770//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//1.00E-07//70aa//
 41%//P17564
 C-NT2RP3002799
 C-NT2RP3002810//HISTIDINE-RICH PROTEIN KE4.//2.20E-10//260aa//26%//Q31125
 15 C-NT2RP3002818//INSERTION ELEMENT IS2A HYPOTHETICAL 48.2 KD PROTEIN.//5.70E-226//303aa//97%//
 P51026
 C-NT2RP3002955
 C-NT2RP3002985
 C-NT2RP3003059//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//3.80E-152//1007bp//
 20 82%//U78090
 C-NT2RP3003121
 C-NT2RP3003133//Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds.//0//1998bp//
 91%//AB011414
 C-NT2RP3003138//Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.//0//2159bp//98%//
 25 AF071592
 C-NT2RP3003155
 C-NT2RP3003157
 C-NT2RP3003185//TROPOMYOSIN 1, FUSION PROTEIN 33.//2.80E-06//402aa//23%//P49455
 C-NT2RP3003264
 30 C-NT2RP3003346
 C-NT2RP3003403
 C-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//6.30E-270//
 743bp//90%//AF071317
 C-NT2RP3003500//SCY1 PROTEIN.//9.20E-27//601aa//23%//P53009
 35 C-NT2RP3003572
 C-NT2RP3003576
 C-NT2RP3003665//Homo sapiens mRNA for beta-ureidopropionase, complete cds.//0//1690bp//99%//AB013885
 C-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PRO-
 TEIN) (12E7).//2.20E-13//146aa//42%//P14209
 40 C-NT2RP3003680//Homo sapiens mRNA; cDNA DKFZp434J154 (from clone DKFZp434J154); complete cds.//0//
 2047bp//95%//AL080155
 C-NT2RP3003799//Rattus norvegicus Srg1 (Sytr1) mRNA, complete cds.//9.00E-238//1529bp//84%//U71294
 C-NT2RP3003800//Rattus norvegicus tyrosine protein kinase pp60-c-src mRNA, complete cds.//1.90E-163//
 924bp//89%//AF130457
 45 C-NT2RP3003828
 C-NT2RP3003932
 C-NT2RP3003992//Homo sapiens mRNA; cDNA DKFZp564C186 (from clone DKFZp564C186).//0//2739bp//
 99%//AL050019
 C-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein.//6.50E-240//1215bp//94%//X84692
 50 C-NT2RP3004028
 C-NT2RP3004041
 C-NT2RP3004051
 C-NT2RP3004078//H.sapiens HRFX2 mRNA.//0//1806bp//99%//X76091
 C-NT2RP3004093
 55 C-NT2RP3004095
 C-NT2RP3004125//Mus musculus zinc finger protein splice variant FIZ1-B (Fiz1) mRNA, complete cds.//4.60E-
 229//1560bp//78%//AF126747
 C-NT2RP3004148//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-

DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//7.90E-05//271aa//22%//P08640
 C-NT2RP3004155//Homo sapiens COQ7 protein mRNA, complete cds.//1.10E-179//823bp//100%//AF098948
 C-NT2RP3004189//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1.//1.30E-14//242aa//24%//Q00808
 C-NT2RP3004332
 C-NT2RP3004349
 C-NT2RP3004470
 C-NT2RP4000035
 C-NT2RP4000049
 C-NT2RP4000102
 C-NT2RP4000167
 C-NT2RP4000515
 C-NT2RP4000517
 C-NT2RP4000519
 C-NT2RP5003512//Homo sapiens mRNA for KIAA1291 protein, partial cds.//0//1980bp//99%//AB033117
 C-OVARC1000092
 C-OVARC1000533
 C-OVARC1000678
 C-OVARC1000689//Homo sapiens mRNA; cDNA DKFZp434C1415 (from clone DKFZp434C1415); partial cds.//0//2032bp//99%//AL133014
 C-OVARC1000802
 C-OVARC1000890
 C-OVARC1000891
 C-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//0//1961bp//82%//AB005549
 C-OVARC1001072
 C-OVARC1001117
 C-OVARC1001200//Mus musculus mRNA for HS1 binding protein 3.//5.80E-88//658bp//80%//AJ132192
 C-OVARC1001244//H.sapiens mRNA for Drosophila female sterile homeotic (FSH) homologue.//0//1467bp//99%//X62063
 C-OVARC1001329
 C-OVARC1001341
 C-OVARC1001376
 C-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//0//1876bp//98%//AF016507
 C-OVARC1001873
 C-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//1.60E-81//212aa//70%//P34547
 C-PLACE1000547//Homo sapiens GDP-mannose pyrophosphorylase B (GMPBP) mRNA, complete cds.//3.70E-241//1124bp//98%//AF135421
 C-PLACE1001036//Homo sapiens mRNA for KIAA1017 protein, complete cds.//0//2117bp//99%//AB023234
 C-PLACE1001076
 C-PLACE1001118//ZINC FINGER PROTEIN 135.//5.40E-147//443aa//57%//P52742
 C-PLACE1001366
 C-PLACE1001545
 C-PLACE1001608
 C-PLACE1002004
 C-PLACE1002256
 C-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1.//4.50E-76//180aa//83%//P41233
 C-PLACE1002591//CORONIN-LIKE PROTEIN P57.//4.40E-70//208aa//66%//P31146
 C-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//0//2462bp//89%//AF079765
 C-PLACE1003383
 C-PLACE1003864
 C-PLACE1004793//RETROVIRUS-RELATED ENV POLYPROTEIN.//5.20E-47//577aa//25%//P10267
 C-PLACE1004913
 C-PLACE1004979
 C-PLACE1005052//Homo sapiens CGI-16 protein mRNA, complete cds.//6.6E-313//1413bp//99%//AF132950

C-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//2431bp//99%//AB011148
 C-PLACE1005128
 C-PLACE1005162
 5 C-PLACE1005176//Homo sapiens hypothalamus protein HT001 mRNA, complete cds.//3.90E-212//1040bp//
 96%//AF113539
 C-PLACE1005467//PENICILLIN-BINDING PROTEIN 4* (PBP 4*) (PBP 4A).//1.10E-09//93aa//31%//P32959
 C-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A.//
 7.60E-97//1287bp//67%//AJ010046
 10 C-PLACE1005584//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9//ER2.6).//
 6.80E-09//267aa//30%//P29128
 C-PLACE1005611//Mus musculus mRNA for mDjO, complete cds.//2.00E-33//379bp//66%//AB028860
 C-PLACE1005802
 C-PLACE1005850
 C-PLACE1005898
 15 C-PLACE1005932
 C-PLACE1006129//Homo sapiens HSPC057 mRNA, complete cds.//0//2849bp//98%//AF161542
 C-PLACE1006360
 C-PLACE1006795
 C-PLACE1006878//TRNA-SPUCING ENDONUCLEASE SUBUNIT SEN2 (EC 3.1.27.9) (TRNA-INTRON ENDO-
 20 NUCLEASE).//1.90E-08//122aa//36%//P16658
 C-PLACE1007557
 C-PLACE1007807
 C-PLACE1008181
 C-PLACE1008426//Homo sapiens mRNA for KIAA1288 protein, partial cds.//0//3311bp//99%//AB033114
 25 C-PLACE1008455
 C-PLACE1008941
 C-PLACE1009935
 C-PLACE1010310//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//1.20E-18//467aa//30%//P46804
 C-PLACE1011891
 30 C-PLACE10118967//Mus musculus Wnt10a mRNA, complete cds.//2.60E-287//1820bp//85%//U61969
 C-PLACE2000003
 C-PLACE2000132
 C-PLACE2000170
 C-PLACE2000335
 35 C-PLACE3000124
 C-PLACE3000158
 C-PLACE3000207
 C-PLACE3000221
 C-PLACE3000271
 40 C-PLACE3000304
 C-PLACE3000322
 C-PLACE3000341
 C-PLACE3000373
 C-PLACE3000399
 45 C-PLACE3000401
 C-PLACE3000402
 C-PLACE3000406
 C-PLACE3000475
 C-PLACE4000063//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-
 50 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//1.70E-15//740aa//23%//P08640
 C-PLACE4000093
 C-PLACE4000100//Homo sapiens hydroxypyruvate reductase (GRHPR) gene, complete cds.//0//4199bp//97%//
 AF146689
 C-PLACE4000131//Homo sapiens mRNA; cDNA DKFZp586J0917 (from clone DKFZp586J0917); partial cds.//0//
 55 1612bp//97%//AL117455
 C-PLACE4000247
 C-PLACE4000250
 C-PLACE4000252

C-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD protein.//0//5143bp//90%//Z70200
 C-PLACE4000261//PEREGRIN (BR140 PROTEIN).//9.50E-10//128aa//34%//P55201
 C-PLACE4000320
 C-PLACE4000344
 5 C-PLACE4000367
 C-PLACE4000401//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-
 TIVATING ENZYME).//7.20E-22//54aa//62%//Q01576
 C-PLACE4000411//Homo sapiens mRNA; cDNA DKFZp586D0624 (from clone DKFZp586D0624); partial cds.//
 0//2159bp//98%//AL117654
 10 C-PLACE4000487
 C-PLACE4000494
 C-PLACE4000521
 C-PLACE4000548//Homo sapiens mRNA for KIAA0947 protein, partial cds.//0//4864bp//99%//AB023164
 C-SKNMC1000013//Homo sapiens ATP-binding cassette protein M-ABC1 mRNA, nuclear gene encoding mito-
 15 chondrial protein, complete cds.//0//2384bp//99%//AF047690
 C-SKNMC1000091//Homo sapiens mRNA for leucine-zipper protein, complete cds.//6.10E-190//872bp//99%//
 AB021663
 C-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//0//3711bp//99%//AB018333
 C-THYRO1000569//Mus musculus hematopoietic zinc finger protein mRNA, complete cds.//0//1557bp//91%//
 20 AF118566
 C-THYRO1001142
 C-THYRO1001189//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-200//546aa//
 62%//005481
 C-THYRO1001320
 25 C-THYRO1001537//Homo sapiens mRNA; cDNA DKFZp586A0522 (from clone DKFZp586A0522); partial cds.//
 0//1010bp//98%//AL050159
 C-THYRO1001602
 C-THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).//9.30E-34//220aa//38%//Q04652
 C-THYRO1001828
 30 C-Y79AA1000346//Homo sapiens nonclathrin coat protein gamma2-COP mRNA, complete cds.//0//2520bp//99%//
 AF157833
 C-Y79AA1001167
 C-Y79AA1001384//Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds.//0//
 4708bp//99%//AF055084
 35 C-Y79AA1001875//RAS-RELATED PROTEIN RAB-7.//9.40E-12//34aa//97%//P51149
 C-Y79AA1002103//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.00E-257//549aa//76%//P16415
 C-HEMBA1006092
 C-HEMBA1006406
 C-HEMBA1006790
 40 C-HEMBA1000917
 C-HEMBA1002280
 C-MAMMA1000802
 C-MAMMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.00000017//46aa//60%//
 P20931
 45 C-MAMMA1002597
 C-MAMMA1002868
 C-NT2RP2003161
 C-NT2RP2003339
 C-NT2RP3001282
 50 C-PLACE1001761
 C-PLACE1004491
 C-PLACE1004686
 C-PLACE1005574
 C-PLACE1006382
 55 C-PLACE1006792
 C-PLACE3000455
 C-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds.//0//2567bp//88%//AF030430
 C-THYRO1000916

C-HEMBA1000327
 C-HEMBA1000637
 C-HEMBA1001967
 C-MAMMA1000266
 C-NT2RP2002979
 C-PLACE1007866
 C-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE PAK-GAMMA (EC 2.7.1.-) (GAMMA-PAK)
 (P21-ACTIVATED KINASE 2) (PAK-2) (PAK65) (S6/H4 KINASE).//9.80E-25//155aa//45%//Q13177
 C-PLACE4000156//ZINC FINGER PROTEIN 132.//7.10E-15//1476aa//46%//P52740
 C-THYRO1001637
 C-MAMMA1002215
 C-MAMMA1002721
 C-NT2RP2002070

Homology search result 14.

[0334] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences. In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be compared. Each data includes Clone name, Definition in matching data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of matching data. These items are shown in this order, separated by a double-slash mark, //.

C-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.90E-250//554aa//85%//O61712
 C-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE-TRNA LIGASE)
 (LEURS).//6.40E-99//457aa//45%//Q09996
 C-HEMBA1000020//Homo sapiens beta 2 gene.//7.50E-264//1194bp//95%//X02344
 C-HEMBA1000030//Homo sapiens ARF GTPase-activating protein GIT1 mRNA, complete cds.//0//1759bp//99%//
 AF124490
 C-HEMBA1000129//HYPOTHETICAL HEUCASE C8A4.08C IN CHROMOSOME I.//3.80E-25//166aa//36%//
 Q09884
 C-HEMBA1000141//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1135bp//100%//
 AF196304
 C-HEMBA1000150//Homo sapiens putative RNA helicase mRNA, complete cds.//5.20E-213//525bp//99%//
 AF085356
 C-HEMBA1000156//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//
 1.90E-12//368aa//24%//P08553
 C-HEMBA1000158//HEPATOCYTE NUCLEAR FACTOR 3-GAMMA (HNF-3G).//5.00E-16//166aa//36%//P35584
 C-HEMBA1000168//CYCLIN I (MULTIPLE-BAND POLYPEPTIDE D.//2.90E-14//303aa//25%//P35662
 C-HEMBA1000185//RAS-RELATED PROTEIN RAL-A.//3.40E-12//125aa//31%//P48555
 C-HEMBA1000201//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//1612bp//99%//AJ011738
 C-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PRO-
 TEIN).//1.00E-86//146aa//56%//O61221
 C-HEMBA1000303//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//7.10E-254//1440bp//87%//
 AF030131
 C-HEMBA1000304//Rattus norvegicus Ca2+-dependent activator protein (CAPS) mRNA, complete cds.//5.10E-
 131//712bp//91%//U16802
 C-HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1//5.20E-
 49//107aa//91%//O35594
 C-HEMBA1000333//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.//0//1866bp//100%//
 AF174601
 C-HEMBA1000369//Homo sapiens mRNA for PICK1, complete cds.//0//1949bp//98%//AB026491
 C-HEMBA1000411//ANKYRIN.//5.70E-12//127aa//38%//Q02357
 C-HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).//3.30E-45//481aa//29%//Q04652
 C-HEMBA1000491//RAS-LIKE PROTEIN 2.//2.00E-22//188aa//31%//P22279
 C-HEMBA1000518//PECANEX PROTEIN.//2.10E-19//227aa//38%//P18490
 C-HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.//2.40E-44//292aa//36%//Q01755
 C-HEMBA1000531//HEAT SHOCK 70 KD PROTEIN COGNATE 1 (HEAT SHOCK 70 KD PROTEIN 70C) (FRAG-
 MENTS).//2.60E-12//73aa//41%//P02826

- C-HEMBA1000542//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//2.20E-194//663bp//83%//D89340
- C-HEMBA1000555//Mus musculus Msx2 interacting nuclear target protein mRNA, complete cds.//7.90E-226//1501bp//83%//AF156529
- 5 C-HEMBA1000561//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//3.40E-37//674aa//25 %//Q05481
- C-HEMBA1000569//GPI-ANCHORED PROTEIN P137.//6.50E-19//265aabp//32%//Q60865
- C-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//2.10E-144//602bp//77%//AF045573
- 10 C-HEMBA1000591//PTB-ASSOCIATED SPLICING FACTOR (PSF).//2.20E-17//198aa//40%//P23246
- C-HEMBA1000592//Homo sapiens sorting nexin 6 (SNX6) mRNA, complete cds.//0//1465bp//99%//AF121856
- C-HEMBA1000608//HYPOTHETICAL PROTEIN KIA0411 (FRAGMENT)//1.80E-55//179aa//61%//O43295
- C-HEMBA1000657//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//7.20E-158//1366bp//76%//U35776
- 15 C-HEMBA1000651//Homo sapiens DNA binding protein p96PIF mRNA, complete cds.//0//1862bp//99%//AF173868
- C-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD).//1.00E-78//119aa//87%//P51689
- C-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN)//1.60E-30//127aa//40%//P43366
- 20 C-HEMBA1000919//HYPOTHETICAL 65.5 KD TRP-ASP REPEATS CONTAINING PROTEIN F02E8.5 IN CHROMOSOME X.//1.00E-10//288aa//23%//Q19124
- C-HEMBA1001019//CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.-) (P34 PROTEIN KINASE) (CYCLIN-DEPENDENT KINASE 1) (CDK1).//3.10E-10//70aa//58%//P06493
- C-HEMBA1001043//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)(FRAGMENT).//1.40E-12//131aa//38%//Q01485
- 25 C-HEMBA1001059//Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 14.//4.80E-169//786bp//99%//U06088
- C-HEMBA1001071//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//1.50E-92//82aa//100%//P02461
- C-HEMBA1001077//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.//2.00E-80//432bp//94%//AF119043
- 30 C-HEMBA1001088//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//3.50E-50//176aa//57%//P48059
- C-HEMBA1001137//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065)(HA0946) (FRAGMENT).//1.50E-116//197aa//58%//Q06730
- 35 C-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//6.80E-79//179aa//80%//P51646
- C-HEMBA1001197//Homo sapiens rap2 interacting protein x mRNA, complete cds.//0//1511bp//99%//AF112221
- C-HEMBA1001257//Homo sapiens mRNA 2-methylacyl-CoA racemase.//0//1672bp//99%//AJ130733
- C-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//0.00000002//198aa//29%//Q60401
- 40 C-HEMBA1001302//Homo sapiens calcium binding protein precursor, mRNA, complete cds.//9.60E-258//682bp//94%//AF153686
- C-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//1.40E-133//614bp//99%//AF057358
- C-HEMBA1001387//GTP-BINDING PROTEIN TC10.//2.90E-64//104aa//82%//P17081
- 45 C-HEMBA1001405//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//5.60E-25//863bp//60%//AF053091
- C-HEMBA1001446//Homo sapiens rap2 interacting protein x mRNA, complete cds.//9.20E-55//719bp//68%//AF112221
- C-HEMBA1001455//Mus musculus transposon-derived Buster2 transposase-like protein gene, partial cds.//4.20E-290//2008bp//81%//AF205599
- 50 C-HEMBA1001476//Human DNA topoisomerase II (top2) mRNA, complete cds.//1.60E-268//1213bp//100%//J04088
- C-HEMBA1001510//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).//1.70E-16//63aa//61%//P18850
- 55 C-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//4.90E-37//399aa//29%//P29166
- C-HEMBA1001569//SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2).//2.30E-53//110aa//100%//P19065
- C-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//808bp//97%//AJ012449

- C-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//4.90E-156//348aa//83%//Q14141
 C-HEMBA1001620//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.60E-166//506aa//60%//P42803
- 5 C-HEMBA1001635//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA).//1.60E-10//155aa//28%//Q63679
 C-HEMBA1001651//CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 1 (CYTADHERENCE ACCESSORY PROTEIN 1).//6.20E-07//362aa//24%//Q50365
 C-HEMBA1001661//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//4.60E-36//365aa//33%//P33450
- 10 C-HEMBA1001672//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds.//0//1707bp//98%//AF072247
 C-HEMBA1001675//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.//5.40E-09//101aa//35%//P54787
- 15 C-HEMBA1001714//Homo sapiens mRNA for ATPase inhibitor precursor, complete cds.//3.70E-78//200bp//100%//AB029042
 C-HEMBA1001723//Homo sapiens G protein beta subunit mRNA, partial cds.//3.10E-267//1212bp//99%//AF195883
 C-HEMBA1001734//CADHERIN-11 PRECURSOR (OSTEOBLAST-CADHERIN) (OBCADHERIN) (OSF-4).//1.10E-38//87aa//96%//P55288
- 20 C-HEMBA1001744//SCY1 PROTEIN.//9.90E-32//481aa//25%//P53009
 C-HEMBA1001746//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.//7.60E-59//998bp//64%//AF098066
 C-HEMBA1001804//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//1637bp//99%//AF125158
- 25 C-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//3.80E-11//206aa//36%//P11675
 C-HEMBA1001819//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.90E-135//459aa//52%//Q99676
 C-HEMBA1001822//Mus musculus Ese2L protein mRNA, complete cds.//1.90E-235//1329bp//89%//AF132479
 C-HEMBA1001824//Homo sapiens nuclear protein NP94 mRNA, complete cds.//1.40E-199//1180bp//89%//AF159025
- 30 C-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//7.60E-64//1221aa//55%//Q07230
 C-HEMBA1001866//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//5.70E-51//234aa//41%//Q09332
 C-HEMBA1001869//TRITHORAX PROTEIN.//9.60E-05//166aa//27%//P20659
- 35 C-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (ME2GLYDH).//9.30E-36//395aa//26%//Q63342
 C-HEMBA1001913//GCN20 PROTEIN.//2.30E-81//158aa//50%//P43535
 C-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//0//1850bp//99%//AF000145
- 40 C-HEMBA1001967//Homo sapiens NY-REN-57 antigen mRNA, partial cds.//0//1721bp//99%//AF155114
 C-HEMBA1002035//Homo sapiens BAZ1A mRNA for bromodomain adjacent to zinc finger domain 1A, complete cds.//0//2149bp//99%//AB032252
 C-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.30E-271//1583bp//88%//J92703
- 45 C-HEMBA1002102//ANKYRIN.//4.40E-10//106aa//35%//Q02357
 C-HEMBA1002139//ILIM AND SH3 DOMAIN PROTEIN LASP-1 (MLN 50).//7.10E-05//51aa//49%//Q14847
 C-HEMBA1002151//Rattus norvegicus p34 mRNA, complete cds.//1.10E-153//1059bp//82%//AF178669
 C-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.40E-51//180aa//56%//P79293
- 50 C-HEMBA1002177//TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).//6.00E-13//190aa//36%//P43694
 C-HEMBA1002212//TYROSINE-PROTEIN KINASE-2 (EC 2.7.1.112) (FRAGMENT).//3.30E-07//267aa//29%//P18161
 C-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//2.20E-199//392aa//89%//P47226
- 55 C-HEMBA1002241//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//3.70E-06//95aa//33%//P46087
 C-HEMBA1002267//Sus scrofa decorin mRNA, complete cds.//1.10E-46//302bp//90%//AF125537
 C-HEMBA1002341//IP53-BINDING PROTEIN 2 (53BP2) (FRAGMENT).//3.80E-55//109aa//98%//Q62415
 C-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//

- 1847bp//99%//AF092563
 C-HEMBA1002417//mGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1)//1.00E-121//489aa//52%//P39447
- 5 C-HEMBA1002419//TRICHOHYALIN//1.90E-09//299aa//24%//P22793
 C-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74//4.20E-24//109aa//55%//Q00994
 C-HEMBA1002469//DXS8237E PROTEIN (FRAGMENT)//3.50E-50//199aa//61%//P98175
 C-HEMBA1002475//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//1.10E-12//285aa//31%//P17437
- 10 C-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1//6.80E-53//257aa//36%//P48732
 C-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//0.10E-24//2432bp//99%//AJ011972
 C-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds.//0.1605bp//97%//AF016903
 C-HEMBA1002555//Homo sapiens mSin3A associated polypeptide p30 mRNA, complete cds.//5.30E-51//768bp//68%//AF055993
- 15 C-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds.//6.80E-305//951bp//99%//AF075587
 C-HEMBA1002746//DNA POLYMERASE BETA (EC 2.7.7.7)//5.00E-37//268aa//34%//P06746
 C-HEMBA1002768//Mus musculus formin binding protein 17 mRNA, partial cds.//7.80E-237//1522bp//85%//AB011126
- 20 C-HEMBA1002770//Rattus norvegicus mRNA for TIP120, complete cds.//2.90E-176//1024bp//88%//D87671
 C-HEMBA1002776//Fugu rubripes BAW (BAW) mRNA, complete cds.//3.40E-54//319bp//76%//AF153879
 C-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//8.2E-314//1437bp//99%//AF071185
- 25 C-HEMBA1002818//Homo sapiens mRNA for fibulin-4.//2.00E-304//1383bp//99%//AJ132819
 C-HEMBA1002876//HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME n.//1.50E-44//188aa//52%//Q09297
 C-HEMBA1002935//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//1.30E-15//371aa//25%//Q05481
 C-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)//2.00E-34//300aa//34%//P16157
- 30 C-HEMBA1002951//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110)//4.40E-06//324aa//24%//P32380
 C-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17) (DPDE4)//1.20E-27//63aa//100%//P14646
- 35 C-HEMBA1002997//CENTROMERIC PROTEIN E (CENP-E PROTEIN)//3.80E-25//534aa//24%//Q02224
 C-HEMBA1002999//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//1.40E-171//1552bp//75%//U02086
 C-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA.//0.1558bp//99%//AF054182
- 40 C-HEMBA1003071//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR (ALS)//1.30E-09//121aa//40%//P35858
 C-HEMBA1003077//SLIT PROTEIN PRECURSOR//2.60E-15//199aa//31%//P24014
 C-HEMBA1003096//Mouse 19.5 mRNA, complete cds.//5.60E-117//1139bp//72%//M32486
 C-HEMBA1003098//Homo sapiens NY-REN-6 antigen mRNA, partial cds.//6.20E-273//1253bp//99%//AF155096
- 45 C-HEMBA1003136//MANNULOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNULOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE)//8.50E-51//221aa//33%//P41940
 C-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//0.1583bp//99%//AJ005670
 C-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE (EC 2.1.1.61)//5.90E-74//134aa//53%//P44551
- 50 C-HEMBA1003199//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.//8.50E-87//285bp//90%//AF129534
 C-HEMBA1003235//TROPOMYOSIN//2.30E-06//109aa//33%//Q02088
 C-HEMBA1003250//PROTEIN KINASE APK1A (EC 2.7.1.-)//7.20E-41//245aa//42%//Q06548
- 55 C-HEMBA1003281//POLIOVIRUS RECEPTOR PRECURSOR//6.00E-11//239aa//32%//P32506
 C-HEMBA1003286//Homo sapiens mRNA for beta-1,4-galactosyltransferase IV, complete cds.//5.40E-229//1043bp//99%//AB024436
 C-HEMBA1003291//SNF1-RELATED PROTEIN KINASE KIN10 (EC 2.7.1.-) (AKIN10)//7.60E-28//126aa//51%//

Q38997

C-HEMBA1003369//CENTROMERIC PROTEIN E (CENP-E PROTEIN) //2.00E-08//248aa//23%//Q02224

C-HEMBA1003408//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (VERSION 1) //7.80E-13//297aa//30%//P18616

5 C-HEMBA1003417//Homo sapiens BAG-family molecular chaperone regulator-2 mRNA, complete cds //1.50E-255//1179bp//99%//AF095192

C-HEMBA1003418//TRICHOHYALIN //8.70E-19//281aa//31%//P37709

C-HEMBA1003438//Homo sapiens gene for NBS1, complete cds //0//511bp//94%//AB013139

10 C-HEMBA1003538//COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.2.41.41) //2.40E-110//242aa//58%//P00736

C-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (TSLET-2) //8.80E-189//360aa//96%//P50480

C-HEMBA1003555//NUCLEOTIDE-BINDING PROTEIN (NBP) //2.10E-68//251aa//52%//P53384

C-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)(Y)(S)(G)(O) GAMMA-2 SUBUNIT (GAMMA-1) //1.20E-31//171aa//100%//P16874

15 C-HEMBA1003568//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)) //7.90E-49//279aa//32%//P19474

C-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1 //6.90E-206//445aa//74%//Q13330

C-HEMBA1003581//ITALIN //4.40E-45//52aa//98%//P26039

20 C-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP) //4.40E-10//118aa//35%//P19682

C-HEMBA1003615//Homo sapiens ART-4 mRNA, complete cds //0//1713bp//99%//AB026125

C-HEMBA1003617//Homo sapiens ubiquitin-like product Chap1/Dsk2 mRNA, complete cds //6.90E-178//501bp//97%//AB015344

C-HEMBA1003645//TIPD PROTEIN //2.40E-10//289aa//23%//O15736

25 C-HEMBA1003662//TBX2 PROTEIN (T-BOX PROTEIN 2) //1.20E-75//151aa//99%//Q13207

C-HEMBA1003679//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN) //1.00E-09//611aa//22%//P23253

C-HEMBA1003680//PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-) //2.40E-92//423aa//47%//P34629

30 C-HEMBA1003684//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN) //2.00E-73//526aa//32%//Q13105

C-HEMBA1003690//HISTONE DEACETYLASE HDA1 //2.10E-59//249aa//47%//P53973

C-HEMBA1003742//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds //1.70E-44//501bp//67%//AF037339

35 C-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA) //3.70E-124//347aa//55%//Q16665

C-HEMBA1003773//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds //5.80E-81//511bp//86%//U17343

C-HEMBA1003783//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds //1.10E-190//1204bp//84%//AF084259

40 C-HEMBA1003805//Mus musculus KH domain RNA binding protein QKI-5A mRNA, complete cds //0//988bp//95%//AF090402

C-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1) //8.10E-31//134aa//52%//P40484

C-HEMBA1003866//Mus musculus semaphorin VIa mRNA, complete cds //1.20E-105//1192bp//70%//AF030430

45 C-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT) //3.80E-16//89aa//46%//P16372

C-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds //8.50E-221//1188bp//78%//AF091234

C-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT) //1.60E-166//416aa//72%//Q14141

50 C-HEMBA1004168//Homo sapiens geminin mRNA, complete cds //3.90E-208//951 bp//99%//AF067855

C-HEMBA1004199//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III //8.40E-60//243aa//39%//P34529

C-HEMBA1004202//RAS-RELATED PROTEIN RAB-13 //6.20E-30//208aa//37%//P51153

C-HEMBA1004203//NUCLEOLAR PROTEIN NOP2 //1.50E-12//258aa//29%//P40991

C-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds //0//1892bp//99%//U50748

55 C-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds //5.70E-217//1217bp//88%//AF095927

C-HEMBA1004248//INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 (IMMEDIATE-EARLY PROTEIN CL-6) //2.00E-43//98aa//84%//Q08755

- C-HEMBA1004275//Homo sapiens PHD-finger protein (GRCS) mRNA, complete cds.//1.10E-152//1403bp//69%//AF043725
- C-HEMBA1004276//Homo sapiens AP-4 adaptor complex beta4 subunit mRNA, complete cds.//4.80E-257//738bp//99%//AF092094
- 5 C-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.//0//1982bp//99%//AF022795
- C-HEMBA1004295//Homo sapiens NY-REN-25 antigen mRNA, partial cds.//9.40E-31//381bp//65%//AF155103
- C-HEMBA1004321//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.30E-93//357aa//42%//Q99676
- C-HEMBA1004353//C-MYC BINDING PROTEIN MM-1.//3.00E-71//89aa//96%//Q99471
- 10 C-HEMBA1004354//CHL1 PROTEIN.//9.90E-26//130aa//42%//P22516
- C-HEMBA1004356//H. sapiens MSSP-2 mRNA.//3.00E-243//573bp//98%//X77494
- C-HEMBA1004389//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//1437bp//99%//AF125158
- 15 C-HEMBA1004408//PEPTIDYL-PROLYL-CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN-10).//3.20E-32//148aa//52%//P52017
- C-HEMBA1004479//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//3.10E-51//152aa//40%//Q61221
- C-HEMBA1004499//Homo sapiens delta-tubulin mRNA, complete cds.//3.40E-92//483bp//95%//AF201333
- 20 C-HEMBA1004509//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//2.70E-12//200aa//28%//Q13107
- C-HEMBA1004534//Homo sapiens gamma-filamin (ABPL) mRNA, complete cds.//1.2e-316//1445bp//99%//AF089841
- C-HEMBA1004573//Homo sapiens mRNA for HELG protein.//2.00E-59//483bp//68%//AJ277291
- 25 C-HEMBA1004604//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.//0//1612bp//99%//AF193844
- C-HEMBA1004669//SON PROTEIN (SON3).//7.30E-17//288aa//36%//P18583
- C-HEMBA1004697//MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) (FRAGMENT).//2.90E-05//303aa//21%//P35749
- 30 C-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.90E-39//143aa//52%//P42743
- C-HEMBA1004752//Homo sapiens mRNA for LAK-4p, complete cds.//4.60E-109//650bp//89%//AB002405
- C-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds.//9.10E-34//515bp//66%//U49082
- C-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds.//2.60E-246//1249bp//94%//L39060
- 35 C-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.40E-111//314aa//58%//P08547
- C-HEMBA1004795//CDC4-UKE PROTEIN (FRAGMENT).//3.80E-69//198aa//66%//P50851
- C-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//8.20E-154//317aa//94%//Q00004
- 40 C-HEMBA1004889//Human C3f mRNA, complete cds.//6.70E-24//341aapb//26%//U72515
- C-HEMBA1004929//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//2.50E-05//148aa//24%//P25386
- C-HEMBA1004930//26S PROTEASOME SUBUNIT S5B (KIAA0072) (HA1357).//3.30E-27//65aa//100%//Q16401
- C-HEMBA1004972//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEURO FILAMENT PROTEIN) (NF-H).//0.0000096//286aa//23%//P12036
- 45 C-HEMBA1004973//ZINC-BINDING PROTEIN A337/4.10E-08//121aa//33%//Q02084
- C-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//0//1813bp//99%//AF041474
- C-HEMBA1005029//Homo sapiens CGI-13 protein mRNA, complete cds.//0//1487bp//99%//AF132947
- C-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16).//3.40E-101//106aa//98%//P35290
- 50 C-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//0//2762bp//99%//AF080561
- C-HEMBA1005201//Homo sapiens CGI-07 protein mRNA, complete cds.//0//1608bp//99%//AF132941
- C-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.90E-179//361aa//95%//Q00004
- 55 C-HEMBA1005206//Drosophila simulans anon73Bl gene and Su(P) gene.//1.90E-111//376bp//63%//AJ250308
- C-HEMBA1005219//NUCLEAR PROTEIN SNF7.//5.30E-10//189aa//25%//P39929
- C-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial.//3.90E-241//1095bp//99%//AJ007581
- C-HEMBA1005359//ZINC FINGER PROTEIN 137.//3.90E-85//206aa//69%//P52743
- C-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds.//9.00E-77//620bp//74%//

AF071787

C-HEMBA1005394//Mus musculus pantothenate kinase 1 beta (panK1beta) mRNA, complete cds.//3.90E-126//1097bp//75%//AF200357

C-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.//2.00E-213//537bp//99%//AF041248

C-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-)//1.90E-129//332aa//61%//O02193

C-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1) //3.10E-154//285aa//99%//Q68089

C-HEMBA1005530//Homo sapiens anaphase-promoting complex subunit 7 (APC7) mRNA, complete cds.//0//1578bp//98%//AF191340

C-HEMBA1005548//Homo sapiens MAFB/Kreisler basic region/leucine zipper transcription factor (MAFB) mRNA, complete cds.//1.00E-220//1014bp//99%//AF134157

C-HEMBA1005558//NUCLEAR PROTEIN SNF7.//6.40E-16//170aa//31%//P39929

C-HEMBA1005576//Mus musculus mRNA for plexin 2, complete cds.//1.20E-122//870bp//82%//D86949

C-HEMBA1005581//Homo sapiens SLIT2 (SLIL2) mRNA, complete cds.//0//1721bp//100%//AF133270

C-HEMBA1005582//TROPOMYOSIN 1, NON-MUSCLE ISOFORM (TROPOMYOSIN II) (CYTOSKELETAL TROPOMYOSIN) //0.00000009//213aa//27%//P09492

C-HEMBA1005595//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) //2.30E-54//562aa//29%//P34036

C-HEMBA1005621//Homo sapiens Mad2-like protein mRNA, complete cds.//8.00E-211//962bp//99%//AF072933

C-HEMBA1005666//Homo sapiens mRNA for DIPB protein.//8.60E-147//685bp//99%//AJ249128

C-HEMBA1005689//EPHRIIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 8) (LERK-8) (EPH-RELATED RECEPTOR TRANSMEMBRANE LIGAND ELK-L3) //2.10E-37//98aa//81%//Q15768

C-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) //4.40E-17//167aa//34%//P25296

C-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU/M-TYPE) //2.00E-36//342aa//33%//P00789

C-HEMBA1005931//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1) //5.60E-15//76aa//51%//P51522

C-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//2371bp//100%//AF082516

C-HEMBA1006031//Homo sapiens mRNA for putative phospholipase, complete cds.//0//1413bp//99%//AB019435

C-HEMBA1006038//LAMININ ALPHA-5 CHAIN (FRAGMENT) //3.10E-33//81aa//64%//Q61001

C-HEMBA1006067//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.//8.20E-12//297bp//64%//AF098066

C-HEMBA1006130//SEL-10 PROTEIN //0.000000043//219aa//25%//Q93794

C-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//0//1551bp//99%//AF048693

C-HEMBA1006198//PROLINE-RICH PROTEIN MP-2 PRECURSOR //1.90E-19//215aa//39%//P05142

C-HEMBA1006248//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT) //8.60E-23//151aa//37%//P16372

C-HEMBA1006253//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR //0.00000002//62aa//53%//P42698

C-HEMBA1006268//Homo sapiens HQ0024c mRNA, complete cds.//3.50E-157//845bp//92%//AF073836

C-HEMBA1006272//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-) //1.30E-123//200aa//73%//P10265

C-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE) //1.00E-210//490aa//77%//P25500

C-HEMBA1006283//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2 //0.000000012//176aa//30%//P32505

C-HEMBA1006291//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-) //4.20E-12//215aa//23%//P70473

C-HEMBA1006309//Homo sapiens aspartyl aminopeptidase mRNA, complete cds.//5.30E-169//774bp//100%//AF005050

C-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//3.70E-225//1189bp//88%//AF076183

C-HEMBA1006344//RADIXIN.//1.50E-31//333aa//28%//P26043

C-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-) //1.60E-130//332aa//62%//O02193

C-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6) //3.50E-105//381aa//54%//P28160

C-HEMBA1006398//Human L1 element L1.6 putative pi 50 gene, complete cds.//2.00E-277//1728bp//85%//U93563

C-HEMBA1006445//Homo sapiens putative tumor suppressor NOEY2 mRNA, complete cds.//1.40E-270//1224bp//

- 100%/U96750
C-HEMBA1006474//40 KD PROTEIN.//1.40E-39//292aa//34%/Q01552
C-HEMBA1006485//PUROMYCIN-SENSITIVE AMINOPEPTIDASE (EC 3.4.11.-) (PSA).//1.90E-81//153aa//97%/P55786
- 5 C-HEMBA1006507//DIAPHANOUS PROTEIN HOMOLOG 2.//1.40E-46//316aa//32%/O60879
C-HEMBA1006521//3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE).//4.00E-33//177aa//42%/P25716
C-HEMBA1006559//Mus musculus PRAJA1 (Praja1) mRNA, complete cds.//2.80E-208//1107bp//83%/U06944
- 10 C-HEMBA1006583//Drosophila melanogaster Scribble (scrib) mRNA, complete cds.//1.70E-63//1002bp//65%/AF190774
C-HEMBA1006624//DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG.//0.00000069//109aa//38%/Q58323
C-HEMBA1006650//ARP2/3 COMPLEX 20 KD SUBUNIT (P20-ARC).//9.00E-40//113aa//82%/O15509
- 15 C-HEMBA1006652//60S RIBOSOMAL PROTEIN L7.//2.40E-44//206aa//47%/P14148
C-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMC1-TFG2 INTERGENIC REGION.//3.30E-22//241aa//31%/P53196
C-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//0.00000043//111aa//40%/Q01485
- 20 C-HEMBA1006758//Homo sapiens protocadherin beta 13 (PCDH-beta13) mRNA, complete cds.//0//1832bp//91%/AF152492
C-HEMBA1006807//Homo sapiens mRNA for SPOP.//5.70E-125//1109bp//75%/AJ000644
C-HEMBA1006877//OXYSTEROL-BINDINGPROTEIN.//2.00E-59//378aa//39%/P16258
C-HEMBA1006885//Homo sapiens gene for Proline synthetase associated, complete cds.//0//1467bp//96%/AB018566
- 25 C-HEMBA1006914//Human anthracycline-associated resistance ARX mRNA, complete cds.//0//1837bp//99%/U35832
C-HEMBA1006941//Homo sapiens PKCq-interacting protein PICOT (PICOT) mRNA, complete cds.//2.10E-271//1234bp//99%/AF118649
C-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.60E-143//740bp//94%/AF004828
- 30 C-HEMBA1006976//H. sapiens mRNA for Gal-beta(1-3/4)GlcNAc alpha-2,3-sialyltransferase.//1.90E-80//447bp//89%/X74570
C-HEMBA1007018//DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (UC57/59) (DYNEIN LIGHT CHAIN A) (DLC-A).//2.40E-188//391aa//89%/Q90828
C-HEMBA1007087//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//8.30E-271//253aa//30%/Q10568
- 35 C-HEMBA1007121//Homo sapiens bisphosphate 3'-nucleotidase mRNA, complete cds.//1.70E-252//1118bp//92%/AF125042
C-HEMBA1007151//Homo sapiens synphilin 1 mRNA, complete cds.//0//1900bp//99%/AF076929
C-HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds.//3.80E-271//642bp//99%/AF062085
C-HEMBA1007194//Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds.//0//1588bp//99%/AF139658
C-HEMBA1007224//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1590bp//99%/AF196304
- 40 C-HEMBA1007243//Chinese hamster hpmt mRNA, complete cds.//2.00E-58//650bp//70%/J00060
C-HEMBA1007251//Homo sapiens F-box protein FBX29 (FBX29) mRNA, partial cds.//5.00E-58//330bp//95%/AF176707
C-HEMBA1007300//Homo sapiens 3',5'-cyclic nucleotide phosphodiesterase 10A1 (PDE10A) mRNA, splice variant 1, complete cds.//0//1519bp//99%/AF127479
- 50 C-HEMBA1007301//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//6.20E-18//115aa//33%/P13941
C-HEMBA1000036//Homo sapiens CGI-51 protein mRNA, complete cds.//0//1665bp//99%/AF151809
C-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//2.80E-187//1582bp//80%/AF084928
C-HEMBA1000083//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//1.90E-22//426aa//25%/P11799
- 55 C-HEMBA1000119//Homo sapiens ASMTL gene.//0//1891bp//99%/Y15521
C-HEMBA1000144//GUANYLATE CYCLASE ACTIVATING PROTEIN 2 (GCAP2) (RETINAL GUANYLYL CYCLASE ACTIVATOR PROTEIN P24).//1.40E-24//71aa//77%/P51177

- C-HEMBA1000217//Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds.//0//1038bp//99%//AF090385
- C-HEMBA1000226//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE EEEEDB.5//2.70E-12//112aa//47%//Q09530
- 5 C-HEMBA1000264//CHL1 PROTEIN.//9.50E-19//104aa//45%//P22516
- C-HEMBA1000266//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHROMOSOME V.//6.10E-09//242aa//26%//Q23256
- C-HEMBA1000317//FIBULIN-1, ISOFORM D PRECURSOR.//7.10E-62//458aa//35%//P37888
- 10 C-HEMBA1000593//Homo sapiens transferrin receptor 2 alpha (TFR2) mRNA, complete cds.//1.30E-107//503bp//99%//AF067864
- C-HEMBA1000631//LONGEVITY-ASSURANCE PROTEIN 1 (LONGEVITY ASSURANCE FACTOR 1).//4.10E-19//232aa//28%//P78970
- C-HEMBA1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//2.20E-28//273aa//31%//P27671
- 15 C-HEMBA1000693//Homo sapiens neuroan1 mRNA, complete cds.//0//2952bp//94%//AF040723
- C-HEMBA1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//6.20E-130//692bp//93%//U53475
- C-HEMBA1000763//Homo sapiens CGI-89 protein mRNA, complete cds.//0//1676bp//96%//AF151847
- C-HEMBA1000781//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.//1.20E-126//613bp//97%//AF111105
- 20 C-HEMBA1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//5.10E-54//232aa//43%//P39956
- C-HEMBA1000831//Homo sapiens breast cancer nuclear receptor-binding auxiliary protein (BRX) mRNA, complete cds.//5.80E-60//301bp//99%//AF126008
- 25 C-HEMBA1000915//SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (EC 3.4.21.-).//1.10E-08//129aa//31%//P29122
- C-HEMBA1000927//Homo sapiens A-type potassium channel modulatory protein 2 (KCHIP2) mRNA, complete cds.//1.30E-126//592bp//99%//AF199598
- C-HEMBA1000947//Homo sapiens clone HAW100 putative ribonuclease III mRNA, complete cds.//0//2292bp//99%//AF116910
- 30 C-HEMBA1000973//Mus musculus schlafen3 (Sfn3) mRNA, complete cds.//3.40E-120//580bp//67%//AF099974
- C-HEMBA1000985//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//8.60E-18//178aa//30%//P28575
- C-HEMBA1001011//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.40E-73//230aa//45%//P51523
- 35 C-HEMBA1001056//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//2.90E-19//264aa//34%//P46087
- C-HEMBA1001058//Homo sapiens neuronal thread protein ADTC-NTP mRNA, complete cds.//3.60E-52//331bp//80%//AF010144
- C-HEMBA1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.40E-307//1447bp//97%//AF034803
- 40 C-HEMBA1001112//Homo sapiens sec61 homolog mRNA, complete cds.//6.00E-145//961 bp//83 %//AF077032
- C-HEMBA1001137//Homo sapiens mRNA for putative phospholipase, complete cds.//0//3069bp//99%//AB019435
- C-HEMBA1001151//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//4.20E-210//1835bp//76%//AF110267
- C-HEMBA1001175//ANKYRIN.//7.00E-11//169aa//31%//Q02357
- 45 C-HEMBA1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).//5.40E-93//196aa//54%//P46938
- C-HEMBA1001242//Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds.//1.80E-284//713bp//100%//AF089897
- C-HEMBA1001282//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//7.00E-43//394aa//34%//P16157
- 50 C-HEMBA1001288//COPPER HOMEOSTASIS PROTEIN CUTC.//7.80E-46//163aa//51%//P46719
- C-HEMBA1001294//GTP-BINDING PROTEIN TC10.//1.20E-79//196aa//80%//P17081
- C-HEMBA1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.30E-129//724bp//86%//U92703
- C-HEMBA1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//2.10E-65//458bp//79%//D63850
- 55 C-HEMBA1001339//DXS8237E PROTEIN (FRAGMENT).//4.60E-06//124aa//37%//P98175
- C-HEMBA1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.10E-58//292bp//99%//AF097441

- C-HEMBB1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0.1586bp//99%//AF100757
- C-HEMBB1001429//Homo sapiens leucine aminopeptidase mRNA, complete cds.//0.1933bp//99%//AF061738
- C-HEMBB1001443//Rattus norvegicus pyruvate dehydrogenase phosphatase isoenzyme 1 mRNA, complete cds.//3.00E-130//553bp//86%//AF062740
- 5 C-HEMBB1001482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-57//941aa//27%//Q05481
- C-HEMBB1001562//CYCLIN II (MULTIPLE-BAND POLYPEPTIDE II).//1.40E-06//373aa//21%//Q28092
- C-HEMBB1001564//VACUOLAR ATP SYNTHASE SUBUNIT H (EC 3.6.1.34) (V-ATPASE H SUBUNIT) (V-ATPASE M9.2 SUBUNIT) (9.2 KD MEMBRANE ACCESSORY PROTEIN).//9.60E-32//80aa//78%//Q15342
- 10 C-HEMBB1001673//Homo sapiens gene for new zinc finger protein, complete cds.//0.1919bp//99%//AB012770
- C-HEMBB1001736//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 (EIF3 P116) (EIF3 P110).//4.60E-15//391aa//25%//P55884
- C-HEMBB1001749//TRANSCRIPTIONAL ACTIVATOR GCN5.//1.70E-16//84aa//47%//Q03330
- C-HEMBB1001802//Human desmin mRNA, complete cds.//0.1523bp//98%//U59167
- 15 C-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//0.1514bp//99%//AF056209
- C-HEMBB1001839//GASTRULA ZINC FINGER PROTEIN XLGCF42.1 (FRAGMENT).//6.90E-11//87aa//35%//P18720
- C-HEMBB1001871//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S1).//5.40E-75//241aa//48%//P47853
- 20 C-HEMBB1001872//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR) (CELL SURFACE GLYCOPROTEIN F4/80).//1.90E-22//210aa//27%//Q61549
- C-HEMBB1001905//TRICHOHYALIN.//2.10E-10//268aa//27%//P37709
- C-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds.//1.60E-131//874bp//86%//U47742
- 25 C-HEMBB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E).//6.90E-132//561aa//50%//Q24574
- C-HEMBB1001950//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.) (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1.60E-41//370aa//31%//P54304
- 30 C-HEMBB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYP1VC1).//2.70E-49//139aa//55%//P29981
- C-HEMBB1002044//Mus musculus mRNA for vascular cadherin-2.//0.3562bp//81%//Y08715
- C-HEMBB1002134//ZINC-FINGER PROTEIN NEURO-D4.//8.10E-56//176aa//67%//P56163
- C-HEMBB1002193//TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE DTK) (TK19-2).//8.70E-61//77aa//74%//P55144
- 35 C-HEMBB1002217//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-132//399aa//44%//Q05481
- C-HEMBB1002266//NEURONAL PROTEIN.//2.10E-46//121aa//76%//P41737
- C-HEMBB1002342//Homo sapiens PKCq-interacting protein PICOT (PICOT) mRNA, complete cds.//1.50E-229//1045bp//99%//AF118649
- 40 C-HEMBB1002442//ILIN-10 PROTEIN.//9.70E-14//121aa//31%//P34692
- C-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds.//7.70E-258//774bp//99%//U43885
- C-HEMBB1002510//GYP7 PROTEIN.//3.10E-50//192aa//42%//P48365
- C-HEMBB1002550//HYPOTHETICAL UOG-1 PROTEIN.//5.00E-28//266aa//33%//P27544
- 45 C-HEMBB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds.//0.1417bp//99%//AF089749
- C-HEMBB1002607//Homo sapiens vitamin D3 receptor interacting protein (DRIP80) mRNA, complete cds.//2.00E-136//660bp//98%//AF105421
- C-HEMBB1002705//Homo sapiens CGI-27 protein mRNA, complete cds.//7.80E-285//841bp//96%//AF132961
- 50 C-MAMMA1000020//H. sapiens mRNA for flavin-containing monooxygenase 5 (FMO5).//8.20E-198//868bp//99%//Z47553
- C-MAMMA1000045//ENV POLYPROTEIN [CONTAINS: SURFACE PROTEIN GP85; MEMBRANE PROTEIN GP37].//1.90E-07//249aa//27%//P03396
- C-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//1.50E-90//323aa//48%//P47226
- C-MAMMA1000085//PUTATIVE CYSTEINYL-TRNA SYNTHETASE C2SE6.06C (EC 6.1.1.16) (CYSTEINE-TRNA LIGASE) (CYSRS).//2.10E-90//427aa//39%//Q09860
- 55 C-MAMMA1000173//Homo sapiens src homology 3 domain-containing protein HIP-55 mRNA, complete cds.//2.60E-164//1044bp//87%//AF197060
- C-MAMMA1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.40E-134//359aa//63%//

P51523

C-MAMMA1000284//P.walt mRNA for rnp associated protein 55.//2.20E-109//864bp//776%//X99836

C-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds.//0//1466bp//99%//AB015132

5 C-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//2.00E-30//119aa//53%//Q09232

C-MAMMA1000612//Homo sapiens G protein beta subunit mRNA, partial cds.//8.30E-178//1992bp//84%//AF195883

C-MAMMA1000625//GYP7 PROTEIN.//2.10E-41//198aa//40%//P48365

10 C-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.).//4.40E-33//250aa//33%//P42660

C-MAMMA1000684//Homo sapiens opioid growth factor receptor mRNA, complete cds.//0//2391bp//99%//AF172451

C-MAMMA1000713//IL-RBULOKINASE (EC 2.7.1.16).//7.70E-17//246aa//29%//P94524

15 C-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//1.00E-77//395aa//45%//O14646

C-MAMMA1000734//Homo sapiens mRNA for SEC63 protein.//0//1587bp//99%//AJ011779

C-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//9.00E-299//1033aa//55%//P87115

20 C-MAMMA1000824//ACTIN.//6.20E-20//284aa//28%//P53500

C-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4).//7.80E-40//101aa//54%//O27540

C-MAMMA1000897//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (TTI HEAVY CHAIN H3) (SERUM-DERIVED HYALURONAN-ASSOCIATED PROTEIN) (SHAP).//1.00E-14//576aa//37%//Q06033

C-MAMMA1000956//Homo sapiens CLDN8 gene for claudin-8.//0//1767bp//99%//AJ250711

25 C-MAMMA1001008//Homo sapiens aspartic-like protease mRNA, complete cds.//2.50E-276//1263bp//99%//AF117892

C-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CG-R) (LSH-R) (LUTEINIZING HORMONE RECEPTOR) (FRAGMENT).//1.20E-26//276aa//28%//Q090674

C-MAMMA1001038//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN]//2.60E-107//190aa//95%//Q15746

30 C-MAMMA1001041//SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1).//1.60E-16//113aa//41%//Q01082

C-MAMMA1001059//Homo sapiens mRNA for DEAD Box Protein 5.//0//1440bp//99%//AJ237946

C-MAMMA1001075//Homo sapiens CGI-72 protein mRNA, complete cds.//1.30E-181//397bp//98%//AF151830

35 C-MAMMA1001080//Homo sapiens SNC73 protein (SNC73) mRNA, complete cds.//1.6E-312//1596bp//94%//AF067420

C-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN).//4.00E-49//125aa//68%//P51521

C-MAMMA1001139//SRE-2 PROTEIN.//5.80E-35//239aa//38%//Q09273

C-MAMMA1001181//ABC1 PROTEIN HOMOLOG PRECURSOR.//1.30E-07//81aa//45%//Q92338

40 C-MAMMA1001198//Homo sapiens eps15R mRNA, partial cds.//0//2253bp//99%//AB015346

C-MAMMA1001222//EBNA-2 NUCLEAR PROTEIN.//6.60E-09//255aa//29%//P12978

C-MAMMA1001259//Mus musculus F-box protein FBX18 mRNA, partial cds.//2.30E-271//1414bp//89%//AF184275

45 C-MAMMA1001260//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//2.10E-52//630aa//30%//P34537

C-MAMMA1001305//RHO-GTPASE-ACTIVATING PROTEIN 1 (GTPASE-ACTIVATING PROTEIN RHOGAP) (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//2.20E-98//283aa//63%//Q07960

50 C-MAMMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.00000017//46aa//60%//P20931

C-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//1.40E-165//312aa//99%//P02750

C-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) (FRAGMENT).//6.50E-129//260aa//92%//P52623

55 C-MAMMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU-TYPE).//5.70E-55//86aa//97%//P07384

C-MAMMA1001576//Human gamma-tubulin mRNA, complete cds.//7.50E-276//1561bp//90%//M61764

C-MAMMA1001627//Homo sapiens mRNA for transcription factor TBX6.//5.20E-189//871bp//99%//AJ007989

C-MAMMA1001633//ZINC FINGER PROTEIN 165.//6.30E-39//160aa//55%//P49910

- C-MAMMA1001679//F-ACTIN CAPPING PROTEIN BETA SUBUNIT (CAPZ).//0.00000058//29aa//100%//P47756
 C-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.//0//1603bp//99%//AF095687
- 5 C-MAMMA1001735//TUBULIN BETA-5 CHAIN (BETA-TUBULIN CLASS-V).//5.90E-240//445aa//97%//P09653
 C-MAMMA1001743//Y BOX BINDING PROTEIN-1 (Y-BOX TRANSCRIPTION FACTOR).//8.50E-32//171aa//36%//P21573
- C-MAMMA1001751//Homo sapiens tandem pore domain potassium channel TWIK-2 (KCNK6) mRNA, complete cds.//0//2332bp//99%//AF117708
- 10 C-MAMMA1001754//Homo sapiens Vacuolar proton pump subunit SFD alpha isoform mRNA complete cds.//0//1987bp//99%//AF112204
- C-MAMMA1001768//CELL DIVISION CYCLE PROTEIN 48 HOMOLOG MJ1156.//3.80E-45//351aa//38%//Q58556
- C-MAMMA1001771//M.musculus mRNA for semaphorin B.//2.60E-200//1272bp//79%//X85991
- 15 C-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene.//1.30E-198//1157bp//80%//Y13148
- C-MAMMA1001837//ZINC FINGER PROTEIN 29 (ZFP-29).//2.60E-77//507aa//38%//Q07230
- C-MAMMA1001868//TRICHOHYALIN.//2.70E-19//359aa//25%//P22793
- C-MAMMA1002143//Homo sapiens Cdc42 effector protein 4 mRNA, complete cds.//1.70E-252//1170bp//99%//AF099664
- 20 C-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN).//6.00E-66//157aa//70%//P15880
- C-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE 1) (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) (TSA) (PRP) (NATURAL KILLER CELL ENHANCING FACTOR B) (NKEF-B).//5.20E-61//60aa//90%//P32119
- C-MAMMA1002219//Rattus norvegicus rexo70 mRNA, complete cds.//1.30E-181//861bp//98%//AF032667
- 25 C-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR).//8.80E-217//310aa//86%//PP70541
- C-MAMMA1002268//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//1.00E-190//1624bp//76%//AF068748
- C-MAMMA1002297//Homo sapiens mRNA for Rab6 GTPase activating protein.//1.10E-214//881bp//97%//AJ011679
- 30 C-MAMMA1002329//M.musculus mRNA for semaphorin B.//3.80E-45//332bp//84%//X85991
- C-MAMMA1002351//Mus musculus dynactin subunit p25 (p25) mRNA, complete cds.//4.30E-119//773bp//86%//AF190795
- C-MAMMA1002385//RIBONUCLEOPROTEIN RB97D.//1.50E-07//206aa//29%//Q02926
- 35 C-MAMMA1002428//LYSOSOME MEMBRANE PROTEIN II (LIMP II) (85 KD LYSOSOMAL MEMBRANE SIALOGLYCOPROTEIN) (LGP85) (CD38 ANTIGEN-LIKE 2).//1.10E-24//96aa//68%//Q014108
- C-MAMMA1002470//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1.00E-11//128aa//36%//P47623
- C-MAMMA1002485//Homo sapiens stanniocalcin-related protein mRNA, complete cds.//0//1822bp//99%//AF098462
- 40 C-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION.//1.20E-34//337aa//31%//P43571
- C-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.//0//1910bp//99%//AF065214
- 45 C-MAMMA1002573//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//2.60E-19//666aa//23%//P08640
- C-MAMMA1002617//ZINC FINGER PROTEIN 135.//7.60E-89//252aa//75%//P52742
- C-MAMMA1002619//PROBABLE UBIQUITTIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITTIN THIOLESTERASE) (UBIQUITTIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//9.50E-16//159aa//37%//Q09831
- 50 C-MAMMA1002622//VILLIN.//7.20E-35//53aa//64%//P02640
- C-MAMMA1002637//KINESIN LIGHT CHAIN (KLC).//1.30E-198//550aa//70%//Q07866
- C-MAMMA1002650//Mus musculus ODA-8S protein mRNA, complete cds.//5.40E-57//480bp//68%//AF194030
- C-MAMMA1002655//Homo sapiens mRNA for ganglioside sialidase, complete cds.//0//1515bp//99%//AB008185
- 55 C-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COALIGASE) (ACYL-AC-TIVATING ENZYME).//1.10E-45//618aa//26%//P27550
- C-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//4.3e-317//1942bp//85%//AF018261
- C-MAMMA1002769//Homo sapiens cell cycle progression restoration 8 protein (CPR8) mRNA, complete cds.//

2.20E-25//330bp//77%//AF011794

C-MAMMA1002842//Mus musculus c-Cbl associated protein CAP mRNA, complete cds.//2.60E-58//373bp//61%//U58883

C-MAMMA1002844//TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT).//4.90E-10//334aa//22%//P52178

C-MAMMA1002858//Rat cMG1 mRNA.//3.70E-238//1147bp//92%//X52590

C-MAMMA1002869//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//1.40E-160//305aa//65%//P48059

C-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN).//5.70E-30//214aa//35%//P48060

C-MAMMA1002937//ZINC FINGER PROTEIN 135.//8.30E-99//393aa//43%//P52742

C-MAMMA1002972//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27.//1.10E-05//69aa//42%//P40343

C-MAMMA1003011//HISTONE MACRO-H2A.1.//2.70E-123//370aa//66%//Q02874

C-MAMMA1003013//DNA POLYMERASE BETA (EC 2.7.7.7).//1.40E-46//332aa//36%//P06746

C-MAMMA1003035//RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//1.90E-13//108aa//33%//P23851

C-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds.//0.1533bp//99%//AF077952

C-MAMMA1003057//MD6 PROTEIN.//3.10E-225//419aa//97%//Q60584

C-MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//1.10E-234//1178bp//86%//AF071316

C-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA).//2.20E-105//217aa//89%//P46735

C-MAMMA1003146//Homo sapiens mRNA for GalT3 protein.//4.30E-218//996bp//99%//Y15062

C-MAMMA1003150//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.//5.00E-13//592aa//24%//P47179

C-MAMMA1003166//Homo sapiens MLL septin-like fusion protein (MSF) mRNA, complete cds.//3.10E-158//592bp//97%//AF123052

C-NT2RM1000001//D.melanogaster sap47-2 mRNA.//1.50E-10//417bp//62%//X80110

C-NT2RM1000039//HYPOTHETICAL 41.4 KD PROTEIN IN SRLQ-HYFF INTERGENIC REGION (EC 1.18.1.-) (ORF4) (ORF2).//2.90E-14//299aa//25%//P37596

C-NT2RM1000055//Rattus norvegicus mRNA for TIP120, complete cds.//0.13016bp//89%//D87671

C-NT2RM1000080//UNC-1 PROTEIN.//5.90E-25//211aa//31%//Q21190

C-NT2RM1000086//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//8.40E-52//364aa//32%//P34537

C-NT2RM1000092//MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2).//1.00E-07//362aa//23%//P39843

C-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//1.20E-10//150aa//28%//P87072

C-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUFS6 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds.//7.80E-110//516bp//99%//AF044959

C-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3.30E-38//469aa//27%//P49902

C-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//1.20E-10//150aa//28%//P87072

C-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//1.10E-10//94aa//47%//O42643

C-NT2RM1000199//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0.12476bp//99%//AJ245820

C-NT2RM1000244//Homo sapiens TRAF4 associated factor 1 mRNA, partial cds.//2.00E-126//592bp//99%//U81002

C-NT2RM1000252//H. sapiens E-MAP-115 mRNA.//9.70E-35//569bp//64%//X73882

C-NT2RM1000256//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.//0.13012bp//99%//AB016789

C-NT2RM1000257//MAGO NASHI PROTEIN.//7.90E-69//143aa//91%//P49028

C-NT2RM1000260//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP100 mRNA, complete cds.//0.12766bp//99%//AF055995

C-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V-ATPASE 28 KD ACCESSORY PROTEIN).//1.50E-106//118aa//97%//P39942

- C-NT2RM1000354//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//7.40E-245//2101bp//68%//AF111423
- C-NT2RM1000355//Homo sapiens transmembrane protein BRI (BRI) mRNA, complete cds.//7.0//1599bp//99%//AF152462
- 5 C-NT2RM1000377//Homo sapiens dual specificity phosphatase MKP5 (MKP5) mRNA, complete cds.//3.20E-196//1016bp//94%//AF179212
- C-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.00000019//67aa//31%//P53915
- C-NT2RM1000421//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775
- 10 C-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//1.40E-185//1486bp//81%//AF084928
- C-NT2RM1000499//Caenorhabditis elegans mRNA for centaurin gamma 1A.//3.00E-17//927bp//58%//AJ132700
- C-NT2RM1000539//Homo sapiens mRNA for Lsm5 protein.//3.00E-158//733bp//99%//AJ238097
- C-NT2RM1000553//Homo sapiens putative glycolipid transfer protein mRNA, complete cds.//3.40E-177//814bp//99%//AF103731
- 15 C-NT2RM1000555//UNR PROTEIN.//0//678aa//98%//P18395
- C-NT2RM1000563//TRANSMISSION-B LOCKING TARGET ANTIGEN S230 PRECURSOR.//0.0000068//199aa//30%//Q08372
- C-NT2RM1000623//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775
- 20 C-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.50E-75//301aa//39%//P43636
- C-NT2RM1000661//Homo sapiens translation initiation factor 4e mRNA, complete cds.//5.70E-210//960bp//99%//AF038957
- C-NT2RM1000666//DNA-BINDING PROTEIN A.//2.20E-09//165aa//34%//P16989
- C-NT2RM1000691//Homo sapiens mRNA for PLU-1 protein.//0//3104bp//99%//AJ132440
- 25 C-NT2RM1000702//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//5.60E-08//187aa//27%//P49695
- C-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds.//0//3524bp//99%//AF027208
- C-NT2RM1000746//Homo sapiens polyamine modulated factor-1 (PMF1) mRNA, complete cds.//6.70E-227//1043bp//99%//AF141310
- 30 C-NT2RM1000770//DXS6673E PROTEIN.//1.40E-39//194aa//48%//Q14202
- C-NT2RM1000772//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//7.30E-15//280aa//27%//Q00808
- C-NT2RM1000800//Mus musculus partial mRNA for B-IND1 protein (B-indi gene).//1.10E-98//571bp//89%//Z97207
- C-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds.//0//3524bp//99%//AF027208
- 35 C-NT2RM1000826//UNR PROTEIN.//0//678aa//98%//P18395
- C-NT2RM1000833//Homo sapiens sec61 homolog mRNA, complete cds.//0//3541 bp//99%//AF08445 8
- C-NT2RM1000850//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//9.70E-42//333aa//36%//P16157
- C-NT2RM1000852//Homo sapiens putative ATP-dependent RNA helicase ROK1 mRNA, complete cds.//0//2206bp//99%//AF077033
- 40 C-NT2RM1000874//Homo sapiens death effector domain-containing testicular molecule mRNA, complete cds.//1.40E-244//1113bp//99%//AF043733
- C-NT2RM1000882//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//4.30E-122//1394bp//69%//AF126799
- 45 C-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//5107bp//99%//AF082516
- C-NT2RM1000885//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1.80E-56//630aa//30%//P34537
- C-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//1020aa//89%//P07000
- 50 C-NT2RM1000898//ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR).//8.90E-26//229aa//29%//P02583
- C-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//1.00E-15//266aa//26%//P46577
- C-NT2RM1001003//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.//0//2230bp//99%//AF030233
- 55 C-NT2RM1001008//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//1.60E-13//119aa//36%//Q09701
- C-NT2RM1001059//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB4.//3.60E-11//180aa//28%//

Q99383

C-NT2RM1001072//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODESTERASE GAMMA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II) (PLC-148)//8.30E-47//259aa//35%//P08487

5 C-NT2RM1001092//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//3.60E-115//332aa//52%//Q05481

C-NT2RM1001102//Human HEM45 mRNA, complete cds.//2.30E-27//482bp//63%//U88964

C-NT2RM1001115//ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14)//5.60E-06//239aa//27%//P54197

10 C-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2)//2.20E-144//362aa//71%//P25167

C-NT2RM2000030//DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DH IC) (CYTOPLASMIC DYNEIN INTERMEDIATE CHAIN)//0.00000043//136aa//31%//P54703

15 C-NT2RM2000092//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8)//1.30E-36//160aa//40%//P50102

C-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1574bp//99%//AF067223

20 C-NT2RM2000260//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN)//3.60E-19//181aa//34%//P14918

C-NT2RM2000322//SPERMIDINE SYNTHASE (EC 2.5.1.16) (PUTRESCINE AMINOPROPYLTRANSFERASE) (AMINOPROPYLTRANSFERASE)//8.10E-06//167aa//29%//O48660

C-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN//1.80E-14//245aa//29%//P11274

C-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//0//1506bp//99%//U48251

25 C-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLEOTIDE//1.70E-68//419aa//36%//P50849

C-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHE-
ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-
NENT)//1.60E-54//344aa//33%//P32802

30 C-NT2RM2000407//Mus musculus semaphorin VIa mRNA, complete cds.//9.70E-201//826bp//84%//AF030430

C-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73//1.00E-222//237aa//89%//Q08469

C-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION//1.00E-07//157aa//28%//P36113

35 C-NT2RM2000469//NITROGEN PERMEASE REACTIVATOR PROTEIN (EC 2.7.1.-)//8.90E-06//377aa//24%//P22211

C-NT2RM2000490//SYNAPTOTAGMIN (P65)//1.80E-13//166aa//34%//P14823

C-NT2RM2000502//Rattus norvegicus W307 mRNA, complete cds.//1.70E-58//381bp//86%//U78304

40 C-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//1673bp//99%//AF061243

C-NT2RM2000522//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//1.30E-12//282aa//32%//P17437

C-NT2RM2000566//Homo sapiens integrin alpha-7 mRNA, complete cds.//0//2519bp//96%//AF032108

45 C-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS)//1.70E-187//1741aa//46%//P73505

C-NT2RM2000588//HISTONE DEACETYLASE HDA1//2.80E-60//384aa//40%//P53973

C-NT2RM2000594//Homo sapiens DNA cytosine-5 methyltransferase 3 beta 3 (DNMT3B) mRNA, complete cds.//0//2712bp//99%//AF156487

C-NT2RM2000599//Homo sapiens F-box protein Liliina (LILINA) mRNA, complete cds.//4.90E-70//838bp//69%//AF179221

50 C-NT2RM2000609//Homo sapiens CTL1 gene.//0//1559bp//99%//AJ245620

C-NT2RM2000612//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//2.60E-106//1069bp//74%//U35776

C-NT2RM2000624//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75)//4.40E-32//319aa//35%//Q08170

55 C-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2)//3.70E-142//285aa//90%//P32391

C-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)//3.80E-23//184aa//36%//Q15404

C-NT2RM2000718//Homo sapiens endocrine regulator mRNA, complete cds.//0//1731bp//99%//AF121141

- C-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//2.90E-103//249aa//73%//P28160
- C-NT2RM2000740//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//5.70E-53//266aa//43%//P41877
- 5 C-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP).//9.50E-279//545aa//98%//P23514
- C-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//1.70E-200//927bp//99%//AB015046
- C-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//8.20E-154//285aa//99%//Q60809
- 10 C-NT2RM2001065//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1554bp//99%//AF100757
- C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//2.40E-15//266aa//26%//P46577
- C-NT2RM2001105//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//1.20E-28//805bp//61%//AF053091
- 15 C-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.30E-20//267aa//35%//P05143
- C-NT2RM2001201//EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5).//1.50E-07//95aa//35%//P48724
- C-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10).//3.60E-10//177aa//32%//P97924
- 20 C-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMIDOHYDROLASE).//1.30E-180//328aa//99%//P13264
- C-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.60E-166//312aa//98%//P53995
- C-NT2RM2001324//ZYXIN.//6.80E-55//200aa//41%//Q04584
- 25 C-NT2RM2001345//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//2.90E-08//334aa//22%//Q00808
- C-NT2RM2001424//Homo sapiens mRNA for EIB-55kDa-associated protein.//0//1621bp//99%//AJ007509
- C-NT2RM2001499//LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2).//7.40E-121//437aa//57%//P52569
- C-NT2RM2001547//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.90E-27//90aa//42%//P38660
- 30 C-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//4.30E-61//312aa//44%//P19474
- C-NT2RM2001592//Rattus norvegicus rexo70 mRNA, complete cds.//3.10E-156//909bp//88%//AF032667
- C-NT2RM2001605//Homo sapiens mRNA for PLU-1 protein.//0//3114bp//99%//AJ132440
- 35 C-NT2RM2001613//Homo sapiens sec61 homolog mRNA, complete cds.//0//2601 bp//99%//AF084458
- C-NT2RM2001632//KES1 PROTEIN.//1.40E-31//342aa//34%//P35844
- C-NT2RM2001635//NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145).//1.20E-142//566aa//56%//P52591
- 40 C-NT2RM2001648//Homo sapiens sec61 homolog mRNA, complete cds.//0//2421 bp//99%//AF084458
- C-NT2RM2001652//Homo sapiens guanine nucleotide exchange factor mRNA, complete cds.//0//2608bp//99%//AF111162
- C-NT2RM2001659//ZINC/CADMIUM RESISTANCE PROTEIN.//3.40E-39//161aa//34%//P20107
- 45 C-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA complete cds.//0//2471bp//99%//AF044195
- C-NT2RM2001668//Homo sapiens putative WHSC1 protein (WHSC1) mRNA, alternative splice product ending in intron 11, complete cds.//6.20E-16//464bp//62%//AF083391
- C-NT2RM2001670//ZINC FINGER PROTEIN 29 (ZFP-29).//6.50E-104//407aa//43%//Q07230
- C-NT2RM2001671//Oryctolagus cuniculus sarcolemmal associated protein (SLAP1) mRNA, complete cds.//0//1843bp//94%//U21155
- 50 C-NT2RM2001688//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I.//4.60E-20//253aa//30%//Q09674
- C-NT2RM2001698//Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds.//6.20E-253//1170bp//99%//AB028600
- C-NT2RM2001700//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3.99.-) (VLCAD) (FRAGMENT).//5.70E-130//536aa//49%//P05044
- 55 C-NT2RM2001716//Homo sapiens BPTF mRNA for bromodomain PHD finger transcription factor, complete cds.//0//1774bp//98%//AB032251
- C-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-

ZYME).//7.20E-16//381aa//27%//Q09931

C-NT2RM2001743//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//0//1498bp//99%//AF011792

C-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210.//8.80E-11//119aa//36%//Q92609

C-NT2RM2001760//Homo sapiens sec61 homolog mRNA, complete cds.//0//2379bp//99%//AF084458

C-NT2RM2001771//ZINC FINGER PROTEIN 135.//6.40E-154//394aa//64%//P52742

C-NT2RM2001782//Homo sapiens GDP-mannose pyrophosphorylase A (GMPPA) mRNA, complete cds.//0//1470bp//99%//AF135422

C-NT2RM2001785//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//0//2150bp//99%//AF126799

C-NT2RM2001803//Homo sapiens IkkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//0//2249bp//99%//AF044195

C-NT2RM2001823//CHD1 PROTEIN.//1.80E-106//631aa//39%//P32657

C-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds.//0//2415bp//97%//AF013759

C-NT2RM2001866//PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN2 (EC 3.1.13.4) (PAB1P-DEPENDENT POLY(A)-NUCLEASE).//3.00E-54//337aa//39%//P53010

C-NT2RM2001896//CELL DIVISION PROTEIN FTSJ.//5.10E-26//204aa//34%//P28692

C-NT2RM2001930//M. musculus mRNA for semaphorin G.//5.20E-135//894bp//83%//X97818

C-NT2RM2001935//Homo sapiens single-strand selective monofunctional uracil DNA glycosylase mRNA, complete cds.//0//1454bp//99%//AF125182

C-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//2.70E-27//216aa//34%//P28320

C-NT2RM2001950//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION.//0.0000001//212aa//23%//P38250

C-NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.//0//1658bp//98%//AF089816

C-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//1.90E-39//253aa//35%//P37838

C-NT2RM2001997//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//1.30E-10//232aa//28%//Q12730

C-NT2RM2001998//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME L/3.10E-12//206aa//30%//Q09782

C-NT2RM2002004//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTANTIGEN HOMOLOG).//2.90E-08//83aa//44%//P40796

C-NT2RM2002014//HYPOTHETICAL 81.4 KD PROTEIN IN GREB-FEOA INTERGENIC REGION.//1.10E-89//425aa//41%//P46837

C-NT2RM2002030//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.//0//1959bp//99%//AB016789

C-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.00000099//338aa//24%//Q07878

C-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//5.00E-62//104aa//57%//Q61990

C-NT2RM2002091//Drosophila melanogaster eyeld (eld) mRNA, complete cds.//7.10E-29//805bp//61%//AF053091

C-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//0//1807bp//99%//AJ010840

C-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//0//1868bp//99%//AF030435

C-NT2RM2002128//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//4.90E-13//487aa//26%//P49695

C-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//8.00E-31//105aa//47%//P47805

C-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//8.50E-191//1524bp//81%//AF084928

C-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//7.10E-155//381aa//72%//P25167

C-NT2RM4000030//LAS1 PROTEIN.//5.60E-12//184aa//32%//P36146

C-NT2RM4000046//GOLIATH PROTEIN (G1 PROTEIN).//0.000008//112aa//31%//Q06003

C-NT2RM4000104//ZINC FINGER PROTEIN 135.//1.50E-81//251aa//53%//P52742

C-NT2RM4000139//R. norvegicus trg mRNA.//2.30E-114//1161bp//72%//X68101

- C-NT2RM4000155//THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE--TRNA LIGASE) (THRRS).//1. 20E-157//321aa//61%/IP26639
- C-NT2RM4000156//H.sapiens HPBRII-7 gene.//3.60E-21//785bp//60%/X67336
- C-NT2RM4000167//Homo sapiens mRNA for Chromokinesin (KIF 4 gene).//0//1946bp//99%/IAJ271784
- 5 C-NT2RM4000169//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//4.80E-13//688aa//23%/IP25386
- C-NT2RM4000191//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.//9.20E-75//439aa//41%/IP16381
- C-NT2RM4000202//ZINC FINGER PROTEIN MOK-2 (HOK-2).//4.90E-32//170aa//41%/IQ16600
- C-NT2RM4000215//MAK16 PROTEIN.//1.30E-68//295aa//49%/IP10962
- 10 C-NT2RM4000229//Gallus gallus actin filament-associated protein (AFAP-110) mRNA, complete cds.//1.10E-27//633bp//64%/L20303
- C-NT2RM4000233//Mus musculus semaphorin Via mRNA, complete cds.//3.40E-231//1395bp//86%/AF030430
- C-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//2.20E-276//1124bp//97%/M99438
- 15 C-NT2RM4000344//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//0//2030bp//99%/AJ132637
- C-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//1.50E-21//208aa//35%/Q24371
- C-NT2RM4000356//RAS-RELATED PROTEIN RAB-17.//5.90E-80//213aa//75%/IP35292
- C-NT2RM4000386//Mus musculus ODZ3 (Odz3) mRNA, partial cds.//0//2156bp//87%/AF195418
- 20 C-NT2RM4000421//Homo sapiens mRNA for nuclear transport receptor.//0//1730bp//99%/AJ133769
- C-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.//4.10E-271//2085bp//77%/AF062476
- C-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//8.00E-20//393aa//24%/Q10297
- 25 C-NT2RM4000471//Homo sapiens cysteine desulfurase (nIfs) mRNA, complete cds.//0//2092bp//99%/AF097025
- C-NT2RM4000486//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.80E-11//242aa//31%/P04280
- C-NT2RM4000496//ISAP1 PROTEIN.//8.30E-53//434aa//29%/P39955
- C-NT2RM4000515//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H) (FRAGMENT).//1.10E-11//394aa//24%/P16884
- 30 C-NT2RM4000531//ZINC FINGER PROTEIN 29 (ZFP-29).//2.40E-89//389aa//43%/Q07230
- C-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).//1.00E-59//595aa//28%/Q04652
- C-NT2RM4000595//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//8.70E-15//403aa//30%/P26337
- 35 C-NT2RM4000611//VEGETATABLE INCOMPATIBILITY PROTEIN HET-E-1.//2.90E-09//108aa//31%/Q00808
- C-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-TIVATING ENZYME).//2.70E-146//420aa//60%/IP27550
- C-NT2RM4000657//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III).//3.00E-68//297aa//40%/IP51178
- 40 C-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL137471.//2.0E-28//180aa//30%/IP74168
- C-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.//1.00E-136//1104bp//77%/AF022789
- C-NT2RM4000733//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000041//207aa//29%/IP52154
- C-NT2RM4000734//Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds.//0//2071bp//99%/AF221712
- 45 C-NT2RM4000741//Homo sapiens hSGT1 mRNA for hSGT1p, complete cds.//0//2184bp//99%/D88208
- C-NT2RM4000751//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.90E-125//301aa//53%/Q99676
- C-NT2RM4000798//Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 mRNA, complete cds.//0//2603bp//99%/AF084521
- 50 C-NT2RM4000820//VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45 SUBUNIT).//1.10E-24//138aa//44%/P40662
- C-NT2RM4000857//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//6.70E-22//250aa//29%/IP02750
- C-NT2RM4000996//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//8.00E-211//738aa//50%/Q05481
- 55 C-NT2RM4001047//MO25 PROTEIN.//8.00E-140//333aa//80%/Q06138
- C-NT2RM4001054//Homo sapiens sec61 homolog mRNA, complete cds.//3.10E-190//1315bp//81%/AF077032
- C-NT2RM4001084//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I.//0.000000032//165aa//33%/Q09820

- C-NT2RM4001092//ZINC FINGER PROTEIN GLO37/3.10E-24//265aa//33%//P38682
 C-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F.8 IN CHROMOSOME II.//5.90E-86//292aa//48%//Q09417
- 5 C-NT2RM4001140//HOMEBOX PROTEIN MSH-D.//1.00E-11//103aa//38%//Q01704
 C-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN.//4.10E-197//445aa//78%//Q27969
 C-NT2RM4001178//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//1.10E-48//218aa//43%//Q03532
 C-NT2RM4001200//ZINC FINGER PROTEIN 135.//9.50E-135//375aa//60%//P52742
 C-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//0//2310bp//99%//AF004828
- 10 C-NT2RM4001217//Mus musculus actin-binding protein (ENC-1) mRNA, complete cds.//3.10E-148//1445bp//72%//U65079
 C-NT2RM4001256//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//4.30E-55//289bp//77%//AF129131
 C-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-UKE (EC 2.7.1.137) (PI3-KINASE) (PTDINS-3-KINASE) (PI3K).//3.50E-35//124aa//65%//P54676
- 15 C-NT2RM4001316//ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.3) (MCAD).//2.30E-31//334aa//30%//P08503
 C-NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds.//1.80E-39//728bp//64%//D89016
 C-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).//1.00E-28//171aa//37%//P32626
 C-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HOL1 INTERGENIC REGION.//8.10E-30//265aa//33%//P53742
- 20 C-NT2RM4001347//Homo sapiens NY-REN-25 antigen mRNA, partial cds.//0//2300bp//99%//AF155103
 C-NT2RM4001371//Homo sapiens IDN3 mRNA, partial cds.//0//2524bp//99%//AB019494
 C-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//2.20E-237//1079bp//99%//AF098799
- 25 C-NT2RM4001411//Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA, complete cds.//0//1962bp//87%//AF020526
 C-NT2RM4001412//Homo sapiens nGAP mRNA, complete cds.//0//1918bp//99%//AF047711
 C-NT2RM4001444//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS).//1.40E-118//444aa//46%//P73505
- 30 C-NT2RM4001483//ZINC FINGER PROTEIN 136.//5.10E-106//357aa//55%//P52737
 C-NT2RM4001566//NECDIN.//9.80E-44//227aa//41%//P25233
 C-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//1.50E-284//1082bp//90%//AF071317
- 35 C-NT2RM4001592//HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC REGION.//7.60E-56//213aa//49%//P31380
 C-NT2RM4001597//M. musculus red-1 gene.//12.10E-171//1414bp//78%//X92750
 C-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).//2.60E-32//203aa//39%//Q12600
- 40 C-NT2RM4001629//MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LARGE HOMOLOG 3).//1.50E-93//278aa//38%//Q13368
 C-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REGION.//2.70E-84//410aa//42%//P37339
 C-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT).//8.90E-141//354aa//72%//Q14141
- 45 C-NT2RM4001731//Homo sapiens F-box protein Liliina (LILINA) mRNA, complete cds.//0//1922bp//100%//AF179221
 C-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.).//4.10E-186//639aa//58%//Q05512
 C-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1).//7.90E-66//311aa//35%//Q03164
- 50 C-NT2RM4001810//AGGRECAN CORE PROTEIN PRECURSOR (CARTILAGE-SPECIFIC PROTEOGLYCAN CORE PROTEIN) (CSPCP) (CHONDROITIN SULFATE PROTEOGLYCAN CORE PROTEIN 1).//5.10E-07//263aa//30%//P16112
 C-NT2RM4001813//LECTIN BRA-2.//0.00000048//114aa//30%//P17346
 C-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds.//8.10E-300//1395bp//98%//M37712
- 55 C-NT2RM4001823//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)7/2.90E-55//325aa//37%//P28160
 C-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.90E-161//481aa//56%//P51523
 C-NT2RM4001858//T-BOX CONTAINING PROTEIN TBX6L (FRAGMENT).//6.50E-22//126aa//46%//P79779

- C-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//4.30E-244//1248bp//94%//Y17711
- C-NT2RM4001876//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//6.50E-23//184aa//36%//Q15404
- 5 C-NT2RM4001880//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-).//5.90E-09//268aa//26%//P47486
- C-NT2RM4001930//Homo sapiens dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl glucosyltransferase (ALG6) mRNA, complete cds.//0//1930bp//99%//AF102851
- C-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//0//2087bp//99%//AF098162
- 10 C-NT2RM4001969//R. norvegicus mRNA for IP63 protein.//2.60E-261//1563bp//84%//X99330
- C-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.80E-112//457aa//47%//P51523
- C-NT2RM4001987//NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM 180) [CONTAINS: N-CAM 140].//3.20E-17//281aa//30%//P16170
- 15 C-NT2RM4002013//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1 INTERGENIC REGION.//6.90E-94//589aa//35%//P42935
- C-NT2RM4002034//Homo sapiens hiwi mRNA, partial cds.//1.90E-53//1585bp//60%//AF104260
- C-NT2RM4002062//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//1.90E-31//80aa//52%//P36419
- 20 C-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//0//1865bp//99%//U82267
- C-NT2RM4002066//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP230 mRNA, complete cds.//1.50E-211//1123bp//71%//AF117755
- C-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//9.30E-293//1751bp//83%//AF072758
- 25 C-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//2.80E-105//556aa//41%//Q04652
- C-NT2RM4002093//Homo sapiens neural polypyrimidine tract binding protein (PTB) mRNA, complete cds.//0//2550bp//99%//AF176085
- C-NT2RM4002109//Homo sapiens mRNA for Chromokinesin (KIF 4 gene).//0//2572bp//99%//AJ271784
- C-NT2RM4002145//SLIT PROTEIN PRECURSOR.//1.40E-09//127aa//33%//P24014
- 30 C-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.90E-70//454bp//85%//AF035940
- C-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, complete cds.//0//2671bp//99%//AF084535
- C-NT2RM4002174//MRPPROTEIN.//9.10E-68//264aa//51%//P21590
- C-NT2RM4002189//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//6.20E-33//688aa//27%//P08640
- 35 C-NT2RM4002194//Mus musculus semaphorin VIa mRNA, complete cds.//5.20E-297//1753bp//87%//AF030430
- C-NT2RM4002205//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//3.00E-37//122aa//72%//Q07803
- C-NT2RM4002213//Homo sapiens protein phosphatase methylesterase-1 (PME-1) mRNA, complete cds.//0//2452bp//100%//AF157028
- 40 C-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//3.70E-19//147aa//41%//P40809
- C-NT2RM4002251//ALPHA-1,3-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.101) (N-GLYCOSYLOLOGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE I) (GNT- I) (GLCNAC-T I).//2.20E-36//320aa//38%//P27808
- C-NT2RM4002323//ANTIGEN GOR (FRAGMENT).//0.00000001//154aa//33%//P48778
- 45 C-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-TIVATING ENZYME).//1.30E-29//275aa//30%//P27095
- C-NT2RM4002438//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//1.10E-49//611 bp//70%//AF129131
- 50 C-NT2RM4002460//ENV POLYPROTEIN (COAT POLYPROTEIN) [CONTAINS: COAT PROTEINS GP70, GP20].//0.0000016//226aa//24%//P51515
- C-NT2RM4002527//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.90E-15//366aa//27%//Q00808
- C-NT2RM4002532//PROTEIN HOM1.//2.00E-16//276aa//28%//P55137
- C-NT2RM4002558//Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds.//0//1797bp//99%//AF055899
- 55 C-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//0//1915bp//87%//AF022962
- C-NT2RM4002571//H. sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T2).//4.60E-78//921bp//69%//X85019
- C-NT2RM4002594//MSP1 PROTEIN HOMOLOG.//2.70E-68//236aa//58%//P54815

- C-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA UGASE) (ASPRS).//2.30E-101//488aa//45%//O32038
- C-NT2RP1000018//Homo sapiens mRNA for NIK, partial cds.//O//1747bp//99%//AB013385
- C-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//O//1652bp//99%//AJ012449
- 5 C-NT2RP1000040//Mus musculus donson protein (Donson) mRNA, partial cds.//5.90E-150//1025bp//82%//AF193608
- C-NT2RP1000086//H. sapiens mRNA for zinc finger protein, Hsa12.//O//1162bp//99%//X98834
- C-NT2RP1000111//COP1 REGULATORY PROTEIN.//A.00E-116//296aa//51%//P93471
- C-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//A.50E-50//181aa//60%//P51859
- 10 C-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//3.40E-270//951bp//98%//AF011792
- C-NT2RP1000202//ANKYRIN.//1.00E-25//302aa//34%//Q02357
- C-NT2RP1000272//Mus musculus mRNA for neural specific sr protein NSSR 2, complete cds.//1.40E-267//1155bp//87%//AB015895
- 15 C-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.30E-275//1249bp//99%//AF053551
- C-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//B.70E-47//155aa//58%//P32447
- C-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//I.70E-15//162aa//30%//P25343
- C-NT2RP1000363//R. norvegicus LL5 mRNA.//I.70E-262//1175bp//83%//X74226
- 20 C-NT2RP1000376//Homo sapiens Ca²⁺-independent phospholipase A2 long isoform (iPLA2) mRNA, complete cds.//O//2252bp//96%//AF102989
- C-NT2RP1000413//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN).//I.190E-153//230aa//99%//P55161
- C-NT2RP1000439//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//1.80E-94//1019bp//63%//AF111423
- 25 C-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN).//I.2.40E-10//227aa//25%//Q08257
- C-NT2RP1000460//NUCLEAR MOVEMENT PROTEIN NUDC.//I.3.80E-19//149aa//36%//P17624
- C-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//I.2.60E-94//254aa//47%//P34580
- 30 C-NT2RP1000478//TUBULIN BETA-5 CHAIN (CLASS-V).//A.50E-240//445aa//97%//P09653
- C-NT2RP1000481//Homo sapiens antigen NY-CO-3 (NY-CO-3) mRNA, partial cds.//I.7.5E-315//1445bp//99%//AF039688
- C-NT2RP1000493//POSSIBLE DNA-REPAIR PROTEIN XP-E (POSSIBLE XERODERMA PIGMENTOSUM GROUP E PROTEIN) (UV-DAMAGED DNA-BINDING PROTEIN) (UV-DBB).//I.3.60E-30//534aa//23%//P33194
- 35 C-NT2RP1000513//Human NifU-like protein (hNifU) mRNA, partial cds.//6.50E-17//1516bp//99%//U47101
- C-NT2RP1000522//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//B.20E-83//345aa//47%//Q61068
- 40 C-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//I.1.10E-27//193aa//35%//P49020
- C-NT2RP1000574//HOMEBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//I.3.50E-75//151aa//94%//P97367
- C-NT2RP1000630//NECDIN.//I.2.40E-44//227aa//41%//P25233
- 45 C-NT2RP1000677//SODIUM-DEPENDENT ORGANIC ANION TRANSPORTER (ORGANIC ANION TRANSPORTING POLYPEPTIDE).//I.1.20E-78//483aa//31%//P46721
- C-NT2RP1000701//Homo sapiens phospholipase A2 activating protein (PLA2P) mRNA, complete cds.//O//1687bp//99%//AF145020
- C-NT2RP1000733//Human mRNA for GSPT1-TK protein, complete cds.//O//2057bp//99%//E14379
- 50 C-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds.//O//2186bp//99%//AF101434
- C-NT2RP1000746//Homo sapiens 60S acidic ribosomal protein PO mRNA, complete cds.//I.9.70E-196//901bp//99%//AF173378
- C-NT2RP1000782//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//I.1.20E-30//232aa//30%//O35566
- 55 C-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//B.20E-83//334aa//55%//Q07960
- C-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//O//1494bp//99%//

AF067223

C-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.80E-176//829bp//98%//AF047020

C-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.20E-30//232aa//30%//Q35566

C-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds.//0//1555bp//99%//AF064094

C-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//5.20E-20//306aa//33%//Q09531

C-NT2RP1000915//AUTOANTIGEN NGP-1.//1.70E-19//343aa//25%//Q13823

C-NT2RP1000947//Human E2 ubiquitin conjugating enzyme Ubch5B (UBCH5B) mRNA, complete cds.//4.60E-105//504bp//99%//U39317

C-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//1.40E-23//370aa//28%//Q04652

C-NT2RP1000958//AUTOANTIGEN NGP-1.//1.40E-19//343aa//25%//Q13823

C-NT2RP1000959//Human acidic ribosomal phosphoprotein P0 mRNA, complete cds.//2.50E-236//966bp//99%//M17885

C-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//8.90E-299//554aa//99%//P19338

C-NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds.//2.20E-78//1529bp//61%//L01790

C-NT2RP1001013//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.70E-253//425aa//98%//P51522

C-NT2RP1001033//Homo sapiens delta-tubulin mRNA, complete cds.//2.10E-285//1290bp//100%//AF201333

C-NT2RP1001073//Homo sapiens U6 snRNA-associated Sm-like protein LSm5 mRNA, complete cds.//8.10E-107//504bp//99%//AF182291

C-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//0//2085bp//99%//U82267

C-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9.//2.30E-116//319aa//46%//Q06218

C-NT2RP1001113//Homo sapiens CTL2 gene.//0//2790bp//98%//AJ245621

C-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//5.20E-108//1278bp//69%//U79139

C-NT2RP1001185//Human isovaleryl-coA dehydrogenase (IVD) mRNA, complete cds.//1.90E-158//729bp//99%//M34192

C-NT2RP1001247//Homo sapiens TGF-beta type secreted signaling protein LEFTYA mRNA, complete cds.//0//2006bp//100%//AF081513

C-NT2RP1001253//Homo sapiens oscillin (hLn) mRNA, complete cds.//0//2020bp//99%//AF029914

C-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//32%//Q12024

C-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//32%//Q12024

C-NT2RP1001310//Homo sapiens mitochondrial carrier homolog 1 isoform a mRNA, partial cds; nuclear gene for mitochondrial product.//0//1732bp//99%//AF176006

C-NT2RP1001313//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//7.50E-121//1394bp//69%//AF126799

C-NT2RP1001361//Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA, complete cds.//6.50E-116//541bp//100%//AF070652

C-NT2RP1001385//HYPOTHETICAL 48.8 KD PROTEIN IN SSU81-SCS2 INTERGENIC REGION.//2.70E-22//284aa//25%//P40074

C-NT2RP1001395//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.//0//1782bp//99%//AF210052

C-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//8.90E-141//396aa//67%//P91917

C-NT2RP1001449//Mus musculus Gng31g mRNA, complete cds.//7.20E-165//800bp//87%//AF069954

C-NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).//1.20E-137//629bp//100%//AJ005257

C-NT2RP1001482//Mouse oncogene (ect2) mRNA, complete cds.//2.10E-158//755bp//86%//L11316

C-NT2RP1001494//MALE STERILITY PROTEIN 2.//7.20E-40//261aa//27%//Q08891

C-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IP5).//1.60E-166//506aa//60%//P42803

C-NT2RP1001546//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.60E-30//232aa//30%//Q35566

C-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//5.80E-121//271aa//89%//P47758

C-NT2RP1001665//CALMODULIN.//0.0000051//83aa//30%//P02594

- C-NT2RP2000006//DNAJ PROTEIN (40 KD HEAT SHOCK CHAPERONE PROTEIN) (HSP40).//9.80E-17//179aa//55%//O34136
- C-NT2RP2000008//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.40E-177//1726aa//47%//P51523
- 5 C-NT2RP2000032//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)7/1.80E-22//184aa//34%//Q01730
- C-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//0//1390bp//98%//AF061749
- 10 C-NT2RP2000054//Homo sapiens putative ring zinc finger protein NY-REN-43 antigen mRNA, complete cds.//0//2245bp//99%//AF155109
- C-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP-EP-SILON).//9.40E-16//145aa//100%//P49446
- C-NT2RP2000067//Mus musculus ODZ3 (Odz3) mRNA, partial cds.//0//3546bp//99%//AF195418
- 15 C-NT2RP2000070//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//3.40E-51//383aa//32%//P33450
- C-NT2RP2000076//Homo sapiens partial mRNA for polyhomeotic 2 protein (PH2 gene).//7.90E-20//265bp//73%//AJ242730
- C-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//0//2244bp//99%//AB018356
- 20 C-NT2RP2000126//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//2.50E-117//541aa//42%//P41877
- C-NT2RP2000133//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.//0//1490bp//99%//AF175966
- C-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//4.40E-226//423aa//99%//P35585
- 25 C-NT2RP2000153//GAR2 PROTEIN.//9.80E-23//311aa//28%//P41891
- C-NT2RP2000157//MLO2 PROTEIN.//2.60E-11//62aa//40%//Q09329
- C-NT2RP2000161//DIS3 PROTEIN HOMOLOG.//4.10E-35//184aa//44%//Q17632
- 30 C-NT2RP2000183//DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL SPECIFIC PROTEIN NSP60).//3.30E-16//114aa//44%//O02675
- C-NT2RP2000195//Homo sapiens androgen induced protein (AIG-1) mRNA, complete cds.//7.80E-152//704bp//99%//AF153605
- C-NT2RP2000224//INSULIN RECEPTOR SUBSTRATE-1 (IRS-1).//0.000043//103aa//28%//P35568
- 35 C-NT2RP2000248//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//3.40E-21//210aa//33%//P56558
- C-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//9.70E-41//278aa//36%//P40556
- C-NT2RP2000258//ACTIVATOR 1 140 KD SUBUNIT (REPLICATION FACTOR C LARGE SUBUNIT) (AI 140 KD SUBUNIT) (RF-C 140 KD SUBUNIT) (ACTIVATOR 1 LARGE SUBUNIT) (DNA-BINDING PROTEIN PO-GA).//7.10E-12//213aa//23%//P35251
- 40 C-NT2RP2000270//Human putative G-protein coupled receptor (SH120) mRNA, complete cds.//1.30E-242//1043bp//99%//U78723
- C-NT2RP2000288//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME 1.//1.60E-27//576aa//25%//Q10297
- 45 C-NT2RP2000297//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.30E-186//256aa//60%//Q99676
- C-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds.//4.30E-279//1193bp//99%//U82381
- C-NT2RP2000329//GTP-AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2.00E-111//226aa//92%//P08760
- 50 C-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds.//0//2331bp//99%//U83981
- C-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds.//0//1886bp//99%//L28010
- C-NT2RP2000420//ZINC FINGER PROTEIN 165.//8.50E-33//155aa//52%//P49910
- C-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//0//1757bp//99%//AF102265
- 55 C-NT2RP2000448//KES1 PROTEIN.//8.70E-54//392aa//38%//P35844
- C-NT2RP2000523//APOLOPROTEIN B MRNA EDITING PROTEIN (HEPR) (APOBEC-1).//6.00E-16//124aa//34%//P41238
- C-NT2RP2000660//SAP1 PROTEIN.//5.20E-68//474aa//32%//P39955

- C-NT2RP2000668//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.30E-27//349aa//32%/Q01577
- C-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE)//2.70E-100//488aa//44%/O32038
- 5 C-NT2RP2000764//NIFS PROTEIN.//6.60E-36//252aa//42%/P12623
- C-NT2RP2000809//Homo sapiens BAG-family molecular chaperone regulator-5 mRNA, complete cds.//0//3347bp//99%/AF095195
- C-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//5.-60E-08//179aa//29%/Q99104
- 10 C-NT2RP2000814//GELATION FACTOR (ACTIN BINDING PROTEIN 120) (ABP-120).//1.10E-07//96aa//29%/P13466
- C-NT2RP2000816//MAGNESIUM-CHELATASE 30 KD SUBUNIT.//7.90E-08//172aa//28%/P26174
- C-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds.//0//1562bp//99%/U08011
- 15 C-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2.//0//694aa//99%/O60841
- C-NT2RP2000892//Rattus norvegicus db83 mRNA, complete cds.//2.90E-191//1094bp//85%/AB006135
- C-NT2RP2000931//MATRIN 3.//2.40E-289//467aa//95%/P43244
- C-NT2RP2000943//Homo sapiens sec24D protein mRNA, complete cds.//0//2767bp//99%/AF130464
- 20 C-NT2RP2000965//Homo sapiens mRNA for fls353, complete cds.//0//1989bp//96%/AB024704
- C-NT2RP2001070//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/IMP OXIDASE).//5.80E-46//222aa//45%/Q20939
- C-NT2RP2001081//SYNAPTOTAGMIN IV.//4.20E-118//430aa//54%/P50232
- C-NT2RP2001127//Homo sapiens mRNA for PLU-1 protein.//0//2514bp//99%/AJ132440
- C-NT2RP2001168//VERPROLIN.//1.50E-09//143aa//33%/P37370
- 25 C-NT2RP2001174//GASTRULA ZINC FINGER PROTEIN XLCGF46.1 (FRAGMENT).//6.00E-10//88aa//38%/P18722
- C-NT2RP2001233//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.00E-128//409aa//45%/Q05481
- C-NT2RP2001245//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHAIN) (NMMHC).//2.20E-10//366aa//28%/P14105
- 30 C-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-ALPHA HOMOLOG) (BRAIN PROTEIN 147) (FRAGMENT).//4.40E-91//179aa//99%/P28663
- C-NT2RP2001295//ZINC/CADMIUM RESISTANCE PROTEIN.//8.30E-39//161aa//34%/P20107
- C-NT2RP2001327//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//5.50E-116//311aa//71%/Q13829
- 35 C-NT2RP2001378//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//2.00E-11//403aa//25%/Q02817
- C-NT2RP2001392//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//8.40E-192//581aa//54%/P93647
- C-NT2RP2001394//Homo sapiens mRNA for SCML2 protein.//0//2068bp//99%/Y18004
- 40 C-NT2RP2001397//Homo sapiens mRNA for cyclin B2, complete cds.//1.9E-316//1428bp//100%/AB020981
- C-NT2RP2001420//Mus musculus nuclear protein NIP45 mRNA, complete cds.//9.00E-112//742bp//82%/U76759
- C-NT2RP2001440//Homo sapiens mRNA for 14-3-3gamma, complete cds.//0//3712bp//99%/AB024334
- C-NT2RP2001460//TRICHOHYAUN.//1.00E-14//521aa//24%/P37709
- 45 C-NT2RP2001511//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//3.20E-297//2206bp//75%/AF093097
- C-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ALARAL1.//0//2502bp//99%/Y14494
- C-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//0//2326bp//99%/AF035586
- C-NT2RP2001560//VAV2 PROTEIN.//0.00000015//219aa//27%/Q60992
- 50 C-NT2RP2001576//HYPOTHETICAL 62.2 KD PROTEIN C4G8.12C IN CHROMOSOME 1.//8.20E-29//294aa//31%/Q09637
- C-NT2RP2001597//RYANODINE RECEPTOR, CARDIAC MUSCLE.//0.000000036//127aa//36%/P30957
- C-NT2RP2001601//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1748bp//99%/AF196304
- 55 C-NT2RP2001613//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT).//6.10E-12//184aa//31%/P24391
- C-NT2RP2001634//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//0//2445bp//99%/U97067
- C-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kd subunit brain-specific isoform mR-

NA, complete cds.//0/1287bp/99%/AF058718

C-NT2RP2001663//ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE), (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).//1.10E-47//126aa//53%/P42897

5 C-NT2RP2001740//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//7.90E-52//220aa//44%/Q61068

C-NT2RP2001748//FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS) (FARNESYL DIPHOSPHATE SYNTHETASE) (DIMETHYLALLYLTRANSFERASE (EC 2.5.1.1) / GERANYLTRANSFERASE (EC 2.5.1.10)) (KIAA0032).//5.40E-47//96aa//79%/P14324

10 C-NT2RP2001756//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.70E-49//411aa//32%/P51523

C-NT2RP2001839//SCY1 PROTEIN.//5.40E-32//621aa//24%/P53009

C-NT2RP2001869//ZINC FINGER PROTEIN 191.//7.10E-26//126aa//52%/O14754

15 C-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AIF-1) (IONIZED CALCIUM BINDING ADAPTER MOLECULE 1).//1.20E-45//141aa//65%/P55008

C-NT2RP2001883//Human sapiens CGI-01- protein mRNA, complete cds.//0/2306bp/99%/AF132936

C-NT2RP2001898//Homo inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end.//0/2518bp//98%/M74161

20 C-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5.//2.30E-38//395aa//30%/P53946

C-NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA, complete cds.//4.70E-177//1538bp//74%/AF062378

C-NT2RP2001985//Homo sapiens high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha mRNA, complete cds.//2.00E-38//435bp//67%/AF090989

25 C-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//6.50E-129//279aa//85%/Q08469

C-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//1.70E-47//247aa//52%/P35331

C-NT2RP2002046//Homo sapiens mRNA for transcription factor.//0/1664bp/99%/AJ130894

30 C-NT2RP2002058//Homo sapiens WD repeat protein WDR3 (WDR3) mRNA, complete cds.//0/2510bp/99%/AF083217

C-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//1.60E-226//1301bp//88%/U87306

C-NT2RP2002078//PECANEX PROTEIN.//1.80E-09//195aa//32%/P18490

35 C-NT2RP2002079//HISTONE H1, GONADAL.//4.40E-11//214aa//34%/P02256

C-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//0/33 89bp/99%/AJ.007509

C-NT2RP2002105//H.sapiens MSH-R gene for melanocyte stimulating hormone receptor.//0/1644bp/98%/X65634

40 C-NT2RP2002124//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//4.30E-44//155aa//37%/Q13107

C-NT2RP2002185//Homo sapiens ubiquitin mRNA, complete cds.//0/1789bp/99%/AF176069

C-NT2RP2002193//Homo sapiens PIAS3 mRNA for protein inhibitor of activated STAT3, complete cds.//0/2809bp/99%/AB021868

45 C-NT2RP2002252//Mus musculus (clone pVZmSin3A9) mSin3A9 mRNA, complete cds.//0/3118bp/91%/L38621

C-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//0/1528bp/98%/AF005418

C-NT2RP2002270//AF-9 PROTEIN.//1.20E-07//74aa//36%/P42568

C-NT2RP2002312//Homo sapiens mRNA for CDS2 protein.//0/233bp/99%/Y16521

50 C-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds.//8.40E-254//1158bp/99%/AB015594

C-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//4.30E-240//1105bp/99%/AF038958

C-NT2RP2002408//Homo sapiens mRNA for TOLLIP protein.//3.20E-210//1136bp/93%/AJ242972

C-NT2RP2002442//HESA PROTEIN.//2.80E-14//163aa//30%/P46037

55 C-NT2RP2002464//DNA CROSS-LINK REPAIR PROTEIN PSO2/SNM1.//6.50E-07//171aa//27%/P30620

C-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//0/2180bp/99%/AB005289

60 C-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC1744).//4.60E-144//537aa//49%/Q02386

C-NT2RP2002520//Homo sapiens transcription factor RFX-B (RFXB) mRNA, complete cds.//3.70E-34//668bp//61%/AF105427

- C-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//6.20E-19//288aa//26%/Q11073
- C-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-155//562aa//50%/P51523
- 5 C-NT2RP2002595//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//7.50E-35//181aa//42%/P12815
- C-NT2RP2002806//Rattus norvegicus Rabin3 mRNA, complete cds.//9.20E-147//874bp//87%/U19181
- C-NT2RP2002609//2-HYDROXYMUCONIC SEMIALDEHYDE HYDROLASE (EC 3.1.1.-) (HMSH).//2.80E-08//109aa//37%/P19076
- 10 C-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.).//1.70E-51//326aa//38%/P55345
- C-NT2RP2002701//HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME II.//1.90E-14//210aa//30%/O14345
- C-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1.//4.90E-85//489aa//43%/P55194
- 15 C-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.//3.50E-74//727bp//72%/AF041107
- C-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.//9.90E-54//964bp//64%/D89016
- C-NT2RP2002862//60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN).//8.80E-10//203aa//27%/P29764
- C-NT2RP2002880//GLUCOSE REPRESSION MEDIATOR PROTEIN.//0.000039//206aa//23%/P14922
- 20 C-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//1.90E-136//623bp//100%/AF038392
- C-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II.//4.10E-87//395aa//40%/Q18964
- C-NT2RP2002939//ZINC FINGER PROTEIN 136.//5.40E-70//282aa//42%/P52737
- 25 C-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//4.60E-80//147aa//100%/P51669
- C-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//1.00E-08//98aa//36%/P10129
- C-NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds.//0//2209bp//99%/AB026190
- 30 C-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//716aa//91%/P70700
- C-NT2RP2003000//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//L90E-11//132aa//38%/Q13829
- C-NT2RP2003121//Mus musculus enhancer of polycmb (Epc1) mRNA, complete cds.//2.30E-82//642bp//68%/AF079765
- 35 C-NT2RP2003125//RING CANAL PROTEIN (KELCH PROTEIN).//2.40E-38//539aa//25%/Q04652
- C-NT2RP2003137//UBIQUITIN.//0.000026//70aa//30%/P13117
- C-NT2RP2003157//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.30E-13//185aa//38%/Q08170
- 40 C-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds.//0//2091bp//99%/D67025
- C-NT2RP2003164//Homo sapiens mRNA for protein kinase.//0//2313bp//99%/AJ132545
- C-NT2RP2003177//Homo sapiens recombination and sister chromatid cohesion protein homolog (hrec8) mRNA, partial cds.//0//1641bp//99%/AF006264
- C-NT2RP2003228//H. sapiens PI-Cdc21 mRNA.//0//2870bp//98%/X74794
- 45 C-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.60E-186//1551bp//77%/AF023657
- C-NT2RP2003243//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//99%/AJ242978
- C-NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.//0//1580bp//99%/AF15811
- 50 C-NT2RP2003272//Homo sapiens ubiquitin mRNA, complete cds.//0//1789bp//99%/AF176069
- C-NT2RP2003277//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1).//1.90E-16//145aa//43%/P30771
- C-NT2RP2003286//PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4) (RNA-3'-PHOSPHATE CYCLASE) (RNA CYCLASE).//4.20E-88//374aa//47%/Q23400
- 55 C-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meldaing protein, complete cds.//0//1526bp//99%/AB006572
- C-NT2RP2003307//KINESIN LIGHT CHAIN (KLC).//2.20E-199//550aa//70%/Q07866
- C-NT2RP2003308//CROOKED NECK PROTEIN.//5.40E-244//622aa//67%/P17886

- C-NT2RP2003329//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN //3.60E-14//332aa//32%//P26337
- C-NT2RP2003347//BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN HOMOLOG //0.000022//261aa//24%//P48754
- 5 C-NT2RP2003391//Homo sapiens mRNA for nuclear transport receptor //0//1509bp//99%//AJ133769
- C-NT2RP2003394//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1 //5.50E-13//302aa//26%//P25386
- C-NT2RP2003401//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1) //9.60E-78//346aa//43%//Q61068
- 10 C-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT //5.00E-131//269aa//91%//P38378
- C-NT2RP2003466//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds //0//2194bp//99%//AF126799
- 15 C-NT2RP2003480//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds //0//3012bp//99%//AF125158
- C-NT2RP2003506//NADPH-CYTQCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR) //5.40E-14//106aa//46%//P04175
- C-NT2RP2003513//Homo sapiens mRNA for paralectin //0//2137bp//97%//Y14770
- 20 C-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/PDGF2) mRNA, complete cds //0//1746bp//95%//M12783
- C-NT2RP2003522//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds //0//1764bp//99%//AF125158
- 25 C-NT2RP2003543//HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE SLR1673 (EC 2.1.1.-) //1.70E-17//148aa//34%//P74261
- C-NT2RP2003564//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)) //2.10E-59//270aa//46%//P19474
- C-NT2RP2003596//Mus musculus Fas-apoptosis inhibitory molecule (Faim) mRNA, complete cds //4.80E-82//530bp//85%//AF130367
- 30 C-NT2RP2003604//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds //0//2442bp//99%//AF030233
- C-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase //9.40E-243//1624bp//82%//AJ006215
- C-NT2RP2003702//Homo sapiens 17 beta-hydroxysteroid dehydrogenase type VII (HSD17B7) mRNA, complete cds //2.1e-313//978bp//99%//AF098786
- 35 C-NT2RP2003704//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L //1.80E-72//350bp//100%//AJ132637
- C-NT2RP2003713//Homo sapiens ubiquitin-specific protease 3 (USP3) mRNA, complete cds //0//2018bp//99%//AF073344
- 40 C-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7) //5.40E-29//85aa//72%//Q05481
- C-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2) //1.70E-75//147aa//93%//P51669
- C-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP) //0//869aa//80%//P53620
- 45 C-NT2RP2003781//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II //5.50E-63//253aa//50%//Q09201
- C-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X //3.70E-21//137aa//43%//Q11076
- 50 C-NT2RP2003857//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN) //0.0000016//117aa//29%//Q91955
- C-NT2RP2003871//Homo sapiens transposon-derived Buster1 transposase-like protein gene, complete cds //0//2807bp//99%//AF205601
- C-NT2RP2003912//SERINE/THREONINE-PROTEIN KINASE NEK1 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 1) //6.10E-183//387aa//87%//P51954
- 55 C-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B) //1.50E-23//200aa//30%//Q09175
- C-NT2RP2003981//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS8 //1.40E-16//664aa//720%//

P39702

C-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//
2.30E-53//141aa//78%//P20290

C-NT2RP2004041//SYNAPSINS IA AND B.//0.0000074//159aa//32%//P17599

5 C-NT2RP2004066//Mus musculus Msx2 interacting nuclear target protein mRNA, complete cds.//2.70E-288//
1994bp//81%//AF156529

C-NT2RP2004098//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE).//5.40E-30//319aa//31%//Q01513

10 C-NT2RP2004170//Homo sapiens mRNA for transducin (beta) like 1 protein.//1.10E-138//1236bp//74%//Y12781
C-NT2RP2004187//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).//

5.60E-31//424aa//28%//Q07231

C-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds.//3.80E-52//397bp//82%//
AF003998

15 C-NT2RP2004232//Homo sapiens EPK2 mRNA for serine/threonine kinase, complete cds.//0//2272bp//99%//
AB015982

C-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds.//0//3044bp//99%//AB015718

C-NT2RP2004242//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//
9.90E-12//427aa//26%//P19246

20 C-NT2RP2004245//Mus musculus pantothenate kinase 1 beta (panK1beta) mRNA, complete cds.//6.40E-117//
1122bp//72%//AF200357

C-NT2RP2004270//PROTEIN PTM1 PRECURSOR.//1.40E-16//334aa//24%//P32857

C-NT2RP2004366//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS 13.//1.30E-51//505aa//
29%//Q07878

25 C-NT2RP2004389//PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR.//9.30E-15//
126aa//39%//P38120

C-NT2RP2004392//MNN4 PROTEIN7.//1.40E-11//143aa//27%//P36044

C-NT2RP2004396//Homo sapiens mRNA for activator of S phase Kinase, complete cds.//5.40E-243//1108bp//
99%//AB028069

C-NT2RP2004425//Mus musculus axotrophin mRNA, complete cds.//0//2321bp//86%//AF155739

30 C-NT2RP2004476//Homo sapiens cyclin L ania-6a mRNA, complete cds.//0//2075bp//99%//AF180920

C-NT2RP2004538//Mus musculus kinesin-like protein KIF1B (Kif1b) mRNA, complete cds.//0//1387bp//86%//
AF090190

C-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03.//3.00E-117//625aa//40%//
Q09903

35 C-NT2RP2004587//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//
7.30E-07//352aa//23%//P07197

C-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//8.50E-233//1061bp//99%//AJ006291

C-NT2RP2004681//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//
2.60E-07//426aa//23%//P19246

40 C-NT2RP2004689//HYPOTHETICAL 192.5 KD PROTEIN C6G9.10C IN CHROMOSOME 1.//5.60E-64//616aa//
33%//Q92355

C-NT2RP2004710//Mus musculus formin binding protein 30 mRNA, complete cds.//1.50E-280//1464bp//85%//
U40750

45 C-NT2RP2004732//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//
7.30E-07//352aa//23%//P07197

C-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).//1.30E-
26//190aa//41%//P38692

C-NT2RP2004791//PUTATIVE LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.4) (LEUCINE--TRNA
LIGASE) (LEURS).//9.50E-73//153aa//59%//Q10490

50 C-NT2RP2004799//PROBABLE SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC
6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//3.70E-135//414aa//62%//P53588

C-NT2RP2004816//H58 PROTEIN.//9.00E-173//327aa//98%//P40336

C-NT2RP2004920//TRANSCRIPTIONAL REGULATOR ATRX (X-LINKED NUCLEAR PROTEIN) (HETERO-
CHROMATIN PROTEIN 2) (HP1 ALPHA-INTERACTING PROTEIN) (HP1-BP38 PROTEIN).//4.20E-09//804aa//

22%//Q61687

55 C-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds.//0//2103bp//99%//AB007144

C-NT2RP2004959//P54 PROTEIN PRECURSOR.//0.00000095//297aa//20%//P13692

C-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1 (K51) mRNA, complete cds.//1.00E-

228//1666bp//75%//UJ56732

C-NT2RP2004978//ACTIN-LIKE PROTEIN ARP8.//3.30E-47//353aa//30%//Q12386

C-NT2RP2005003//52 KD RO PROTEIN (SJOGEN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))//1.80E-99//376aa//43%//P19474

C-NT2RP2005012//Homo sapiens mRNA for SEC63 protein.//0//1693bp//99%//AJ011779

C-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//3.30E-47//155aa//59%//P32447

C-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL ADDITION ENZYME) (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFERASE)//4.00E-91//218aa//44%//Q92089

C-NT2RP2005116//PUTATIVE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 ALPHA SUBUNIT (EIF-3 ALPHA)//2.00E-173//273aa//57%//P34466

C-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//0//2388bp//98%//X98743

C-NT2RP2005139//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).//0.000000022//139aa//35%//Q05921

C-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//0.00E-01//1437bp//98%//AF045583

C-NT2RP2005162//Homo sapiens aspartyl aminopeptidase mRNA, complete cds.//0//1615bp//99%//AF005050

C-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//2769bp//98%//AJ007509

C-NT2RP2005204//Homo sapiens SUMO-1-activating enzyme E1N subunit (SUA1) mRNA, complete cds.//0//1262bp//99%//AF090385

C-NT2RP2005239//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2087bp//99%//AF097025

C-NT2RP2005276//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2122bp//99%//D89053

C-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//0//2992bp//99%//AF060219

C-NT2RP2005315//Homo sapiens meningioma-expressed antigen 5 (MEA5) mRNA, partial cds.//1.90E-170//780bp//100%//AF036144

C-NT2RP2005325//Homo sapiens LIM-homeodomain protein HLX2 (LHX2) mRNA, complete cds.//0//1643bp//99%//AF124735

C-NT2RP2005336//TRICHOHYALIN.//5.40E-10//545aa//22%//P37709

C-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPASE 5 (EC 3.6.1.38).//2.10E-124//636aa//38%//P32660

C-NT2RP2005358//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds.//0//2199bp//99%//AF072247

C-NT2RP2005360//Homo sapiens sentrin/SUMO-specific protease (SEN1) mRNA, complete cds.//1.30E-52//753bp//67%//AF149770

C-NT2RP2005393//AUTOANTIGEN NGP-1.//7.20E-39//224aa//35%//Q13823

C-NT2RP2005407//OXYSTEROL-BINDING PROTEIN.//5.30E-63//410aa//40%//P22059

C-NT2RP2005436//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.20E-13//185aa//38%//Q08170

C-NT2RP2005441//Homo sapiens hypothalamus protein HT002 mRNA, complete cds.//4.10E-202//962bp//98%//AF113540

C-NT2RP2005457//Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA, complete cds.//1.20E-13 //0//608bp//99%//AF070652

C-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2.//3.00E-44//252aa//41%//P38127

C-NT2RP2005476//Human p190-B (p190-B) mRNA, complete cds.//3.40E-108//668bp//88%//U17032

C-NT2RP2005490//Mus musculus D3M3me (D3M3me) mRNA, complete cds.//1.80E-175//1102bp//83%//AF053628

C-NT2RP2005491//PARAMYOSIN (PMY) (ANTIGEN B).//0.00000015//279aa//26%//P35418

C-NT2RP2005496//ZINC FINGER PROTEIN 135.//2.90E-146//398aa//59%//P52742

C-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55).//5.20E-81//166aa//88%//P36876

C-NT2RP2005509//Homo sapiens CGI-45 protein mRNA, complete cds.//0//1825bp//99%//AF151803

C-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//3994bp//99%//AF092563

C-NT2RP2005525//Mus musculus kanadapin mRNA, complete cds.//2.40E-304//1687bp//85%//AF035526

C-NT2RP2005531//PROTEIN 4.1 (BAND 4.1) (P4.1).//5.50E-70//393aa//39%//P11171

C-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1560bp//98%//AJ012449

C-NT2RP2005549//PUTATIVE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLLGLYOXALALASE (DOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLLGLYOXAL LYASE).//2.00E-20//181aa//36%/Q39366

C-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds.//1.00E-46//576bp//70%/AF062529

C-NT2RP2005605//QUEUINE TRNA-RIBOSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME).//8.20E-23//164aa//28%/Q32053

C-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//8.9E-31//1455bp//98%/AF062085

C-NT2RP2005635//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1.00E-11//128aa//36%/P47623

C-NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).//1.20E-13//174aa//45%/P56101

C-NT2RP2005669//Homo sapiens death effector domain-containing testicular molecule mRNA, complete cds.//1.60E-248//1126bp//99%/AF043733

C-NT2RP2005694//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.40E-200//908bp//99%/AF089814

C-NT2RP2005694//X-LINKED RETINITIS PIGMENTOSA GTPASE REGULATOR.//2.60E-10//175aa//27%/Q92834

C-NT2RP2005701//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//3.00E-63//323aa//39%/Q62158

C-NT2RP2005712//Homo sapiens myosin X (MYO10) mRNA, partial cds.//10//2681 bp//99%/AF132022

C-NT2RP2005719//GPI-ANCHORED PROTEIN P137.//4.00E-14//99aa//43%/Q14444

C-NT2RP2005722//Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds.//10//2545bp//99%/AB011414

C-NT2RP2005723//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN).//3.00E-09//169aa//28%/P38074

C-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//10//1968bp//99%/AF068868

C-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//10//1966bp//99%/AF082516

C-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A (EIF-4A).//1.70E-61//374aa//38%/P47943

C-NT2RP2005767//G. gallus PB1 gene.//5.00E-163//1158bp//81%/X90849

C-NT2RP2005773//Homo sapiens pyrroline 5-carboxylate reductase isoform (P5CR2) mRNA, complete cds.//2.70E-180//656bp//99%/AF151351

C-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN-BINDING PROTEIN) (SABP).//2.10E-213//249aa//85%/Q02038

C-NT2RP2005776//POLY(A) POLYMERASE TYPE 2 (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//4.40E-55//358aa//42%/P51005

C-NT2RP2005784//Homo sapiens ubiquitin-conjugating enzyme variant Kua (UBE2V) mRNA, complete cds.//10//2191bp//92%/AF155120

C-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//2.30E-39//318aa//31%/P40004

C-NT2RP2005835//SHP1 PROTEIN.//1.80E-28//208aa//32%/P34223

C-NT2RP2005841//Homo sapiens mRNA for ALEX3, complete cds.//3.50E-52//1091bp//59%/AB039669

C-NT2RP2005933//NUCLEOPORIN NUP57 (NUCLEAR PORE PROTEIN NUP57).//5.00E-11//155aa//34%/P48837

C-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//1.50E-67//388aa//44%/P25500

C-NT2RP2006043//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.50E-13//185aa//38%/Q08170

C-NT2RP2006071//Homo sapiens adaptor protein APPL mRNA, complete cds.//5.80E-120//1257bp//64%/AF169797

C-NT2RP2006219//H. sapiens mRNA for DCCR6 protein.//1.10E-214//1026bp//97%/X96484

C-NT2RP2006238//Rattus norvegicus CTD-binding SR-like protein rAB mRNA, complete cds.//10//1669bp//88%/U49055

C-NT2RP2006275//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//2.00E-59//388aa//32%/P46821

C-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.80E-274//1236bp//99%/AF035262

C-NT2RP2006436//ANTERIOR-RESTRICTED HOMEBOX PROTEIN (RATKHE POUCH HOME BOX).

- 3.40E-07//50aa//50%//Q61658
 C-NT2RP2006456//Homo sapiens leucine-rich glioma-inactivated protein precursor (LG1) mRNA, complete cds.//1.30E-37//484bp//65%//AF055636
 C-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//0//2181bp//99%//AJ006266
 5 C-NT2RP2006534//5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-1 CHAIN (EC 2.7.1.-) (AMPK ALPHA-1 CHAIN) (FRAGMENT)//3.20E-11//32aa//96%//Q13131
 C-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds.//3.10E-272//1220bp//95%//AF038966
 C-NT2RP2006571//CYTOCHROME P450 2G1 (EC 1.14.14.1) (CYP1G1) (P450-NMB) (OLFACTIVE)//4.20E-134//486aa//50%//P24461
 10 C-NT2RP2006573//2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37) (CNP)//0.0000055//169aa//25%//P09543
 C-NT2RP2006598//Homo sapiens retinoid x receptor interacting protein mRNA, complete cds.//3.10E-295//1193bp//99%//AF113538
 15 C-NT2RP3000031//HISTONE DEACETYLASE HDA1//1.10E-71//350aa//42%//P53973
 C-NT2RP3000046//MITOCHONDRIAL GTPASE MSS1 PRECURSOR.//4.60E-78//421aa//37%//P32559
 C-NT2RP3000047//NPL4 PROTEIN.//1.10E-85//526aa//36%//P33755
 C-NT2RP3000050//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.20E-150//490aa//53%//Q05481
 20 C-NT2RP3000068//SON OF SEVENLESS PROTEIN HOMOLOG 1 (SOS-1) (MSOS-1).//2.20E-06//165aa//27%//Q62245
 C-NT2RP3000085//ACETYL-PROPIONYL-COENZYME A CARBOXYLASE ALPHA CHAIN[CONTAINS: BIOTIN CARBOXYLASE (EC 6.3.4.14); BIOTIN CARBOXYL CARRIER PROTEIN (BCCP)].//1.90E-123//436aa//50%//P46401
 25 C-NT2RP3000109//P54 PROTEIN PRECURSOR.//0.0000065//358aa//22%//P13692
 C-NT2RP3000207//GLUCOAMYLASE S1S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//2.90E-11//721aa//23%//P08640
 C-NT2RP3000233//RING CANAL PROTEIN (KELCH PROTEIN).//9.30E-84//453aa//42%//Q04652
 C-NT2RP3000252//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2388bp//99%//AF120334
 30 C-NT2RP3000299//Rattus norvegicus mRNA for Crk-associated substrate, pi 30, complete cds.//0//2730bp//82%//D29766
 C-NT2RP3000320//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//100%//AJ242978
 C-NT2RP3000333//Rattus norvegicus db83 mRNA, complete cds.//2.90E-191//1094bp//85%//AB006135
 35 C-NT2RP3000344//Homo sapiens mitochondrial inner membrane preprotein translocase Tim17a mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.50E-246//1124bp//99%//AF108622
 C-NT2RP3000350//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2392bp//99%//AF120334
 C-NT2RP3000359//GTP-AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2.00E-111//226aa//92%//P08760
 40 C-NT2RP3000361//Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1/Zer1 and Prp6.//0//2072bp//98%//AB019219
 C-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.10E-107//206aa//99%//P35293
 C-NT2RP3000393//Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds.//5.80E-266//1373bp//86%//AF061817
 45 C-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)//1.70E-139//679aa//41%//O43143
 C-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//0//2364bp//99%//AF071185
 C-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//2.90E-15//319aa//26%//P37908
 50 C-NT2RP3000441//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.//3.40E-42//645bp//67%//AF098066
 C-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//0//1934bp//99%//X16667
 C-NT2RP3000527//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//4.80E-28//536aa//27%//P28160
 C-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//1.90E-12//192aa//30%//P15151
 55 C-NT2RP3000562//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//2165bp//99%//AF093097
 C-NT2RP3000578//HES1 PROTEIN.//1.30E-22//229aa//27%//P35843

- C-NT2RP3000590//UVS-2 PROTEIN.//1.30E-22//458aa//24%//P33288
 C-NT2RP3000596//TRICHOHYALIN.//2.50E-17//304aa//28%//Q07283
 C-NT2RP3000603//NEUROGENIC DIFFERENTIATION FACTOR 1.//3.70E-11//90aa//42%//Q13562
 C-NT2RP3000605//Mus musculus mRNA for wizL, complete cds.//0.//2232bp//82%//AB012265
 5 C-NT2RP3000624//Rattus norvegicus mRNA for SECIS binding protein 2 (sbp2 gene).//5.80E-234//1562bp//81%//AJ251245
 C-NT2RP3000632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.00E-140//499aa//46%//P51523
 10 C-NT2RP3000739//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//1.40E-24//155aa//37%//Q10149
 C-NT2RP3000742//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).//4.10E-165//371aa//49%//P10895
 15 C-NT2RP3000753//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//2.00E-10//565aa//24%//P12036
 C-NT2RP3000759//ADP-RIBOSYLATION FACTOR.//7.00E-28//176aa//34%//Q94650
 C-NT2RP3000825//NEUROGENIC LOCUS NOTCH 3 PROTEIN.//2.50E-36//417aa//31%//Q61982
 C-NT2RP3000826//Homo sapiens mRNA for seven transmembrane protein TM7SF3, complete cds.//0.//2522bp//99%//AB032470
 20 C-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).//8.30E-108//331aa//50%//P27448
 C-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//6.90E-69//1611bp//61%//U53445
 C-NT2RP3000869//Drosophila melanogaster AAA family protein Bor (bor) mRNA, complete cds.//2.60E-138//1673bp//67%//AF22709
 25 C-NT2RP3000875//MEVALONATE KINASE (EC 2.7.1.36) (MK).//7.70E-87//175aa//98%//Q03426
 C-NT2RP3000917//DHP1 PROTEIN.//1.00E-193//428aa//55%//P40848
 C-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//2.70E-185//585bp//88%//AF015264
 30 C-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A.//1.90E-46//173aa//98%//P39027
 C-NT2RP3000994//MATERNAL EFFECT PROTEIN STAUFEN.//0.0000006//78aa//48%//P25159
 C-NT2RP3001055//Drosophila melanogaster separation anxiety protein (san) mRNA, complete cds.//3.80E-38//462bp//70%//AF225902
 35 C-NT2RP3001057//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//9.00E-201//584aa//54%//Q05481
 C-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//7.10E-47//537bp//74%//AF060219
 C-NT2RP3001096//Rattus norvegicus leprecan (lepre1) mRNA, complete cds.//1.70E-94//787bp//66%//AF087433
 40 C-NT2RP3001107//PEREGRIN (BR140 PROTEIN).//3.30E-44//260aa//40%//P55201
 C-NT2RP3001111//Homo sapiens TRF-proximal protein mRNA, complete cds.//1.50E-149//731bp//97%//AF097725
 C-NT2RP3001113//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//2.90E-11//631aa//23%//P25386
 45 C-NT2RP3001120//ZINC FINGER, PROTEIN 136.//7.80E-170//512aa//58%//P52737
 C-NT2RP3001140//F-SPONDIN PRECURSOR.//9.90E-238//419aa//96%//P35446
 C-NT2RP3001150//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000031//207aa//29%//P52154
 C-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//0.//2732bp//99%//AJ006266
 50 C-NT2RP3001176//HYPOTHETICAL 65.3 KD PROTEIN IN MAD1-SCY1 INTERGENIC REGION.//1.70E-10//196aa//27%//P53154
 C-NT2RP3001216//CYCLIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT).//0.0000023//137aa//33%//P35663
 C-NT2RP3001221//GAMMA-BUTYROBETAINE-2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-BUTYROBETAINE HYDROXYLASE).//1.90E-31//353aa//30%//P80193
 55 C-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CONTAINS: LIGHT CHAIN LC1].//1.20E-166//395aa//51%//P14873
 C-NT2RP3001253//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//1.70E-10//540aa//23%//P32380

- C-NT2RP3001268//Homo sapiens zinc finger protein ZNF228 (ZNF228) mRNA, complete cds.//0.3606bp//99%//AF198358
- C-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein.//1.30E-99//669bp//83 %//Y18101
- 5 C-NT2RP3001307//Gallus gallus RPE65 mRNA, complete cds.//4.20E-29//530bp//63%//AB017594
- C-NT2RP3001338//ZINC FINGER PROTEIN 81 (FRAGMENT) //2.40E-16//175aa//28%//P51508
- C-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN) //3.60E-25//129aa//34%//P32089
- 10 C-NT2RP3001383//Mus musculus ARL-6 interacting protein-6 (Aip-6) mRNA, partial cds.//3.40E-40//355bp//79%//AF133913
- C-NT2RP3001384//Homo sapiens mRNA for LA95 protein.//0.1214bp//99%//AJ243467
- C-NT2RP3001398//TRANSCRIPTIONAL REPRESSOR CTCF.//1.30E-61//374aa//36%//P49711
- C-NT2RP3001399//SSU72 PROTEIN.//1.30E-16//84aa//52%//P53538
- 15 C-NT2RP3001407//SCY1 PROTEIN.//0.00000033//143aa//25%//P53009
- C-NT2RP3001426//DNAJ PROTEIN (FRAGMENT) //1.00E-16//177aa//46%//O33529
- C-NT2RP3001427//WERNER SYNDROME HEUCASE HOMOLOG //2.70E-10//159aa//33%//O09053
- C-NT2RP3001428//NUCLEOPROTEIN TPR.//1.40E-128//152aa//99%//P 12270
- C-NT2RP3001453//ANTIGEN PEPTIDE TRANSPORTER 2 (APT2) (HISTOCOMPATIBILITY ANTIGEN MODIFIER 2) //3.20E-90//157aa//59%//P36371
- 20 C-NT2RP3001457//Drosophila melanogaster Melted (melt) mRNA, partial cds.//4.60E-20//792bp//59%//AF205831
- C-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A.//9.10E-13//87aa//43%//P11632
- C-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//0.1475bp//99%//U13395
- 25 C-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//0.2295bp//99%//AF064801
- C-NT2RP3001527//Human Sp140 protein (Sp140) mRNA, complete cds.//4.30E-29//793bp//93%//U63420
- C-NT2RP3001528//SPOOB-ASSOCIATED GTP-BINDING PROTEIN.//1.00E-61//1345aa//42%//P20964
- C-NT2RP3001538//HYPOTHETICAL 39.0 KD PROTEIN T28D9.3 IN CHROMOSOME II.//9.10E-10//158aa//31%//Q10022
- 30 C-NT2RP3001554//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1] //1.40E-76//388aa//32%//P46821
- C-NT2RP3001580//Mus musculus strain C57BL/J germ cell-less protein (Gcl) mRNA, complete cds.//0.1730bp//85%//AF163665
- 35 C-NT2RP3001587//Human anthracycline-associated resistance ARX mRNA, complete cds.//0.2617bp//99%//U35832
- C-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210.//6.80E-18//91aa//38%//Q92609
- C-NT2RP3001646//WD-40 REPEAT PROTEIN MS12.//8.80E-09//132aa//31%//O22468
- C-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP) //0.1557bp//98%//AJ012449
- 40 C-NT2RP3001672//Homo sapiens Sex comb on midleg homolog 1 isoform 2 (SCMH1) mRNA, complete cds.//0.2836bp//99%//AF149046
- C-NT2RP3001679//Homo sapiens rec mRNA, complete cds.//0.2495bp//99%//AB023584
- C-NT2RP3001688//Homo sapiens DNA binding protein p96PIF mRNA, complete cds.//0.1869bp//99%//AF173868
- 45 C-NT2RP3001690//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.00000024//481aa//21%//P25386
- C-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR.//3.40E-33//161aa//32%//P54356
- C-NT2RP3001712//Homo sapiens HP1-BP74 protein mRNA, complete cds.//0.1788bp//99%//AF113534
- C-NT2RP3001723//Homo sapiens cell recognition molecule Caspr2 (CASPR2) mRNA, complete cds.//1.40E-58//1138bp//63%//AF193613
- 50 C-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//1.10E-240//902bp//99%//AF054177
- C-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds.//6.90E-132//774bp//88%//AF008554
- 55 C-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT) //7.10E-132//294aa//84%//Q14141
- C-NT2RP3001739//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//1.40E-15//190aa//32%//Q09701
- C-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRP M).//1.80E-117//462aa//55%//P52272

- C-NT2RP3001799//MYOSIN HEAVY CHAIN, STRIATED MUSCLE.//1.60E-11//348aa//27%//P24733
- C-NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN).//7.40E-18//249aa//30%//Q04652
- C-NT2RP3001854//Homo sapiens novel retinal pigment epithelial cell protein (NORPEG) mRNA, complete cds.//0//2742bp//99%//AF155135
- 5 C-NT2RP3001855//HOMEBOX PROTEIN PKNOX1 (HOMEBOX PROTEIN PREP-1).//8.10E-125//302aa//60%//P55347
- C-NT2RP3001857//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//1.20E-14//242aa//24%//Q00808
- C-NT2RP3001898//Homo sapiens mRNA for UDP-N-acetylglucosamine: alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV, complete cds.//0//1587bp//100%//AB000624
- 10 C-NT2RP3001931//Rattus norvegicus clone C48 CDK5 activator-binding protein mRNA, complete cds.//4.30E-91//656bp//81%//AF177478
- C-NT2RP3001938//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//1.30E-22//227aa//33%//P08458
- C-NT2RP3001944//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//3.10E-92//314aa//51%//Q09251
- 15 C-NT2RP3001969//TRICHOHYALIN.//2.70E-11//442aa//23%//P37709
- C-NT2RP3002004//H. sapiens mRNA for FAST kinase.//1.50E-192//475bp//94%//X86779
- C-NT2RP3002007//SAP1 PROTEIN.//1.1 OE-68//474aa//32%//P39955
- C-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//5.30E-25//139aa//48%//Q09232
- 20 C-NT2RP3002045//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT.//1.00E-299//397aa//94%//P18484
- C-NT2RP3002056//RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1).//2.00E-48//475aa//35%//P29374
- C-NT2RP3002062//Homo sapiens BAG-family molecular chaperone regulator-5 mRNA, complete cds.//0//3764bp//99%//AF095195
- 25 C-NT2RP3002081//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//4.10E-233//1896bp//69%//AF11423
- C-NT2RP3002108//DEC1 PROTEIN (MDM20 PROTEIN).//7.90E-09//181aa//22%//Q12387
- C-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING PROTEIN GST1-HS).//2.80E-253//474aa//93%//P15170
- 30 C-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP.//1.90E-151//223aa//91%//Q02614
- C-NT2RP3002273//SCD6 PROTEIN.//1.30E-09//295aa//28%//P45978
- C-NT2RP3002303//PROBABLE UNDECAPRENYL PYROPHOSPHATE SYNTHETASE (EC 2.5.1.31) (UPP SYNTHETASE) (DI-TRANS-POLY-CIS-DECAPRENYL CISTRANSFERASE).//8.60E-49//243aa//43%//Q58767
- 35 C-NT2RP3002330//Homo sapiens eRF5 mRNA, complete cds.//0//2443bp//99%//U87791
- C-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15).//4.20E-70//590bp//76%//X16396
- C-NT2RP3002399//DNA REPLICATION LICENSING FACTOR MCM4 (CDC21 HOMOLOG) (P1-CDC21).//8.60E-79//416aa//34%//P33991
- 40 C-NT2RP3002501//THREONINE DEHYDRATASE CATABOLIC (EC 4.2.1.16) (THREONINE DEAMINASE).//3.70E-43//318aa//37%//P05792
- C-NT2RP3002529//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS45.//8.90E-95//542aa//38%//P38932
- C-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III.//5.80E-40//161aa//52%//Q10010
- 45 C-NT2RP3002602//PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (EC 5.3.4.1) (ERP60) (58 KD MICROSOMAL PROTEIN) (P58) (HIP-70) (Q-2).//2.90E-19//173aa//28%//P11598
- C-NT2RP3002628//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//2.50E-26//90aa//42%//P38660
- 50 C-NT2RP3002631//Homo sapiens Ran binding protein 11 mRNA, complete cds.//0//1703bp//99%//AF111109
- C-NT2RP3002650//Mus musculus growth suppressor 1L (Gros1) mRNA, complete cds.//0//2109bp//87%//AF165163
- C-NT2RP3002663//Homo sapiens putative glycolipid transfer protein mRNA, complete cds.//8.10E-263//1243bp//97%//AF103731
- 55 C-NT2RP3002671//ELONGATION FACTOR 2 (EF-2).//2.50E-73//179aa//36%//P13060
- C-NT2RP3002682//Homo sapiens CGI-145 protein mRNA, complete cds.//0//1596bp//98%//AF151903
- C-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kif1b), complete cds.//1.10E-83//1205bp//69%//D17577
- C-NT2RP3002770//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//1.00E-071//107aa//

- 41%/P17564
 C-NT2RP3002785//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//2.50E-55//187aa//39%/Q24371
 C-NT2RP3002810//HISTIDINE-RICH PROTEIN KE4.//2.20E-10//260aa//26%/Q31125
 C-NT2RP3002818//INSERTION ELEMENT IS2A HYPOTHETICAL 48.2 KD PROTEIN.//5.70E-226//303aa//97%/P51026
 5 C-NT2RP3002869//Mus musculus semaphorin Via mRNA, complete cds.//2.50E-232//1282bp//85%/AF030430
 C-NT2RP3002876//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//1.30E-29//805bp//61%/AF053091
 10 C-NT2RP3002909//P53-BINDING PROTEIN 2 (53BP2) (BCL2-BINDING PROTEIN) (BBP).//1.50E-125//512aa//47%/Q13625
 C-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).//2.00E-111//551aa//42%/Q04652
 C-NT2RP3002953//Homo sapiens protocadherin beta 5 (PCDH-beta5) mRNA, complete cds.//0//2388bp//99%/AF152498
 15 C-NT2RP3002969//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2722bp//99%/D89053
 C-NT2RP3002972//Halocynthia roretzi mRNA for HrPET-1, complete cds.//3.90E-52//899bp//64%/AB029333
 C-NT2RP3002988//Homo sapiens IKB kinase-b (IKK-beta) mRNA, complete cds.//1.80E-292//1325bp//99%/AF080158
 C-NT2RP3003032//Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds.//0//2656bp//99%/AF084555
 20 C-NT2RP3003059//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//3.80E-152//1007bp//82%/U78090
 C-NT2RP3003061//ANKYRIN.//1.40E-20//200aa//37%/Q02357
 C-NT2RP3003071//NEUROGENIC PROTEIN BIG BRAIN.//1.10E-05//258aa//24%/P23645
 C-NT2RP3003078//Rattus norvegicus mRNA for ischemia related factor NYW-1, complete cds.//2.60E-112//633bp//88%/AB027149
 25 C-NT2RP3003101//Mouse mRNA for tetracycline transporter-like protein, complete cds.//3.60E-83//807bp//72%/D88315
 C-NT2RP3003133//Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds.//0//1998bp//91%/AB011414
 30 C-NT2RP3003138//Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.//0//2159bp//98%/AF071592
 C-NT2RP3003145//Mus musculus metallocalboxypeptidase CPX-1 mRNA, complete cds.//0//2251bp//81%/AF077738
 C-NT2RP3003185//TROPOMYOSIN1, FUSION PROTEIN 33.//2.80E-06//402aa//23%/P49455
 35 C-NT2RP3003193//ZINC FINGER PROTEIN 135.//7.30E-98//269aa//62%/P52742
 C-NT2RP3003197//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME 1.//5.70E-09//169aa//31%/Q09674
 C-NT2RP3003203//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//2.00E-210//1851 bp//76%/AF110267
 40 C-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//4.30E-187//1750bp//75%/U20286
 C-NT2RP3003230//Homo sapiens mRNA for hCRNN4, complete cds.//0//2350bp//99%/AB030656
 C-NT2RP3003242//Homo sapiens stannocalcin-related protein mRNA, complete cds.//0//2366bp//99%/AF098462
 45 C-NT2RP3003251//52 KD RO PROTEIN (SJOEGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//4.20E-86//366aa//48%/P19474
 C-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//0//2596bp//98%/L36983
 C-NT2RP3003290//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.//1.5E-310//1468bp//82%/AB033922
 50 C-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//1.10E-170//585aa//54%/O64948
 C-NT2RP3003313//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP80 mRNA, complete cds.//0//2476bp//99%/AF117657
 C-NT2RP3003327//52 KD RO PROTEIN (SJOEGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52).//1.30E-35//178aa//44%/Q62191
 55 C-NT2RP3003353//HYPOTHETICAL 26.2 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.//2.80E-07//161aa//28%/P40084
 C-NT2RP3003365//Mus musculus SKD3 mRNA, complete cds.//0//2133bp//85%/U09874

- C-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds.//9.20E-45//782bp//65%//U90653
- C-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//6.30E-270//743bp//90%//AF071317
- 5 C-NT2RP3003490//Homo sapiens mRNA for putative phospholipase, complete cds.//4.50E-81//649bp//67%//AB019435
- C-NT2RP3003491//Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.//5.60E-36//842bp//62%//AF091624
- 10 C-NT2RP3003500//SCY1 PROTEIN.//9.20E-27//601aa//23%//P35009
- C-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC REGION.//4.50E-30//191aa//40%//P40529
- C-NT2RP3003589//Homo sapiens ras-related GTP-binding protein mRNA, complete cds.//0/3131bp//94%//AF106681
- 15 C-NT2RP3003659//HES1 PROTEIN.//5.90E-22//229aa//27%//P35843
- C-NT2RP3003665//Homo sapiens mRNA for beta-ureidopropionase, complete cds.//0/1690bp//99%//AB013885
- C-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//2.20E-13//146aa//42%//P14209
- C-NT2RP3003701//F-SPONDIN PRECURSOR.//1.80E-17//324aa//26%//P35446
- 20 C-NT2RP3003716//SLIT PROTEIN PRECURSOR.//6.60E-10//150aa//34%//P24014
- C-NT2RP3003726//Homo sapiens spermatogenesis associated PD1 mRNA, complete cds.//0/2568bp//99%//U28164
- C-NT2RP3003799//Rattus norvegicus Srg1 (Syr1) mRNA, complete cds.//9.00E-238//1529bp//84%//UJ71294
- 25 C-NT2RP3003800//Rattus norvegicus tyrosine protein kinase pp60-c-src mRNA, complete cds.//1.90E-163//924bp//89%//AF130457
- C-NT2RP3003809//SAV PROTEIN.//1.10E-131//576aa//41%//Q07590
- C-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP).//9.60E-19//174aa//31%//P02720
- 30 C-NT2RP3003831//Homo sapiens ENDOGL-1 (alias ENGL-a) mRNA for endonuclease G-like protein-1, complete cds.//2.2e-316//1436bp//99%//AB020523
- C-NT2RP3003846//Homo sapiens mRNA for putative phospholipase, complete cds.//4.80E-277//1255bp//99%//AB019435
- C-NT2RP3003876//Rattus norvegicus Rabin3 mRNA, complete cds.//4.50E-147//874bp//87%//U19181
- 35 C-NT2RP3003914//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//2.20E-20//76aa//64%//Q09332
- C-NT2RP3003918//Homo sapiens VAMP-associated protein B (VAP-B) mRNA, complete cds.//0/2191bp//99%//AF086628
- 40 C-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein.//6.50E-240//1215bp//94%//X84692
- C-NT2RP3004016//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1).//1.50E-17//226aa//26%//Q13263
- C-NT2RP3004078//H.sapiens HRFX2 mRNA.//0/1806bp//99%//X76091
- 45 C-NT2RP3004125//Mus musculus zinc finger protein splice variant FIZ1-B (Fiz1) mRNA, complete cds.//4.60E-229//1560bp//78%//AF126747
- C-NT2RP3004148//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//7.90E-05//271aa//22%//P08640
- 50 C-NT2RP3004155//Homo sapiens COQ7 protein mRNA, complete cds.//1.10E-179//823bp//100%//AF098948
- C-NT2RP3004189//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//1.30E-14//242aa//24%//Q00808
- C-NT2RP3004206//CROOKED NECK PROTEIN.//1.40E-220//567aa//67%//P17886
- 55 C-NT2RP3004207//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0/2445bp//100%//AJ245820
- C-NT2RP3004209//Homo sapiens ubiquitin processing protease (Ubp-M) mRNA, complete cds.//0/2320bp//99%//AF126736
- C-NT2RP3004242//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//4.70E-13//118aa//33%//P52734
- 60 C-NT2RP3004258//Homo sapiens ZIS1 mRNA, complete cds.//0/1861bp//99%//AF065391
- 65 C-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds.//2.40E-248//1126bp//100%//AF088982
- C-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds.//5.10E-24//597bp//61%//AF007871
- C-NT2RP3004348//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.10E-185//1130bp//82%//

X67877

C-NT2RP3004378//Drosophila melanogaster separation anxiety protein (san) mRNA, complete cds.//3.90E-38//462bp//70%//AF225902

C-NT2RP3004424//Homo sapiens mRNA for stromal antigen 3 (STAG3 gene).//1.00E-66//364bp//93%//AJ007798
5 C-NT2RP3004428//CHROMODOMAIN HELICASE-DNA-BINDING PROTEIN 4 (CHD-4) (MI-2 AUTOANTIGEN 218 KD PROTEIN) (MI2-BETA).//5.20E-09//212aa//25%//Q14839

C-NT2RP3004472//GERM CELL-LESS PROTEIN.//1.60E-61//170aa//40%//Q01820
C-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//3.30E-113//466aa//42%//P34110

10 C-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds.//4.00E-303//1385bp//99%//AB012851
C-NT2RP3004498//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.//2.00E-249//1777bp//80%//U83176

C-NT2RP3004504//M.musculus mRNA for CPEB protein.//1.90E-295//893bp//92%//Y08260

C-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).//3.70E-37//190aa//39%//P40484

15 C-NT2RP3004534//Mouse oncogene (ect2) mRNA, complete cds.//0.0//2075bp//87%//L11316

C-NT2RP3004544//THYROID RECEPTOR INTERACTING PROTEIN 10 (TRIP10) (FRAGMENT).//1.00E-22//1.3aa//53%//Q15642

C-NT2RP3004566//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-95//434aa//43%//P51523

20 C-NT2RP3004569//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).//3.80E-08//150aa//28%//Q01484

C-NT2RP3004572//Homo sapiens TATA binding protein associated factor (TAFII150) mRNA, complete cds.//0.0//1853bp//99%//AF040701

C-NT2RP3004578//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//5.50E-12//396aa//23%//P39922

25 C-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//0.0//1807bp//99%//AJ006266

C-NT2RP3004617//ZINC-BINDING PROTEIN A33.//7.20E-75//464aa//35%//Q02084

C-NT2RP3004618//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0.0//3972bp//98%//AF093097

C-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN).//1.70E-72//254aa//45%//P54352

30 C-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete cds.//0.0//2393bp//99%//AB014679

C-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64.//2.60E-98//239aa//64%//P35526

C-NT2RP4000051//SYNAPTONEMAL COMPLEX PROTEIN SC65.//4.90E-51//335aa//37%//Q64375

35 C-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0.0//2160bp//99%//AJ012449

C-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//0.0//2161bp//99%//AB011538

C-NT2RP4000111//CLEFTAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0.0//728aa//99%//Q10568

40 C-NT2RP4000129//Xenopus laevis F-box protein 28 (Fbx28) mRNA, partial cds.//1.40E-28//296bp//75%//AF176667

C-NT2RP4000147//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//4.30E-18//1543bp//78%//U35776

C-NT2RP4000210//PAIRED AMPHIPATHIC HELIX PROTEIN.//1.00E-71//396aa//36%//P22579

45 C-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//5.90E-15//104aa//40%//P15287

C-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//0.0//1932bp//99%//AJ006470

C-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//2.70E-84//208aa//76%//Q03173

C-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).//5.50E-29//153aa//43%//O23968

C-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME 1.//3.50E-297//1024aa//55%//P87115

50 C-NT2RP4000312//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE).//1.50E-26//237aa//28%//Q01631

C-NT2RP4000323//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//3.00E-07//101aa//32%//P26372

55 C-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//0.0//4782bp//99%//AF044195

C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1).//2.60E-77//262aa//54%//Q75570

- C-NT2RP4000376//Homo sapiens mRNA for phospholipase A2 activating protein.//0//2412bp/99%//AJ238243
 C-NT2RP4000398//ZINC FINGER PROTEIN 140.//2.90E-110//435aa//50%//P52738
 C-NT2RP4000415//Drosophila melanogaster fumble (fumble) mRNA, complete cds.//6.20E-19//902bp//57%//AF221546
- 5 C-NT2RP4000417//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113)(MAN(9)-ALPHA-MANNOSIDASE)(FRAGMENT).//2.60E-51//438aa//33%//P45701
 C-NT2RP4000449//Homo sapiens siirtuin type 1 (SIRT1) mRNA, complete cds.//0//3143bp/99%//AF083106
 C-NT2RP4000455//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//3.00E-07//175aa//27%//P09309
 C-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (EC 3.1.2.15) (UBIQUITIN THI-OLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15)(DEUBIQUITINATING ENZYME 15).//2.50E-37//291aa//38%//P50101
- 10 C-NT2RP4000481//ATP-DEPENDENT RNA HELICASE DOB1 (MRNA TRANSPORT REGULATOR MTR4).//1.90E-67//721aa//29%//Q09475
 C-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//8.80E-50//214aa//50%//P40484
 C-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.50E-106//495aa//45%//P45818
 C-NT2RP4000524//Mus musculus Sec8 mRNA, complete cds.//0//3131bp//87%//AF022962
 C-NT2RP4000528//NPL4 PROTEIN.//9.80E-86//515aa//37%//P33755
 C-NT2RP4000556//SUR4 PROTEIN (SRE1 PROTEIN).//7.40E-14//233aa//31%//P40319
 C-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//2.90E-188//863bp//99%//AF067730
- 20 C-NT2RP4000648//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//3.70E-07//175aa//27%//P09309
 C-NT2RP4000657//SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN SPSE.//1.10E-32//350aa//30%//P39625
 C-NT2RP4000713//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//1.10E-13//295aa//27%//Q11073
- 25 C-NT2RP4000724//RETROVIRUS-RELATED ENV POLYPROTEIN.//3.20E-191//199aa//78%//P10267
 C-NT2RP4000737//Mus musculus F-box protein FBL10 mRNA, partial cds.//4.60E-250//1462bp//84%//AF176524
 C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.000000032//67aa//31%//P53915
- 30 C-NT2RP4000817//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.80E-11//503aa//23%//P08640
 C-NT2RP4000837//Homo sapiens mRNA for zinc finger protein SALL1.//4.30E-94//810bp//65%//Y18265
 C-NT2RP4000839//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1.//8.50E-21//271aa//28%//Q00808
 C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE)(ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//5.70E-82//324aa//48%//O09175
- 35 C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//4.10E-85//174aa//55%//P16415
 C-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//6.20E-91//173aa//87%//O35682
 C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME EI (A1S9 PROTEIN).//9.60E-96//513aa//42%//P22314
 C-NT2RP4000907//Mouse NLRP1 mRNA for leucine-rich-repeat protein, complete cds.//0//2127bp//86%//D45913
- 40 C-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//2.60E-26//227aa//36%//Q06828
 C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//1.50E-76//346aa//43%//Q061068
- 45 C-NT2RP4000928//Homo sapiens mRNA for CDS2 protein.//0//2487bp//99%//Y16521
 C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HELICASE MJ1505.//1.40E-07//185aa//25%//Q58900
 C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//1.40E-26//90aa//42%//P38660
- 50 C-NT2RP4000979//Homo sapiens putative HIV-1 infection related protein mRNA, partial cds.//2.30E-81//389bp//100%//AF094583
 C-NT2RP4000989//UNC-47 PROTEIN.//8.20E-06//173aa//25%//P34579
 C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//838aa//87%//P70700
 C-NT2RP4001004//VACUOLAR PROTEIN 8.//3.70E-16//401aa//26%//P39968
- 55 C-NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds.//3.50E-257//1377bp//91%//U67140
 C-NT2RP4001029//Homo sapiens transcription factor LBP-1b (LBP-1) mRNA, complete cds.//0//2002bp//98%//

AF198487

C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE)//1.50E-92//443aa//44%//Q09996

C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65.//6.70E-51//335aa//37%//Q64375

5 C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2⁺-ATPASE)//1.30E-123//563aa//46%//P13586

C-NT2RP4001080//Homo sapiens mRNA for Rod1, complete cds.//0//1439bp//99%//AB023967

C-NT2RP4001086//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)//2.30E-07//474aa//22%//P12036

10 C-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1)//2.60E-17//121aa//36%//P51400

C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT//1.90E-115//224aa//100%//P38378

C-NT2RP4001122//mPD PROTEIN//1.40E-65//253aa//41%//O15736

15 C-NT2RP4001126//TRICHOHYALIN//2.90E-18//380aa//26%//Q07283

C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLAASE (EC 3.5.1.18) (SDAP)//2.10E-07//93aa//33%//P44514

C-NT2RP4001148//SOF1 PROTEIN//1.30E-104//236aa//52%//P33750

20 C-NT2RP4001149//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//4.40E-187//731bp//100%//AF037339

C-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO)//3.40E-29//385aa//29%//P35331

C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)//4.70E-29//227aa//35%//P52178

25 C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//4.40E-104//1460bp//65%//U95760

C-NT2RP4001207//Homo sapiens Ran binding protein 11 mRNA, complete cds.//0//2940bp//99%//AF111109

C-NT2RP4001213//ZINC FINGER PROTEIN 184 (FRAGMENT)//5.70E-141//511aa//43%//Q99676

C-NT2RP4001219//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1)//6.20E-27//90aa//42%//P38660

30 C-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN)//1.80E-103//508aa//43%//Q04652

C-NT2RP4001256//Homo sapiens mRNA for gamma tubulin ring complex protein (76p gene)//0//2006bp//100%//AJ249677

35 C-NT2RP4001260//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.//0//1866bp//100%//AF174601

C-NT2RP4001274//Human transporter protein (g17) mRNA, complete cds.//4.40E-58//1196bp//61%//U49082

C-NT2RP4001276//TRICHOHYALIN//7.90E-09//126aa//32%//Q07283

C-NT2RP4001313//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT)//5.90E-17//296aa//29%//P24391

40 C-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//8.50E-213//1129bp//92%//AJ001119

C-NT2RP4001336//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN//0.000016//186aa//29%//O24076

C-NT2RP4001339//Homo sapiens mRNA for AMMERC1 protein.//9.20E-160//736bp//99%//AJ007014

45 C-NT2RP4001345//Homo sapiens mRNA for LCAT-like lysophospholipase (LLPL), complete cds.//2.7E-310//1400bp//100%//AB017494

C-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//1.40E-58//2425bp//59%//U53445

50 C-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN)//1.60E-19//222aa//30%//Q08180

C-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1)//9.20E-17//146aa//35%//P18160

C-NT2RP4001379//HYPOTHETICAL 49.1 KD PROTEIN C11D3.06 IN CHROMOSOME 1//2.00E-53//436aa//30%//Q10085

55 C-NT2RP4001389//KESIPROTEIN//1.70E-31//342aa//34%//P35844

C-NT2RP4001407//TRICHOHYALIN//1.90E-05//288aa//21%//P22793

C-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT)//7.70E-190//422aa//82%//Q14141

C-NT2RP4001433//ZINC FINGER PROTEIN 184 (FRAGMENT)//1.20E-138//419aa//54%//Q99676

- C-NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds./2.70E-66//738bp//71%//AF129131
- C-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE EI COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE).//0//962aa//78%//Q02218
- 5 C-NT2RP4001498//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//1.00E-27//374aa//29%//P39010
- C-NT2RP4001529//Homo sapiens transcription factor LBP-1b (LBP-1) mRNA, complete cds.//0//2002bp//98%//AF198487
- C-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENIC REGION.//5.70E-54//242aa//38%//P25666
- 10 C-NT2RP4001551//Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit mRNA, complete cds.//0//3202bp//99%//AF152961
- C-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//4.70E-09//216aa//24%//P96902
- C-NT2RP4001567//ARMADILLO SEGMENT POLARITY PROTEIN.//5.40E-07//213aa//26%//Q02453
- C-NT2RP4001568//ZINC FINGER PROTEIN GCS1.//1.80E-10//109aa//36%//P35197
- 15 C-NT2RP4001574//COATOMER GAMMA SUBUNIT (GAMMA-COP).//0//874aa//96%//P53620
- C-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//0//1087bp//87%//AJ223830
- C-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS).//1.70E-14//373aa//747%//P73505
- 20 C-NT2RP4001634//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//2.80E-14//652aa//22%//Q02224
- C-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19.//5.10E-46//234aa//32%//P40469
- C-NT2RP4001644//MYOSIN UGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//6.40E-19//111aa//45%//P25323
- 25 C-NT2RP4001656//VACUOLAR BIOGENESIS PROTEIN END1 (PEPS PROTEIN).//1.10E-45//310aa//27%//P12868
- C-NT2RP4001696//CLEFTAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//4.00E-10//243aa//25%//Q10568
- C-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//3.00E-10//128aa//32%//Q10282
- 30 C-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//6.40E-170//1168aa//33%//Q09332
- C-NT2RP4001753//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.90E-236//665aa//58%//P51523
- C-NT2RP4001760//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-CIOGENITAL DYSPLASIA PROTEIN).//4.10E-16//263aa//27%//P98174
- 35 C-NT2RP4001790//Homo sapiens zinc finger protein ZFP-95 (ZFP95) mRNA, alternatively spliced, complete cds.//0//3053bp//99%//AF170025
- C-NT2RP4001822//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.20E-30//241aa//30%//Q35566
- 40 C-NT2RP4001823//MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.//1.10E-19//77aa//54%//P55083
- C-NT2RP4001838//Homo sapiens CoREST protein (COREST) mRNA, complete cds.//6.30E-99//555bp//73%//AF155595
- C-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1.//1.40E-85//489aa//43%//P55194
- C-NT2RP4001861//HTUCHOHYALIN.//1.00E-35//307aa//34%//P37709
- 45 C-NT2RP4001896//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//1.40E-08//345aa//72%//Q00808
- C-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.30E-38//258aa//32%//Q12024
- C-NT2RP4001938//TRANSCRIPTIONAL REPRESSOR CTCF.//9.80E-60//303aa//38%//P49711
- C-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISO-ASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE).//1.50E-13//211aa//28%//Q43209
- 50 C-NT2RP4001950//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//1.20E-13//356aa//27%//P13816
- C-NT2RP4001966//Mus musculus ODZ3 (Odz3) mRNA, partial cds.//0//3203bp//87%//AF195418
- C-NT2RP4001975//Homo sapiens golgi membrane protein GP73 mRNA, complete cds.//0//3024bp//99%//AF236056
- 55 C-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//6.90E-24//370aa//27%//Q04652
- C-NT2RP4002047//GTP-BINDING PROTEIN LEPA.//1.50E-168//601aa//52%//O67618
- C-NT2RP4002058//PUTATIVE PRE-MIRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)//1.00E-137//679aa//40%//O43143

- C-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.00E-150//722aa//39%//Q05481
- C-NT2RP4002081//TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA CHAINS (TFIIA P35 AND PI 9 SUBUNITS) (TFIIA-42) (TFIIA).//6.70E-06//250aa//31%//P52655
- 5 C-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.50E-63//159aa//53%//P38938
- C-NT2RP4002791//NUCLEOPROTEIN TPR.//6.50E-05//659aa//23%//P12270
- C-NT2RP5003461//RLR1 PROTEIN.//9.70E-22//177aa//27%//P53552
- C-NT2RP5003477//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1.//5.50E-15//280aa//27%//Q00808
- 10 C-NT2RP5003500//Mus musculus mRNA for heparan sulfate 6-sulfotransferase 2, complete cds.//1.30E-237//820bp//87%//AB024565
- C-NT2RP5003506//Homo sapiens putative G protein-coupled receptor (RAIG1) mRNA, complete cds.//0//2289bp//99%//AF095448
- C-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//3.30E-23//219aa//40%//P37116
- 15 C-OVARC1000001//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//7.00E-217//683bp//99%//AB029290
- C-OVARC1000006//HISTONE H2A.1.//1.10E-55//117aa//99%//P02262
- C-OVARC1000013//APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1).//4.20E-06//102aa//32%//Q14727
- 20 C-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//2.60E-295//1393bp//97%//AF058922
- C-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE).//3.20E-07//60aa//45%//P80022
- C-OVARC1000071//Homo sapiens NTF2-related export protein NXT1 (NXT1) mRNA, complete cds.//1.50E-47//727bp//67%//AF156957
- 25 C-OVARC1000085//Human mRNA for proteasome subunit HC5.//1.00E-151//699bp//100%//D00761
- C-OVARC1000087//HISTONE MACRO-H2A.1.//1.60E-12//174aa//26%//Q02874
- C-OVARC1000091//HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1) (VCAF) (CFF).//8.40E-14//259aa//30%//P51610
- C-OVARC1000106//TROPOMYOSIN 1, FUSION PROTEIN 33.//0.000032//165aa//27%//P49455
- 30 C-OVARC1000139//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//2.70E-12//120aa//32%//Q13107
- C-OVARC1000151//Homo sapiens partial mRNA for putative protein p38 interacting with transcription factor Spl.//2.50E-95//461bp//98%//AJ242975
- 35 C-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//1.80E-32//511bp//65%//AF068332
- C-OVARC1000241//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//8.20E-120//351aa//54%//Q16665
- C-OVARC1000288//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)(LEUCINE AMINOPEPTIDASE IV) (LAPIV) (AMINOPEPTIDASE I)(AMINOPEPTIDASE YSCI).//5.40E-53//384aa//30%//P14904
- 40 C-OVARC1000304//PROTEIN MOV-10.//1.10E-249//519aa//87%//P23249
- C-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//2.70E-40//154aa//38%//P29363
- C-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//9.20E-148//787bp//76%//U19614
- 45 C-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//5.90E-14//200aa//27%//P40004
- C-OVARC1000437//TENSIN.//7.90E-181//340aa//84%//Q04205
- C-OVARC1000465//PROTEIN TRANSPORT PROTEIN SECT.//1.20E-25//227aa//25%//P11075
- 50 C-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE VHR).//3.10E-10//125aa//35%//P51452
- C-OVARC1000479//Rattus norvegicus mRNA for TIP120, complete cds.//0//1872bp//89%//D87671
- C-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.20E-157//892bp//91%//AF051850
- C-OVARC1000556//RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1.-) (S6KII-ALPHA 2) (P90-RSK 2) (RIBOSOMAL S6 KINASE 3) (RSK3) (PP90RSK3).//3.30E-67//132aa//95%//Q15349
- 55 C-OVARC1000564//Homo sapiens sorting nexin 5 (SNX5) mRNA, complete cds.//1.0E-310//1440bp//98%//AF121855
- C-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, com-

plete cds.//0/1812bp/98%/D43772

C-OVARC1000679//Homo sapiens myosin-Ix mRNA, complete cds.//0/808bp/99%/AF117888

C-OVARC1000682//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).//1.10E-209//293aa//95%/P39098

5 C-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds.//0/759bp/98%/AF038661

C-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN.//0.000000017//78aa//48%/P25159

C-OVARC1000751//PROBABLE PROTEIN PHOSPHATASE 2C T23F11 (EC 3.1.3.16) (PP2C).//5.60E-11//74aa//37%/P49596

10 C-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.10E-46//121aa//79%/P08886

C-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR (75 KD GLUCOSE REGULATED PROTEIN) (GRP 75).//3.90E-46//78aa//98%/O35501

C-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//2.80E-258//1183bp/99%/Y17711

C-OVARC1000846//NUCLEOLIN (PROTEIN C23).//0.0000097//109aa//30%/P08199

15 C-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//0/2095bp/99%/AF045584

C-OVARC1000862//M. musculus mRNA for FT1.//5.90E-226//1498bp/81%/Z67963

C-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).//2.20E-50//206aa//52%/P40484

C-OVARC1000885//OXIDOREDUCTASE UCFA (EC 1.-.-.-).//1.30E-32//170aa//34%/P37440

20 C-OVARC1000915//Homo sapiens histone deacetylase 5 mRNA, complete cds.//1.60E-121//591bp/97%/AF132608

C-OVARC1000936//COAT PROTEIN GP37 (ENV PROTEIN GP37).//0.0000054//135aa//28%/P03398

C-OVARC1000937//S-PHASE ENTRY CYCLIN 6.//4.90E-10//61aapb//49%/P32943

C-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//0/1961bp//82%/AB005549

25 C-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//1.20E-17//127aa//33%/Q58343

C-OVARC1000999//ANKYRIN HOMOLOG PRECURSOR.//4.10E-11//189aa//32%/Q06527

C-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//1.50E-178//1113bp//86%/AF001533

C-OVARC1001038//Homo sapiens mRNA for Ariadne-2 protein.//0/1172bp//97%/AJ130978

30 C-OVARC1001051//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN).//1.10E-08//216aa//23%/P42566

C-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSORS.//1.90E-35//76aa//98%/P43490

C-OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.//1.00E-215//1027bp//98%/AF132946

35 C-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//0/1819bp//99%/AF082657

C-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//2.00E-214//769bp//97%/AJ005897

C-OVARC1001107//Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds.//6.10E-276//594bp//98%/AF167572

40 C-OVARC1001113//Homo sapiens diaphanous 1 (HDI/A1) mRNA, complete cds.//5.1e-310//1588bp//93%/AF051782

C-OVARC1001154//Homo sapiens clone 24720 epithelin 1 and 2 mRNA, complete cds.//2.30E-296//1561bp//93%/AF055008

C-OVARC1001171//Homo sapiens translation initiation factor 3 47 kDa subunit mRNA, complete cds.//5.70E-151//436bp//92%/U94855

45 C-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2.//1.10E-11//221aa//25%/P48510

C-OVARC1001200//Mus musculus mRNA for HS1 binding protein 3.//5.80E-88//658bp//80%/AJ132192

C-OVARC1001232//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//5.10E-22//83aa//37%/Q10568

50 C-OVARC1001244//H. sapiens mRNA for Drosophila female sterile homeotic (FSH) homologue.//0/1467bp//99%/X62083

C-OVARC1001271//NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1).//0.0000014//224aa//26%/P25976

C-OVARC1001306//N-MYC PROTO-ONCOGENE PROTEIN.//0.0000073//247aa//27%/P18444

C-OVARC1001342//40S RIBOSOMAL PROTEIN S8.//1.40E-110//207aa//99%/P09058

55 C-OVARC1001372//Homo sapiens liprin-alpha4 mRNA, partial cds.//2.00E-252//1146bp//99%/AF034801

C-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL.//6.00E-148//683bp//99%/AJ224819

C-OVARC1001417//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP170

mRNA, complete cds.//0//1715bp//99%//AF135802
 C-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds.//4.90E-48//586bp//69%//U52426
 C-OVARC1001436//ENL PROTEIN.//0.00000009//81aa//39%//Q03111
 C-OVARC1001476//Mus musculus YGR163w mRNA homologue, complete cds.//1.80E-187//510bp//89%//
 5 AB017616
 C-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//0//1876bp//98%//
 AF016507
 C-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE
 PROTEIN 1).//0//777aa//91%//P98161
 10 C-OVARC1001555//NGG1-INTERACTING FACTOR 3.//4.40E-19//130aa//40%//P53081
 C-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retroseudogene.//0//1167bp//100%//
 AF031165
 C-OVARC1001610//Homo sapiens choline/ethanolaminephosphotransferase (CEPT1) mRNA, complete cds.//0//
 1870bp//99%//AF068302
 15 C-OVARC1001703//Homo musculus ARL-6 interacting protein-2 (Aip-2) mRNA, complete cds.//3.50E-16//399bp//
 61%//AF133670
 C-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).//2.80E-10//106aa//
 38%//Q62267
 C-OVARC1001713//ENDOPEPTIDYL-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DI-
 20 AZEPAM BINDING INHIBITOR) (MA-DI).//4.40E-40//195aa//41%//P07106
 C-OVARC1001726//APICAL-LIKE PROTEIN (APXL PROTEIN).//4.30E-16//116aa//43%//Q13796
 C-OVARC1001731//TROPOMYOSIN ALPHA CHAIN, FIBROBLAST ISOFORM F2.//4.00E-122//282aa//85%//
 P08942
 C-OVARC1001762//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMI-
 25 NO, ACETYLTRANSFERASE 1).//6.40E-85//514aa//34%//P12945
 C-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//
 0//963bp//99%//U97670
 C-OVARC1001809//Mus musculus sphingosine kinase (SPHKla) mRNA, partial cds.//2.70E-190//1624bp//77%//
 AF068748
 30 C-OVARC1001942//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMI-
 NO, ACETYLTRANSFERASE 1).//3.10E-81//497aa//35%//P12945
 C-OVARC1001943//Mus musculus DEBT-91 mRNA, complete cds.//0//2035bp//87%//AF143859
 C-OVARC1001987//Homo sapiens prolactin regulatory element-binding protein (PREB) mRNA, complete cds.//
 0//1083bp//99%//AF203667
 35 C-OVARC1002050//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//0//1019bp//99%//
 AB029290
 C-OVARC1002112//HISTONE MACRO-H2A.1.//3.00E-174//371aa//90%//Q02874
 C-OVARC1002127//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER 2 (BRAIN DIGOXIN CARRI-
 40 ER PROTEIN) (BRAIN-SPECIFIC ORGANIC ANION TRANSPORTER) (OATP-B1).//5.40E-52//306aa//35%//
 Q35913
 C-OVARC100213 8//SAP1 PROTEIN.//7.60E-60//128aa//59%//P39955
 C-OVARC1002156//Danio rerio uridine kinase mRNA, complete cds.//6.00E-16//262bp//64%//AF195851
 C-OVARC1002165//3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 2 (EC 1.3.99.5) (STEROID 5-ALPHA-
 REDUCTASE 2) (SR TYPE 2).//7.60E-08//114aa//37%//P31213
 45 C-OVARC1002182//BETA-TRCP (BETA-TRANSUDIN REPEAT-CONTAINING PROTEIN) (BTRCP).//1.70E-
 09//207aa//30%//Q91854
 C-PLACE1000004//Homo sapiens IDN3-B mRNA, complete cds.//0//2365bp//99%//AB019602
 C-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15)
 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-
 50 ZYME).//1.60E-81//212aa//70%//P34547
 C-PLACE1000040//TRANSFORMING PROTEIN P21/K-RAS 2B.//1.40E-17//185aa//32%//P08643
 C-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//7.90E-54//190bp//94%//L22154
 C-PLACE1000066//SSU72 PROTEIN.//1.10E-39//206aa//43%//P53538
 C-PLACE1000081//Human SEC7 homolog Tic (TIC) mRNA, complete cds.//0//2077bp//99%//U63127
 55 C-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//
 1.80E-62//158aa//81%//P20290
 C-PLACE1000142//3-HYDROXYBUTYRYL-COA DEHYDRATASE (EC 4.2.1.55) (CROTONASE).//2.80E-29//
 134aa//43%//P52046

- C-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//1.30E-305//1417bp//98%//AF058291
- C-PLACE1000185//Homo sapiens mRNA for N-Acetylglucosamine kinase.//4.90E-258//1183bp//99%//AJ242910
- 5 C-PLACE1000213//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//4.50E-05//197aa//26%//P08640
- C-PLACE1000383//Homo sapiens mRNA for TMTR1 protein.//0//753bp//99%//AJ224979
- C-PLACE1000401//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//2.70E-30//352aa//31%//P15151
- 10 C-PLACE1000406//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.20E-132//1334aa//72%//P23246
- C-PLACE1000420//7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE).//2.80E-06//1134aa//29%//P53368
- C-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//0//2041bp//87%//U35245
- 15 C-PLACE1000547//Homo sapiens GDP-mannose pyrophosphorylase B (GMPPB) mRNA, complete cds.//3.70E-241//1124bp//98%//AF135421
- C-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.60E-47//207aa//46%//P51522
- C-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-BINDING PROTEIN 1).//1.60E-270//437aa//86%//P32455
- 20 C-PLACE1000598//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1540bp//99%//AJ012449
- C-PLACE1000610//MSN5 PROTEIN.//0.0000026//136aa//26%//P52918
- C-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2.00E-55//779bp//67%//AF044201
- 25 C-PLACE1000636//MALE STERILITY PROTEIN 2.//1.20E-39//261aa//27%//Q08891
- C-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//0//1992bp//99%//AF180371
- C-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNL110F1857Q7 (RZPD Berlin)).//2.10E-277//1260bp//99%//AJ005896
- 30 C-PLACE1000706//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.//0//1366bp//99%//AF119043
- C-PLACE1000755//Homo sapiens mRNA for Helicase-MOI, complete cds.//4.60E-250//1189bp//97%//AB028449
- C-PLACE1000769//Homo sapiens CGI-18 protein mRNA, complete cds.//0//1985bp//98%//AF132952
- C-PLACE1000786//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//7.10E-09//59aa//47%//P52734
- 35 C-PLACE1000793//NEUROGENIC PROTEIN BIG BRAIN.//1.70E-07//251aa//24%//P23645
- C-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR148W.//2.50E-49//181aa//54%//P32899
- C-PLACE1000909//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//2.60E-19//404aa//26%//P39010
- 40 C-PLACE1000977//BETA-CHIMAERIN (BETA-CHIMERIN).//4.40E-22//129aa//35%//Q03070
- C-PLACE1000979//ZINC FINGER PROTEIN 135.//2.50E-153//326aa//64%//P52742
- C-PLACE1000987//Rattus norvegicus late gestation lung 2 protein (Lgl2) mRNA, complete cds.//5.90E-278//1476bp//92%//AF110195
- 45 C-PLACE1001036//Homo sapiens mRNA for alpha integrin binding protein 63, partial.//0//1988bp//99%//AJ131721
- C-PLACE1001054//Homo sapiens mRNA for RuvB-like DNA helicase TIP49b, complete cds.//4.00E-300//1355bp//100%//AB024301
- C-PLACE1001062//Homo sapiens mRNA for lysine-ketoglutarate reductase/saccharopine dehydrogenase, partial CDS.//1.60E-207//742bp//99%//AJ007714
- C-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//0//1500bp//99%//AF065485
- 50 C-PLACE1001104//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//6.80E-18//529aa//23%//Q99323
- C-PLACE1001118//ZINC FINGER PROTEIN 135.//5.40E-147//443aa//57%//P52742
- C-PLACE1001171//MYOTUBULARIN.//7.10E-84//198aa//73%//Q13496
- C-PLACE1001238//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//2.00E-202//1333bp//80%//D14336
- 55 C-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.30E-54//257aa//46%//Q04652
- C-PLACE1001294//Mus musculus XY body protein (Xybp) mRNA, complete cds.//6.20E-223//1092bp//78%//AF120207
- C-PLACE1001304//Homo sapiens C2H2 (Kruppel-type) zinc finger protein mRNA, complete cds.//0//2145bp//

- 99%//AF159567
C-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds.//5.90E-228//827bp//99%//AF009615
- 5 C-PLACE1001383//ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUESTED).//3.00E-33//138aa//42%//Q61103
C-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//2.30E-61//132aa//48%//Q12929
C-PLACE1001517//Homo sapiens gene for glycosylphosphatidylinositol anchor attachment 1 (GPAA1), complete cds.//4.60E-112//392bp//87%//AB002137
- 10 C-PLACE1001602//CCRA-ASSOCIATED FACTOR 1 (CAF1).//5.70E-130//244aa//99%//Q60809
C-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.40E-118//429aa//48%//P51523
C-PLACE1001672//PROBABLE AMINOTRANSFERASE T01B11.2 (EC 2.6.1.-).//4.30E-66//174aa//45%//P91408
C-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//4.00E-81//263aa//56%//P08635
- 15 C-PLACE1001739//PUTATIVE ATP-DEPENDENT RNA HEUCASE PL10.//3.50E-75//439aa//41%//P16381
C-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//2602bp//99%//AF061243
C-PLACE1001771//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//2900bp//99%//AJ006276
- 20 C-PLACE1001781//PROBABLE PHOSPHOMANNOMUTASE (EC 5.4.2.8) (PMM).//5.40E-63//427aa//35%//Q57290
C-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//0//1995bp//99%//AF058953
- 25 C-PLACE1001845//Mus musculus cyclin ania-6a mRNA, complete cds.//3.30E-31//925bp//62%//AF159159
C-PLACE1001869//L-RIBULOKINASE (EC 2.7.1.16).//2.00E-27//270aa//31%//P94524
C-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1729bp//99%//AF099935
C-PLACE1001983//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//7.50E-16//319aa//26%//P37908
- 30 C-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//1.40E-78//496aa//37%//Q49091
C-PLACE1002046//UGATIN (FRAGMENT).//1.70E-240//560aa//80%//Q61211
C-PLACE1002073//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE).//5.30E-07//188aa//29%//P49606
- 35 C-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).//6.50E-58//112aa//100%//Q76094
C-PLACE1002140//Rattus norvegicus apelin mRNA, complete cds.//1.40E-43//425bp//74%//AF179679
C-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX COMPONENT SWI3) (TRANSCRIPTION FACTOR TYE2).//0.00005//179aa//23%//P32591
- 40 C-PLACE1002395//Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds.//7.90E-100//966bp//75%//AB030505
C-PLACE1002433//CHROMOSOME ASSEMBLY PROTEIN XCAP-E.//5.10E-05//278aa//24%//P50533
C-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1.//4.50E-76//180aa//83%//P41233
C-PLACE1002438//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//4.20E-06//133aa//29%//Q13105
C-PLACE1002450//Human zinc finger protein mRNA, complete cds.//0//2565bp//99%//U69274
- 45 C-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//0//2092bp//84%//U69262
C-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds.//1.70E-113//545bp//98%//AF042273
C-PLACE1002500//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//2.90E-58//465bp//80%//U50927
- 50 C-PLACE1002532//HOMEOBOX PROTEIN DLX-5.//1.20E-152//289aa//96%//P70396
C-PLACE1002571//ACTIN-LIKE PROTEIN 13E.//5.00E-99//386aa//48%//P45890
C-PLACE1002583//GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2 PRECURSOR (GLUTAMATE RECEPTOR 6) (GLUR-6) (GLUTAMATE RECEPTOR BETA-2) (GLUR BETA-2) (FRAGMENT).//5.60E-34//76aa//98%//P39087
- 55 C-PLACE1002591//CORONIN-UKE PROTEIN P57.//4.40E-70//208aa//66%//P31146
C-PLACE1002598//OLIGORIBONUCLEASE (EC 3.1.-).//5.50E-17//76aa//56%//P45340
C-PLACE1002655//ADSEVERIN (SCINDERIN) (SC).//2.50E-278//543aa//92%//Q28046
C-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//0//2462bp//89%//AF079765

- C-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//O//1750bp//99%//AF068180
- C-PLACE1002714//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//J.9.40E-13//500aa//21%//Q99323
- 5 C-PLACE1002722//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//9.00E-45//305aa//33%//Q15391
- C-PLACE1002775//PEREGRIN (BR140 PROTEIN).//3.80E-13//272aa//28%//P55201
- C-PLACE1002782//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//3.80E-43//385bp//77%//U50927
- 10 C-PLACE1002816//HISTONE DEACETYLASE HDA1.//2.20E-48//217aa//46%//P53973
- C-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//5.50E-203//396aa//86%//P51522
- C-PLACE1002908//Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds.//O//1654bp//99%//AB028600
- 15 C-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4).//1.40E-78//496aa//37%//Q49091
- C-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//8.50E-44//225bp//100%//AF032387
- C-PLACE1003045//POLYCYSTIN 2 (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE TYPE II PROTEIN) (POLYCYSTIN) (R48321).//1.70E-05//150aa//24%//Q13563
- 20 C-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//2.60E-79//253aa//60%//Q13268
- C-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//3.80E-37//143aa//51%//P42743
- C-PLACE1003176//Homo sapiens clone pHN1868 tyrosyl-DNA phosphodiesterase protein (TDP1) mRNA, partial cds.//1.70E-148//687bp//99%//AF182003
- 25 C-PLACE1003190//SOF1 PROTEIN.//1.90E-110//325aa//48%//P33750
- C-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//4.90E-76//309aa//47%//Q15391
- C-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN.//7.90E-22//70aa//47%//P21541
- C-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//6.90E-206//396aa//86%//P51522
- 30 C-PLACE1003357//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//O//2435bp//99%//U92715
- C-PLACE1003366//Homo sapiens otoferlin (OTOF) mRNA, complete cds.//1.40E-78//542bp//67%//AF107403
- C-PLACE1003394//Homo sapiens RAB14 protein (RAB14) mRNA, complete cds.//2.60E-139//648bp//99%//AF152463
- 35 C-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//1.30E-40//278aa//36%//P40556
- C-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSOR.//1.70E-23//322aa//26%//Q13201
- C-PLACE1003519//H.sapiens hnRNP-E2 mRNA.//5.10E-218//905bp//99%//X78136
- 40 C-PLACE1003521//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//0.0000011//101aa//32%//Q09475
- C-PLACE1003537//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHE- ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO- NENT).//7.70E-68//404aa//33%//P32802
- C-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.//2.60E-93//270aa//66%//P46975
- 45 C-PLACE1003602//Homo sapiens mRNA expressed in placenta.//5.90E-278//1275bp//99%//D83200
- C-PLACE1003605//HAP5 TRANSCRIPTIONAL ACTIVATOR.//0.0000023//82aa//35%//Q02516
- C-PLACE1003611//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.//6.20E-169//683bp//99%//AF191338
- 50 C-PLACE1003625//ARMADILLO SEGMENT POLARITY PROTEIN.//3.20E-10//380aa//25%//P18824
- C-PLACE1003669//TRICHOHYALIN.//5.60E-09//219aa//30%//P22793
- C-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//8.00E-19//209aa//34%//Q08170
- C-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA complete cds.//6.20E-282//1316bp//98%//AF053305
- 55 C-PLACE1003738//ZINC FINGER PROTEIN 135.//9.60E-118//350aa//46%//P52742
- C-PLACE1003760//Homo sapiens tetraspanin TM4-A mRNA, complete cds.//5.20E-289//1313bp//97%//AF133423

- C-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE) //3.70E-222//651aa//66%//P25500
- 5 C-PLACE1003888//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-II) (FRAGMENT) //6.70E-113//501aa//46%//P10895
- C-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP-AMMONIA LIGASE) (CTP SYNTHETASE) //1.40E-243//584aa//74%//P17812
- C-PLACE1003915//PROBABLE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19) (ARGININE-TRNA UGASE) (ARGRS) //2.40E-108//581aa//40%//Q05506
- 10 C-PLACE1003923//Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds. //0//1670bp//99%//AF033120
- C-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN) //2.40E-124//326aa//73%//P80385
- 15 C-PLACE1004104//Rattus norvegicus rsec5 mRNA, complete cds. //0//2384bp//86%//AF032666
- C-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA CHAIN 4) //6.10E-181//340aa//96%//P29387
- C-PLACE1004149//Rattus norvegicus GERp95 mRNA, complete cds. //3.30E-41//452bp//65%//AF195534
- C-PLACE1004183//Homo sapiens for TOM1-like protein. //0//1279bp//97%//AJ010071
- C-PLACE1004197//BUTYROPHILIN PRECURSOR (BT) //4.50E-10//208aa//27%//Q62556
- 20 C-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds. //0//1882bp//99%//AF069493
- C-PLACE1004256//Mus musculus short coiled coil protein SCOCO (Scoc) mRNA, complete cds. //2.00E-93//960bp//76%//AF115778
- 25 C-PLACE1004258//Homo sapiens vanilloid receptor-like protein 1 (VRL-1) mRNA //0//1144bp//98%//AF129112
- C-PLACE1004270//TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21.-) //9.70E-36//389aa//31%//O15393
- C-PLACE1004277//Homo sapiens two pore domain K⁺ channel (TASK-2) mRNA, complete cds. //0//1498bp//99%//AF084830
- 30 C-PLACE1004302//SOF1 PROTEIN //1.90E-110//325aa//48%//P33750
- C-PLACE1004316//H.sapiens mRNA for apoptosis specific protein. //0//1767bp//99%//Y11588
- C-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds. //0//2512bp//99%//AF100153
- C-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-) //1.20E-39//385aa//33%//Q63448
- C-PLACE1004437//Human NAD⁺-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds. //0//985bp//99%//U49283
- 35 C-PLACE1004460//MATERNAL TUDOR PROTEIN //0.000002//218aa//23%//P25823
- C-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1) //72.90E-56//276aa//41%//P51522
- C-PLACE1004506//Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds. //2.10E-16//402bp//62%//U90878
- 40 C-PLACE1004510//Homo sapiens TATA binding protein associated factor (TAFII150) mRNA, complete cds. //3.40E-227//1037bp//99%//AF040701
- C-PLACE1004550//Homo sapiens CGI-20 protein mRNA, complete cds. //3.50E-274//1305bp//97%//AF132954
- C-PLACE1004564//CLEFTAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT) //0//525aa//99%//Q10568
- 45 C-PLACE1004629//PROTEIN OS-9 PRECURSOR //7.70E-18//264aa//32%//Q13438
- C-PLACE1004646//B.taurus mRNA for retinal pigment epithelial membrane receptor p63. //4.40E-42//985bp//59%//X66277
- C-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds. //1.30E-195//982bp//96%//AF035606
- 50 C-PLACE1004743//PROBABLE N-END-RECOGNIZING PROTEIN (UBIQUITIN-PROTEIN LIGASE E3 COMPONENT) (N-RECOGNIN) //4.40E-35//578aa//27%//O60152
- C-PLACE1004751//Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds. //7.10E-224//790bp//98%//AB022918
- 55 C-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN) //1.90E-32//259aa//32%//P30337
- C-PLACE1004793//RETROVIRUS-RELATED ENV POLYPROTEIN //5.20E-47//577aa//25%//P10267
- C-PLACE1004804//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE) //4.70E-65//695aa//29%//Q01631

- C-PLACE1004814//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//5.90E-19//196aa//36%//Q08170
- C-PLACE1004868//MALE STERILITY PROTEIN 27.3.90E-39//261aa//27%//Q08891
- 5 C-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//9.30E-11//94aa//47%//O42643
- C-PLACE1004918//L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDH-A).//4.90E-48//198aa//44%//P06151
- C-PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1853bp//98%//AF099936
- C-PLACE1004937//SEL-10 PROTEIN.//6.30E-125//357aa//58%//Q93794
- 10 C-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//2.00E-14//205aa//26%//Q11073
- C-PLACE1005052//Homo sapiens CGI-16 protein mRNA, complete cds.//6.6E-313//1413bp//99%//AF132950
- C-PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).//2.60E-56//565aa//30%//Q04652
- C-PLACE1005176//Homo sapiens hypothalamus protein HT001 mRNA, complete cds.//3.90E-212//1040bp//96%//AF113539
- 15 C-PLACE1005187//APAG PROTEIN.//3.80E-13//122aa//36%//P05636
- C-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.30E-27//349aa//32%//Q01577
- C-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.30E-13//269aa//28%//P53352
- 20 C-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2.00E-111//226aa//92%//P08760
- C-PLACE1005331//Homo sapiens Th3 protein mRNA, partial cds.//1.20E-226//748bp//95%//AF209931
- C-PLACE1005373//TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//8.60E-09//194aa//27%//O33335
- 25 C-PLACE1005467//PENICILLIN-BINDING PROTEIN 4* (PBP 4*) (PBP 4A).//1.10E-09//93aa//31%//P32959
- C-PLACE1005494//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//1649bp//99%//AJ006276
- C-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//5.60E-52//173aa//57%//Q09251
- 30 C-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A.//7.60E-97//1287bp//67%//AJ010046
- C-PLACE1005557//60S RIBOSOMAL PROTEIN L27.//1.90E-11//60aa//48%//P46288
- C-PLACE1005584//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPQ (P135 PROTEIN) (IER 2.9/ER2.6).//6.80E-09//267aa//30%//P29128
- 35 C-PLACE1005611//Mus musculus mRNA for mDj10, complete cds.//2.00E-33//379bp//66%//AB028860
- C-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//0//2130bp//99%//AF083255
- 40 C-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE II).//2.10E-148//321aa//83%//P31350
- C-PLACE1005727//Homo sapiens STRIN protein (STRIN) mRNA, complete cds.//2.00E-118//378bp//98%//AF162680
- C-PLACE1005739//INTERFERON-GAMMA INDUCIBLE PROTEIN MG11.//1.30E-237//585aa//72%//Q60710
- 45 C-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//2.50E-79//209aa//53%//P08635
- C-PLACE1005803//Homo sapiens mRNA for transcription factor (SMIF gene).//0//1985bp//99%//AJ275986
- C-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.10E-217//994bp//99%//AF027156
- 50 C-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2040bp//99%//AF065482
- C-PLACE1005876//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//730aa//99%//Q10568
- C-PLACE1005890//BEM46 PROTEIN (FRAGMENT).//9.90E-42//224aa//43%//P54069
- C-PLACE1005921//AIG1 PROTEIN.//3.00E-31//284aa//31%//P54120
- 55 C-PLACE1005951//Homo sapiens prolactin regulatory element-binding protein (PREB) mRNA, complete cds.//1.10E-264//661bp//99%//AF203687
- C-PLACE1005953//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//6.70E-30//198aa//37%//P43636
- C-PLACE1005955//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)/5.40E-54//455aa//32%//P14904

- C-PLACE1005966//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TFII-90)/71.40E-07//254aa//25%/P38129
- C-PLACE1006003//Homo sapiens CGI-94 protein mRNA, complete cds.//2.40E-177//829bp//99%/AF151852
- C-PLACE1006011//Homo sapiens mRNA for poly(ADP-ribose) polymerase-2.//0//1564bp//99%/AJ236876
- 5 C-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.70E-161//744bp//99%/X99906
- C-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.50E-148//681bp//99%/AF039023
- C-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).//2.00E-28//236aa//30%/P98110
- 10 C-PLACE1006167//PAF1 PROTEIN.//7.30E-15//437aa//24%/P38351
- C-PLACE1006170//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HAZ/AP2 ADAPTIN ALPHA C SUBUNIT).//1.70E-169//373aa//88%/P17427
- 15 C-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C.06.//2.70E-116//496aa//48%/Q09747
- C-PLACE1006239//BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).//2.00E-16//244aa//31%/P28675
- C-PLACE1006288//VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 1 (VDAC1) (PLASMA-LEMNAL PORIN) (OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN) (PORIN 31HL) (PORIN 31HM).//4.60E-117//147aa//80%/P21796
- 20 C-PLACE1006318//Mus musculus skm-BOP2 (Bop) mRNA, complete cds.//3.00E-07//376bp//59%/U76374
- C-PLACE1006335//Homo sapiens NY-REN-50 antigen mRNA, partial cds.//0//1649bp//99%/AF155112
- C-PLACE1006368//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//1.30E-18//460aa//24%/Q00547
- 25 C-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//0//1168bp//99%/AF062085
- C-PLACE1006430//ZINC FINGER PROTEIN 165.//2.50E-45//122aa//43%/P49910
- C-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL-AC-TIVATING ENZYME).//1.20E-83//313aa//49%/P27550
- C-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//7.70E-55//142aa//85%/Q90595
- 30 C-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.10E-229//367aa//96%/Q00004
- C-PLACE1006492//Homo sapiens transmembrane protein 2 (TMEM2) mRNA, complete cds.//0//2618bp//99%/AF137030
- C-PLACE1006506//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.//0//2170bp//99%/AF191338
- 35 C-PLACE1006531//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//1967bp//99%/AF093097
- C-PLACE1006534//POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE (EC 2.4.1.41)(PROTEIN-UDP ACETYLGLACTOSAMINYLTRANSFERASE)(UDP-GALNAC:POLYPEPTIDE, N-ACETYLGLACTOSAMINYLTRANSFERASE) (GALNAC-T1).//8.30E-08//100aa//41%/Q10472
- 40 C-PLACE1006552//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//1.20E-09//426aa//21%/P39922
- C-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//0//1464bp//99%/U97670
- C-PLACE1006626//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%/AB028449
- 45 C-PLACE1006678//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-24//734bp//62%/AB015630
- C-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//6.90E-13//177aa//33%/Q59263
- C-PLACE1006754//BILIARY GLYCOPROTEIN 1 PRECURSOR (BGP-1) (ANTIGEN CD66) (CD66A ANTIGEN).//6.20E-63//191aa//43%/P13688
- 50 C-PLACE1006819//UNE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.80E-213//232aa//80%/P08547
- C-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLEST-EASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUI-TOUS NUCLEAR PROTEIN).//2.00E-15//188aa//29%/P35123
- 55 C-PLACE1006878//TRNA-SPLICING ENDONUCLEASE SUBUNIT SEN2 (EC 3.1.27.9) (TRNA-INTRON ENDO-NUCLEASE).//1.90E-08//122aa//36%/P16658
- C-PLACE1006917//HSH49 PROTEIN.//5.50E-12//97aa//35%/Q09181
- C-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III.//6.70E-48//278aa//41%/

Q10000

C-PLACE1006956//ATP-DEPENDENT PERMEASE MDL1.//1.30E-86//522aa//36%//P97998

C-PLACE1006958//Homo sapiens mRNA for heat shock protein apg-1, complete cds.//0//1770bp//99%//AB023421

5 C-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12) (DER12).//3.20E-35//180aa//33%//Q14542

C-PLACE1007105//Homo sapiens muskelin (MKLN1) mRNA, complete cds.//0//2449bp//98%//AF047489

C-PLACE1007140//TRICHOHYALIN.//1.30E-25//816aa//22%//P37709

10 C-PLACE1007226//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.) (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1.00E-42//370aa//31%//P54304

C-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-I₁, hS-I₁-T1, complete cds.//6.50E-216//1068bp//96%//D50495

C-PLACE1007243//UNC-47 PROTEIN.//1.70E-07//211aa//27%//P34579

C-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//0//2052bp//99%//Y15908

15 C-PLACE1007317//Drosophila melanogaster Adrift (adrf1) mRNA, complete cds.//4.10E-17//1037bp//56%//AF117649

C-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//0//2366bp//99%//AF096870

20 C-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13.//0.00000044//127aa//30%//P27715

C-PLACE1007409//WHITTE PROTEIN.//1.10E-64//428aa//32%//Q17320

C-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP).//8.80E-25//140aa//35%//P27487

C-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//5.40E-53//426aa//33%//P52734

25 C-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19).//1.40E-85//385aa//45%//P08728

C-PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds.//8.9E-316//1485bp//98%//AF159164

30 C-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1.00E-49//361aa//36%//P34537

C-PLACE1007598//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.60E-143//666aa//44%//Q99676

C-PLACE1007632//POLIOVIRUS RECEPTOR PRECURSOR.//1.00E-07//228aa//31%//P32506

35 C-PLACE1007649//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//4.50E-05//197aa//26%//P08640

C-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//8.70E-09//279aa//28%//Q26457

C-PLACE1007697//GCN20 PROTEIN.//7.60E-119//717aa//38%//P43535

40 C-PLACE1007705//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.//1.10E-184//1096bp//62%//AB033922

C-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//3431bp//99%//AF061243

C-PLACE1007729//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.50E-44//231aa//42%//P10265

C-PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds.//0//1836bp//99%//AB019602

C-PLACE1007897//Homo sapiens FLASH mRNA, complete cds.//0//2145bp//99%//AF154415

45 C-PLACE1007946//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//2.60E-14//370aa//25%//Q99323

C-PLACE1007954//HYPOTHETICAL 45.5 KD PROTEIN IN FIG1-GIP1 INTERGENIC REGION.//6.70E-13//168aa//31%//P38226

50 C-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//0//2252bp//99%//AF084530

C-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//0//2300bp//99%//AF079529

C-PLACE1007969//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.10E-36//202aa//48%//P52272

55 C-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSYP-110) (SYNAPTIC DENSITY PROTEIN PSD-93).//6.10E-14//128aa//39%//Q63622

C-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NUCLEOPORIN) (P105).//4.6E-318//613aa//94%//P52590

- C-PLACE1008080//Homo sapiens mRNA for HEXIM1 protein, complete cds.//0/12152bp//99%/AB021179
 C-PLACE1008111//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).//3.00E-25//208aa//37%/Q03326
 C-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//1.30E-24//395aa//31%/Q09531
- 5 C-PLACE1008177//TRICHOHYALIN.//2.30E-29//487aa//26%/P37709
 C-PLACE1008201//Rattus rattus zinc finger protein, complete cds.//0/12265bp//83%/L23077
 C-PLACE1008244//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//9.50E-21//148aa//38%/Q00808
 C-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.30E-283//671aa//77%/P53620
- 10 C-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-).//2.30E-18//162aa//37%/P12689
 C-PLACE1008309//Rattus norvegicus putative four repeat ion channel mRNA, complete cds.//5.20E-137//672bp//77%/AF078779
 C-PLACE1008330//EOSINOPHIL LYSOPHOSPHOLIPASE (EC 3.1.1.5) (CHARCOT-LEYDEN CRYSTAL PROTEIN) (LYSOLECITHIN ACYLHYDROLASE) (CLC) (GALACTIN-10).//2.20E-23//94aa//47%/Q05315
 C-PLACE1008356//Homo sapiens meningioma-expressed antigen 5 (MEA5) mRNA, partial cds.//7.1.90E-170//780bp//100%/AF036144
- 15 C-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).//5.30E-26//309aa//30%/Q04652
 C-PLACE1008398//GENE 33 POLYPEPTIDE.//7.30E-114//243aa//87%/P05432
 C-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRAN-SCYTOSIS ASSOCIATED PROTEIN) (TAP).//0/698aa//95%/P41541
- 20 C-PLACE1008426//RESTIN (CYTOPLASMIC LINKER PROTEIN-170) (CLIP-170).//1.80E-11//365aa//25%/Q42184
 C-PLACE1008429//ANKYRIN HOMOLOG PRECURSOR.//3.10E-11//189aa//32%/Q06527
 C-PLACE1008465//Homo sapiens mRNA for rapa-1 (rapa gene).//6.60E-243//1102bp//99%/AJ277275
- 25 C-PLACE1008533//101 KD MALARIA ANTIGEN (P101) (ACIDIC BASIC REPEAT ANTIGEN).//1.10E-09//62aa//48%/P22620
 C-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//7.80E-236//453aa//96%/P37199
 C-PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.//0/1850bp//99%/AJ006591
- 30 C-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (II HEAVY CHAIN H2).//5.20E-90//483aa//38%/O02688
 C-PLACE1008650//PRL1/PRL2-LIKE PROTEIN.//2.00E-127//354aa//62%/O13615
 C-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//0/3002bp//99%/AF03 8406
- 35 C-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds.//0/1670bp//99%/AF060543
 C-PLACE1008808//Homo sapiens mRNA for cell cycle checkpoint protein radA.//2.30E-269//1225bp//99%/AJ004974
 C-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//8.80E-268//1171bp//90%/AF032668
- 40 C-PLACE1009020//NIFS PROTEIN.//3.90E-55//279aa//41%/P12623
 C-PLACE1009027//Homo sapiens mRNA for doublecortin.//0/1919bp//99%/AJ003112
 C-PLACE1009060//BRO1 PROTEIN.//6.70E-19//567aa//24%/P48582
 C-PLACE1009094//FURIN-LIKE PROTEASE 2 PRECURSOR (EC 3.4.21.75) (FURIN 2).//1.90E-44//480aa//30%/P30432
- 45 C-PLACE1009099//ZINC FINGER PROTEIN 41 (FRAGMENT).//1.10E-179//452aa//67%/P51814
 C-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//0/2529bp//99%/AF035586
 C-PLACE1009130//UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.2.-) (ONCOGENIC PROTEIN-ASSOCIATED PROTEIN E6-AP).//2.00E-68//181aa//43%/Q05086
- 50 C-PLACE1009158//Mus musculus mRNA for death inducer-obliator-1 (Dio-1).//5.40E-200//1790bp//75%/AJ238332
 C-PLACE1009186//Homo sapiens small zinc finger-like protein (TIM9b) mRNA, complete cds.//9.60E-255//1179bp//98%/AF150105
 C-PLACE1009246//POLLEN SPECIFIC PROTEIN SF3.//4.40E-16//82aa//43%/P29675
 C-PLACE1009298//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//2.00E-78//262aa//43%/P34110
- 55 C-PLACE1009308//GLUCOSE REPRESSION MEDIATOR PROTEIN.//4.00E-06//439aa//23%/P14922
 C-PLACE1009319//Rattus norvegicus outer membrane protein (OMP25) mRNA, complete cds; nuclear gene for mitochondrial product.//2.10E-132//1229bp//75%/AF107295

- C-PLACE1009368//METAL HOMEOSTASIS FACTOR ATX27/2. 50E-10//151aa//29%//Q12067
 C-PLACE1009398//ZINC FINGER PROTEIN 135.//6.20E-97//361aa//51%//P52742
 C-PLACE1009404//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06 IN CHROMOSOME 1.//4.70E-08//165aa//33%//Q09820
- 5 C-PLACE1009443//Mus musculus F-box protein FBL8 mRNA, complete cds.//1.00E-173//1367bp//77%//AF176523
 C-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//7.80E-71//82aa//89%//P42356
 C-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.10E-289//550aa//93%//P54319
- 10 C-PLACE1009476//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//3.90E-40//179aa//37%//P34580
 C-PLACE1009477//Homo sapiens ubiquitin-fusion degradation protein 2 (UFD2) mRNA, complete cds.//6.60E-147//592bp//99%//AF043117
 C-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FACTOR)7/8.10E-99//228aa//75%//Q99418
- 15 C-PLACE1009571//Homo sapiens PTD002 mRNA, complete cds.//5.90E-185//857bp//99%//AF078857
 C-PLACE1009596//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1.//5.10E-54//291aa//40%//Q00808
 C-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.30E-60//209aa//41%//P25159
 C-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN).//1.50E-285//538aa//99%//P55161
- 20 C-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//0//1854bp//100%//AF062534
 C-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN CHROMOSOME 1.//7.00E-33//166aa//43%//Q09876
 C-PLACE1009721//MSF1 PROTEIN.//1.70E-22//176aa//33%//P35200
- 25 C-PLACE1009731//AIG1 PROTEIN.//1.60E-22//274aa//28%//P54120
 C-PLACE1009763//Homo sapiens mRNA for Nedd8-activating enzyme hUba3, complete cds.//4.30E-294//1329bp//100%//AB012190
 C-PLACE1009798//RLR1 PROTEIN.//1.60E-18//270aa//23%//P53552
 C-PLACE1009845//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//2.30E-59//405aa//33%//P38968
- 30 C-PLACE1009861//CATHEPSIN B-LIKE CYSTEINE PROTEINASE 6 PRECURSOR (EC 3.4.22.-).//6.50E-28//209aa//38%//P43510
 C-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC REGION.//1.90E-108//277aa//43%//P53145
- 35 C-PLACE1009925//Homo sapiens RNA helicase (RIG-I) mRNA, complete cds.//0//1730bp//99%//AF038963
 C-PLACE1009992//LIMULUS CLOTTING FACTOR C PRECURSOR (EC 3.4.21.84).//4.60E-59//450aa//34%//P28175
 C-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds.//5.20E-70//736bp//73 %//U48288
- 40 C-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//6.00E-279//1402bp//94%//X84692
 C-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2019bp//99%//AF065482
 C-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.40E-268//506aa//98%//Q62671
 C-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//7.30E-114//537aa//44%//Q04652
- 45 C-PLACE1010134//TRANSCRIPTION REGULATORY PROTEIN SNF2 (SWI/SNF COMPLEX COMPONENT SNF2) (REGULATORY PROTEIN SWI2) (REGULATORY PROTEIN GAM1) (TRANSCRIPTION FACTOR TYE3).//1.70E-20//156aa//42%//P22082
 C-PLACE1010148//CYUCIN I (MULTIPLE-BAND POLYPEPTIDE I).//4.60E-07//431aa//23%//P35662
 C-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//9.80E-11//95aa//49%//Q01130
- 50 C-PLACE1010231//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR).//5.10E-27//371aa//28%//Q1246
 C-PLACE1010261//SEGREGATION DISTORTER PROTEIN.//1.60E-77//214aa//62%//P25722
 C-PLACE1010310//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//1.20E-18//467aa//30%//P46804
 C-PLACE1010321//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//1.10E-09//350aa//22%//P52178
- 55 C-PLACE1010362//1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE PRECURSOR (EC 3.1.4.10) (PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC).//2.00E-09//126aa//29%//P34024
 C-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds.//0//2082bp//91%//AF003927

- C-PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induced by progesterone), complete cds.//0/1981 bp//99%//AB022718
- C-PLACE1010529//Homo sapiens TANK binding kinase TBK1 (TBK1) mRNA, complete cds.//0/1750bp//99%//AF191838
- 5 C-PLACE1010547//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//1.20E-07//616aa//24%//P25386
- C-PLACE1010579//Homo sapiens CED-6 protein (CED-6) mRNA, complete cds.//8.80E-300//1359bp//99%//AF191771
- 10 C-PLACE1010599//Homo sapiens Pex14 mRNA for peroxisomal membrane anchor protein, complete cds.//0/1904bp//99%//AB017546
- C-PLACE1010622//TROPONIN T, CARDIAC MUSCLE ISOFORMS (TNTC).//0.0000016//120aa//28%//P02642
- C-PLACE1010628//Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds.//7.50E-08//324bp//64%//AF109907
- 15 C-PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS 13.//5.70E-75//423aa//39%//Q01755
- C-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//1.80E-222//808aa//52%//Q09332
- C-PLACE1010702//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//5.20E-151//427aa//55%//P28160
- 20 C-PLACE1010720//Homo sapiens mRNA for chromosome-associated polypeptide-C, complete cds.//4.00E-299//1091bp//99%//AB019987
- C-PLACE1010743//Homo sapiens myosin-IXb splice variant (Myo9b) mRNA, partial cds.//8.90E-91//668bp//82%//AF020267
- C-PLACE1010761//Homo sapiens mRNA for cisplatin resistance-associated overexpressed protein, complete cds.//0/1448bp//99%//AB034205
- 25 C-PLACE1010771//M.musculus HCNGP mRNA.//7.40E-168//966bp//89%//X68061
- C-PLACE1010811//Rattus norvegicus mRNA for protein encoded by bdeight gene, partial.//1.60E-217//858bp//87%//AJ010392
- C-PLACE1010833//CALTRACTIN(CENTRIN).//0.0000001//154aa//28%//P41209
- 30 C-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.30E-143//407aa//58%//Q05481
- C-PLACE1010896//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//1.50E-255//583aa//23%//P35580
- C-PLACE1010926//HYPOTHETICAL 72.2 KD PROTEIN C12C2.05C IN CHROMOSOME II.//7.60E-23//103aa//53%//Q09746
- 35 C-PLACE1010942//Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds.//0/1440bp//99%//AF114487
- C-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//5.30E-98//297aa//48%//P45890
- C-PLACE1011041//Homo sapiens mRNA for BAP2-alpha protein, complete cds.//0/1701bp//97%//AB015019
- 40 C-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1 (EC 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PLC-154).//0/646aa//97%//P10894
- C-PLACE1011056//HISTONE H1, GONADAL.//6.80E-13//154aa//37%//P02256
- 45 C-PLACE1011109//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEFG).//1.50E-22//63aa//88%//Q07803
- C-PLACE1011114//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//2.90E-71//190aa//44%//Q03532
- C-PLACE1011160//Homo sapiens HFB30 mRNA, complete cds.//0/1691bp//99%//AB022663
- 50 C-PLACE1011185//INSERTION ELEMENT IS1 PROTEIN INSB.//1.30E-89//167aa//100%//P03830
- C-PLACE1011219//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).//3.20E-12//212aa//29%//Q03326
- C-PLACE1011229//Homo sapiens ubiquitin-specific protease homolog (UPH) mRNA, complete cds.//2.30E-152//701bp//99%//AF153604
- 55 C-PLACE1011310//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE.//3.50E-20//496aa//25%//P10587
- C-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//7.20E-151//697bp//99%//AF102265
- C-PLACE1011340//Homo sapiens IDN3-B mRNA, complete cds.//1.20E-74//380bp//97%//AB019602
- C-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2).//1.70E-78//383aa//39%//Q61703
- 60 C-PLACE1011399//Homo sapiens CGI-72 protein mRNA, complete cds.//3.20E-90//427bp//99%//AF151830
- C-PLACE1011433//TRANSCRIPTION FACTOR IIIA (FACTOR A) (TFIIIA).//3.00E-10//236aa//25%//P34695
- C-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0/2040bp//99%//AF065482
- 65 C-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//

4. 90E-11//147aa//32%//P52178
 C-PLACE1011576//Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds.//0//1791bp//82%//L11672
- 5 C-PLACE1011586//Rattus norvegicus clone C53 CDK5 activator-binding protein mRNA, complete cds//74.10E-259//1538bp//87%//AF177476
 C-PLACE1011635//Homo sapiens heparan sulfate D-glucosaminyl 3-O-sulfotransferase-3B (3OST3B1) mRNA, complete cds.//0//1559bp//99%//AF105377
 C-PLACE1011664//CROOKED NECK PROTEIN //1.60E-187//505aa//64%//P17886
- 10 C-PLACE1011858//Homo sapiens BAG-family molecular chaperone regulator-2 mRNA, complete cds.//1.30E-255//1179bp//99%//AF095192
 C-PLACE1011896//Mus musculus Wnt10a mRNA, complete cds.//2.60E-287//1820bp//85%//U61969
 C-PLACE1011922//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMHC-B) //1.30E-15//409aa//27%//P35580
- 15 C-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//0//2782bp//99%//AF059617
 C-PLACE101-2031//Homo sapiens sorting nexin 13 (SNX13) mRNA, partial cds.//0//1701bp//100%//AF121862
 C-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III //2.60E-42//104aa//49%//Q09475
- 20 C-PLACE2000015//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN) //1.10E-116//364aa//45%//P42566
 C-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, complete cds.//2.70E-107//981bp//74%//AF082556
 C-PLACE2000034//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48) //2.20E-29//212aa//35%//P10586
- 25 C-PLACE2000039//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C) //6.10E-293//388aa//99%//P38650
 C-PLACE2000062//Homo sapiens mRNA for type II membrane protein similar to HIV gp120-binding C-type lectin, complete cds, clone:HP01347. //6.30E-166//656bp//94%//AB015629
 C-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0//3174bp//99%//AF027219
 C-PLACE2000164//TIPD PROTEIN //2.10E-59//481aa//33%//O15736
- 30 C-PLACE2000216//SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1) //6.60E-115//226aa//99%//Q01082
 C-PLACE2000246//RING CANAL PROTEIN (KELCH PROTEIN) //6.00E-57//239aa//34%//Q04652
 C-PLACE2000274//DYNEIN BETA CHAIN, CILIARY //2.20E-167//880aa//37%//P23098
 C-PLACE2000341//Homo sapiens sodium-dependent multivitamin transporter (SMVT) mRNA, complete cds.//0//1554bp//99%//AF069307
- 35 C-PLACE2000371//TENSIN //2.90E-78//561aa//37%//Q04205
 C-PLACE2000373//F-SPONDIN PRECURSOR //8.60E-16//371aa//28%//P35446
 C-PLACE2000398//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48) //6.30E-37//90aa//98%//P10586
- 40 C-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7) //1.60E-14//180aa//39%//P14209
 C-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS) //9.90E-229//821aa//54%//Q09996
 C-PLACE2000411//Homo sapiens epsilon 2b mRNA, complete cds.//3.80E-271//642bp//99%//AF062085
- 45 C-PLACE2000427//PROBABLE HELICASE MOT1 //1.20E-26//200aa//27%//P32333
 C-PLACE2000438//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1) //2.10E-86//348aa//41%//Q10472
 C-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN) //2.50E-25//165aa//40%//P33450
- 50 C-PLACE2000477//Homo sapiens putative secreted protein (ZS1G11) mRNA, complete cds.//6.70E-127//671bp//94%//AF072733
 C-PLACE3000009//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1)(FRAGMENT) //3.50E-30//400aa//30%//P11414
 C-PLACE3000020//Homo sapiens type III adenylyl cyclase (AC-III) mRNA, complete cds.//0//2253bp//99%//AF038861
- 55 C-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//0//1979bp//90%//Y17267
 C-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC157 //1.90E-08//281aa//22%//P22224
 C-PLACE3000145//TENSIN //1.00E-108//277aa//75%//Q04205

- C-PLACE3000147//Homo sapiens metalloproteinase with thrombospondin type 1 motifs ADAMTS1 (ADAMTS1) mRNA, complete cds.//0/2043bp//99%//AF170084
- C-PLACE3000169//ZINC FINGER PROTEIN 135.1//2.50E-90//358aa//47%//P52742
- 5 C-PLACE3000218//Homo sapiens putative protein O-mannosyltransferase (POMT2) mRNA, complete cds.//0/1862bp//98%//AF105020
- C-PLACE3000242//Human trophinin mRNA, complete cds.//0/2290bp//99%//U04811
- C-PLACE3000244//PROTEIN TSG4 (MEIOTIC CHECK POINT REGULATOR).//0/1435aa//92%//P53995
- C-PLACE3000254//Homo sapiens transcriptional activator SRCAP (SRCAP) mRNA, complete cds.//0/14583bp//83%//AF143946
- 10 C-PLACE3000339//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.60E-08//359aa//23%//P08640
- C-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE SULU (EC 2.7.1.-).//1.00E-54//418aa//38%//P46549
- 15 C-PLACE3000416//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//1.80E-14//565bp//98%//AB029290
- C-PLACE3000477//Homo sapiens phosphoprotein pp75 mRNA, partial cds.//0/3012bp//98%//AF153085
- C-PLACE4000009//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMHC-B).//2.90E-54//626aa//29%//P35580
- 20 C-PLACE4000014//X-LINKED HEUCASE II (X-LINKED NUCLEAR PROTEIN) (XNP).//3.10E-11//348aa//41%//P46100
- C-PLACE4000052//Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA, complete cds.//0/4661bp//99%//AF165281
- C-PLACE4000063//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//1.70E-15//740aa//23%//P08640
- 25 C-PLACE4000100//Homo sapiens hydroxypyruvate reductase (GRHPR) gene, complete cds.//0/4199bp//97%//AF146689
- C-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds.//1.60E-86//190aabbp//88%//AF091234
- C-PLACE4000156//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.40E-235//516aa//51%//Q05481
- 30 C-PLACE4000192//ZINC FINGER PROTEIN 142 (KIA0236) (HA4654).//17.00E-22//369aa//25%//P52746
- C-PLACE4000211//Homo sapiens BAZ2A mRNA for bromodomain adjacent to zinc finger domain 2A, complete cds.//0/5709bp//96%//AB032254
- C-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds.//0/2567bp//88%//AF030430
- 35 C-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD protein.//0/5143bp//90%//Z70200
- C-PLACE4000261//PEREGRIN (BR140 PROTEIN).//9.50E-10//128aa//34%//P55201
- C-PLACE4000269//Rattus norvegicus rexo70 mRNA, complete cds.//0/2034bp//89%//AF032667
- C-PLACE4000326//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1).//8.10E-24//319aa//31%//P30771
- 40 C-PLACE4000369//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP240 mRNA, complete cds.//1.40E-185//1135bp//67%//AF117754
- C-PLACE4000401//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME).//17.20E-22//54aa//62%//Q01576
- C-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//0/5142bp//90%//Z70200
- 45 C-PLACE4000450//Homo sapiens BAZ2A mRNA for bromodomain adjacent to zinc finger domain 2A, complete cds.//0/5709bp//96%//AB032254
- C-PLACE4000489//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//7.50E-60//254aa//44%//P13002
- C-PLACE4000522//NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (XOTCH PROTEIN).//2.40E-191//828aa//48%//P21783
- 50 C-PLACE4000548//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.70E-13//784aa//21%//P08640
- C-PLACE4000558//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE FAF) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF) (DEUBIQUITINATING ENZYME FAF) (FAT FACETS PROTEIN).//1.50E-26//252aa//35%//P55824
- 55 C-PLACE4000561//FIBROPELIN I PRECURSOR (EPIDERMAL GROWTH FACTOR-RELATED PROTEIN 1) (UEGF-1).//9.30E-70//228aa//52%//P10079
- C-PLACE4000650//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).//17.90E-17//201aa//34%//

P49816

C-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//0//6340bp//87%//Y17267
 C-SKNMC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//5.50E-35//431aa//29%//O60100

5 C-SKNMC1000013//Homo sapiens ATP-binding cassette protein M-ABC1 mRNA, nuclear gene encoding mitochondrial protein, complete cds.//0//2384bp//99%//AF047690
 C-SKNMC1000046//Homo sapiens liprin-alpha3 mRNA, partial cds.//1.90E-162//749bp//99%//AF034800
 C-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) [CALCIUM-ACTIVATED NEUTRAL PROTEINASE] (CANP) (M-TYPE).//3.20E-41//87aa//98%//P17655

10 C-SKNMC1000091//Homo sapiens mRNA for leucine-zipper protein, complete cds.//6.10E-190//872bp//99%//AB021663
 C-THYRO1000034//TRICHOHYALIN.//9.40E-10//176aa//30%//P37709
 C-THYRO1000072//MYOSIN UGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//3.40E-16//201aa//29%//P11799

15 C-THYRO1000085//PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B.//2.00E-72//155aa//92%//Q06710
 C-THYRO1000121//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//0//1737bp//87%//U49055
 C-THYRO1000132//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//1.10E-159//824bp//95%//U97018

20 C-THYRO1000173//Homo sapiens AP-mu chain family member muB (HSMU1B) mRNA, complete cds.//0//1713bp//99%//AF020797
 C-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//0//2362bp//99%//AJ005698
 C-THYRO1000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.00E-118//239aa//66%//P51523

25 C-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//0//2161bp//99%//AB016068
 C-THYRO1000327//Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds.//0//1567bp//99%//AF124145
 C-THYRO1000343//ATROPHIN-1 (DENTATORUBRAL-PALUDOLUYSIAN ATROPHY PROTEIN).//4.90E-06//280aa//31%//P54259

30 C-THYRO1000358//SELENIUM-BINDING LIVER PROTEIN.//2.30E-229//237aa//79%//P17563
 C-THYRO1000394//Homo sapiens peroxisomal membrane protein PMP 24 mRNA, complete cds.//1.20E-299//1325bp//99%//AF072864
 C-THYRO1000395//Homo sapiens actin-binding protein (IPP) mRNA, complete cds.//0//2092bp//99%//AF156857

35 C-THYRO1000401//Human Tcd37 homolog (HTcd37) mRNA, partial cds.//1.10E-90//430bp//99%//U67085
 C-THYRO1000488//Homo sapiens HFB30 mRNA, complete cds.//0//2254bp//100%//AB022663
 C-THYRO1000501//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//4.20E-98//408aa//42%//P19474

40 C-THYRO1000569//Mus musculus hematopoietic zinc finger protein mRNA, complete cds.//0//1557bp//91%//AF118566
 C-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds.//0//1901bp//99%//AF075587
 C-THYRO1000605//Homo sapiens histone acetyltransferase (HBOa) mRNA, complete cds.//0//3080bp//99%//AF140360

45 C-THYRO1000662//Homo sapiens XPV mRNA for DNA polymerase eta, complete cds.//0//2341 bp//99%//AB024313
 C-THYRO1000666//Mus musculus mRNA for kinesin like protein 9.//0//2001bp//86%//AJ132889
 C-THYRO1000684//Homo sapiens BAG-family molecular chaperone regulator-5 mRNA, complete cds.//0//3347bp//99%//AF095195

50 C-THYRO1000748//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//3.30E-96//335aa//52%//P98171
 C-THYRO1000756//[ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (EC 2.4.99.-)] (ST6GALNACIII)(STY).//1.80E-55//243aa//42%//Q64686
 C-THYRO1000783//Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds.//1.240E-157//11656bp//70%//U37373

55 C-THYRO1000852//Human branched-chain amino acid aminotransferase (ECA40) mRNA, complete cds.//1.40E-137//689bp//96%//U62739
 C-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//0//2387bp//99%//AF079529

- C-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//7.50E-57//315aa//43%//P32322
- C-THYRO1000951//DIHYDROXYACETONE KINASE 2 (EC 2.7.1.29) (GLYCERONE KINASE).//5.00E-83//566aa//37%//P43550
- 5 C-THYRO1000983//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//6.30E-17//143aa//39%//P35132
- C-THYRO1001003//UBIQUITIN-CONJUGATING ENZYME E2-21.2 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN UGASE) (UBIQUITIN CARRIER PROTEIN).//5.90E-14//84aa//41%//P52491
- C-THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//8.40E-12//167aa//29%//P31948
- 10 C-THYRO1001100//ZINC FINGER X-UNKEED PROTEIN ZXDA (FRAGMENT).//1.20E-67//245aa//62%//P98168
- C-THYRO1001120//Homo sapiens dextx (Dx) mRNA, complete cds.//1.30E-110//1947bp//65%//AF053700
- C-THYRO1001134//Homo sapiens CGI-78 protein mRNA, complete cds.//0.11898bp//99%//AF151835
- C-THYRO1001189//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-200//546aa//62%//Q05481
- 15 C-THYRO1001204//Homo sapiens cathepsin Z precursor (CTS2) gene, exons 4, 5, and 6 and complete cds; and TH1 gene partial sequence.//3.80E-100//478bp//99%//AF136276
- C-THYRO1001287//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE) (FRAGMENT).//3.40E-51//429aa//33%//P45701
- C-THYRO1001313//Homo sapiens sorting nexin 11 (SNX11) mRNA, complete cds.//0.12330bp//94%//AF121861
- 20 C-THYRO1001347//Homo sapiens RAN binding protein 16 mRNA, complete cds.//2.00E-263//3101bp//68%//AF064729
- C-THYRO1001374//CYTOSOLIC ACYL COENZYME A THIOESTER HYDROLASE (EC 3.1.2.2) (LONG CHAIN ACYL-COA THIOESTER HYDROLASE) (CTE-II).//1.80E-13//361aa//22%//O00154
- C-THYRO1001405//PLECTIN.//6.90E-19//450aa//27%//P30427
- 25 C-THYRO1001406//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).//1.10E-131//219aa//81%//O70503
- C-THYRO1001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//2.70E-17//559aa//59%//P35580
- C-THYRO1001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//0.11784bp//99%//AJ002190
- 30 C-THYRO1001656//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.//4.10E-273//1947bp//82%//AF175988
- C-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//0.11820bp//99%//AJ225089
- 35 C-THYRO1001703//NIFR3-LIKEPROTEIN.//2.90E-32//282aa//32%//P45672
- C-THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).//9.30E-34//220aa//38%//Q04652
- C-THYRO1001738//TUBULIN-TYROSINE LIGASE (EC 6.3.2.25) (TTL).//2.40E-20//217aa//30%//P38584
- C-THYRO1001809//MYOCYTE NUCLEAR FACTOR (MNF).//1.40E-74//158aa//89%//P42128
- 40 C-Y79AA1000013//Mus musculus RING finger protein A07 mRNA, complete cds.//8.90E-205//1435bp//81%//AF171060
- C-Y79AA1000033//Homo sapiens CARD4 mRNA, complete cds.//0.12929bp//96%//AF126484
- C-Y79AA1000037//DNA-BINDING PROTEIN BMI-1.//2.40E-30//80aa//60%//P25916
- C-Y79AA1000059//Homo sapiens aryl-hydrocarbon interacting protein-like 1 (AIP1) gene, complete cds.//0.11980bp//96%//AF180472
- 45 C-Y79AA1000181//Homo sapiens CGI-01 protein mRNA, complete cds.//0.11858bp//99%//AF132936
- C-Y79AA1000214//Homo sapiens histone H2A.FZ variant (H2AV) mRNA, complete cds.//7.10E-71//345bp//100%//AF081192
- C-Y79AA1000231//Homo sapiens nucleolar protein NOP5/NOP58 mRNA, complete cds.//0.11515bp//99%//AF123534
- 50 C-Y79AA1000268//Mus musculus Nip21 mRNA, complete cds.//2.10E-50//648bp//64%//AF035207
- C-Y79AA1000313//CALPHOTIN.//0.000011//336aa//23%//Q02910
- C-Y79AA1000328//SEL-10 PROTEIN.//0.000000067//219aa//25%//Q93794
- C-Y79AA1000342//Homo sapiens Ciz1 mRNA, complete cds.//0.12644bp//81%//AB030835
- C-Y79AA1000346//Homo sapiens nonclathrin coat protein gamma2-COP mRNA, complete cds.//0.12520bp//99%//AF157833
- 55 C-Y79AA1000349//M. musculus Spnr mRNA for RNA binding protein.//0.12048bp//93%//X84692
- C-Y79AA1000368//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//4.00E-20//261aa//27%//P25343
- C-Y79AA1000469//Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete

- cds.//18.30E-252//1207bp//85%//U41736
 C-Y79AA1000540//CELL POLARITY PROTEIN TEA1.//2.10E-12//211aa//33%//P87061
 C-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AF2 ADAPTIN ALPHA C SUBUNIT)7//0//652aa//98%//P17427
 5 C-Y79AA1000589//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//2.40E-27//216aa//34%//P28320
 C-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds.//2.00E-287//2031bp//82%//AF080503
 C-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1.//5.80E-254//1477bp//84%//X69942
 10 C-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds.//0//1594bp//99%//AF093670
 C-Y79AA1000748//Rattus norvegicus clone C42 CDK5 activator-binding protein mRNA, complete cds.//6.60E-286//1832bp//84%//AF177477
 C-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//4.90E-91//200aa//64%//Q61990
 15 C-Y79AA1000782//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3.00E-37//469aa//27%//P49902
 C-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//1.10E-236//1076bp//99%//AF098799
 C-Y79AA1000794//Homo sapiens actin-associated protein 2E4/kaptein (2E4) mRNA, 2E4-1 allele, complete cds.//0//1610bp//99%//AF105369
 20 C-Y79AA1000800//Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds.//1.60E-284//1288bp//99%//AF072733
 C-Y79AA1000833//TUBULIN ALPHA-1 CHAIN.//5.00E-173//220aa//79%//P05209
 C-Y79AA1000962//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II)7/4.20E-17//430aa//27%//Q99323
 25 C-Y79AA1000966//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%//AF100757
 C-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//3.90E-248//1468bp//87%//U38253
 C-Y79AA1000985//Human centrosomal protein kendrin mRNA, complete cds.//4.70E-151//985bp//87%//U52962
 30 C-Y79AA1001048//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD).//3.10E-138//583aa//47%//P45953
 C-Y79AA1001211//Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds.//0//1435bp//99%//AF139658
 C-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HYDROXYSTEROID DEHYDROGENASE 1).//7.70E-50//228aa//42%//P51657
 35 C-Y79AA1001236//Homo sapiens cell division protein mRNA, complete cds.//0//1612bp//99%//AF063015
 C-Y79AA1001299//Homo sapiens mRNA for integrase interactor 1b protein (INI1b).//0//996bp//99%//AJ011738
 C-Y79AA1001312//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46).//0.00000023//193aa//30%//Q03309
 40 C-Y79AA1001323//Mus musculus mRNA for GSG1, complete cds.//3.30E-172//1171bp//83%//D87325
 C-Y79AA1001384//Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds.//0//4708bp//99%//AF055084
 C-Y79AA1001391//HOMEBOX PROTEIN HOX-A13 (HOX-1J).//1.20E-58//178aa//66%//P31271
 C-Y79AA1001394//CELL DIVISION PROTEIN FTSH HOMOLOG (EC 3.4.24.-).//1.20E-13//230aa//32%//O83746
 45 C-Y79AA1001402//Homo sapiens paraneoplastic cancer-testis-brain antigen (MA4) mRNA, partial cds.//8.50E-65//784bp//62%//AF083115
 C-Y79AA1001493//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//3.80E-18//151aa//38%//P35132
 C-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//4.50E-193//1333bp//80%//D14336
 50 C-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//7.50E-76//85aa//90%//P42356
 C-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL-AC-TIVATING ENZYME).//1.90E-40//482aa//27%//P27550
 C-Y79AA1001594//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//2.50E-14//410aa//24%//Q00547
 55 C-Y79AA1001603//POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYLGLACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYLGLACTOS-

AMINYLTRANSFERASE) (GALNAC-T1) //1.70E-84//313aa//48%//Q07537
 C-Y79AA1001613//ZINC FINGER PROTEIN 132 //3.80E-91//209aa//41%//P52740
 C-Y79AA1001679//Homo sapiens lambda-crystallin mRNA, complete cds.//3.4e-310//1430bp//98%//AF077049
 C-Y79AA1001692//Mus musculus strain C57BL/J germ cell-less protein (Gc1) mRNA, complete cds.//1.40E-78//
 227aa//40%//Q01820
 C-Y79AA1001705//Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds.//3.40E-
 47//826bp//68%//AF033120
 C-Y79AA1001711//Human 80-kdal ribonucleoprotein (Ro) mRNA, complete cds.//1.20E-258//1185bp//99%//
 J04137
 C-Y79AA1001827//Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA, complete cds.//
 0//1689bp//98%//AF177145
 C-Y79AA1001866//Homo sapiens zinc finger protein ZNF180 (ZNF180) mRNA, complete cds.//0//2927bp//97%//
 AF192913
 C-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTI-
 15 VATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN) //4.50E-08//135aa//31%//P43489
 C-Y79AA1001875//RAS-RELATED PROTEIN RAB-7 //9.40E-12//34aa//97%//P51149
 C-Y79AA1001923//Homo sapiens F-box protein Fbx22 (FBX22) gene, partial cds.//1.70E-52//279bp//97%//
 AF174602
 C-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE
 20 SPAC10F6.02C //1.00E-10//94aa//47%//O42643
 C-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN
 LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42) //9.90E-39//143aa//52%//P42743
 C-Y79AA1002083//H. sapiens mRNA for MUF1 protein.//5.00E-163//752bp//99%//X86018
 C-Y79AA1002103//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT) //3.00E-257//549aa//76%//P16415
 25 C-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1) //9.00E-17//120aa//45%//Q24133
 C-Y79AA1002204//COMPLEXIN 2 (SYNAPHIN 1) (921-L) //7.50E-09//131aa//35%//Q13329
 C-Y79AA1002208//ANKYRIN //8.10E-34//188aa//38%//Q02357
 C-Y79AA1002209//TYROSYL-TRNA SYNTHETASE (EC 6.1.1.1) (TYROSINE--TRNA LIGASE) (TYRRS) //1.60E-
 72//437aa//39%//P00952
 30 C-Y79AA1002210//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-
 TEIN) //0.0000018//140aa//25%//Q13829
 C-Y79AA1002211//PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN HOMOLOG F40A3.3 //1.70E-17//
 146aa//35%//O16264
 C-Y79AA1002229//DNA CROSS-LINK REPAIR PROTEIN PSO2/SNM1 //7.10E-17//213aa//31%//P30620
 35 C-Y79AA1002246//SYNAPTOTAGMIN V //1.60E-28//286aa//32%//O00445
 C-Y79AA1002258//Homo sapiens mRNA for HIP1R, complete cds.//0//2106bp//99%//AB013384
 C-Y79AA1002307//Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds.//0//1209bp//99%//AF116574
 C-Y79AA1002311//R. norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.90E-186//1130bp//82%//
 X67877
 40 C-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit) //6.90E-140//966bp//82%//
 Y18208
 C-Y79AA1002399//Homo sapiens mRNA for sperm protein.//0//1163bp//95%//X91879
 C-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds.//3.9e-317//1902bp//
 86%//U49385
 45 C-Y79AA1002431//TRANSDUCIN-LIKE ENHANCER PROTEIN 2 (ESG2) //9.80E-62//318aa//35%//Q04725
 C-Y79AA1002433//Homo sapiens chromatin- specific transcription elongation factor FACT 140 kDa subunit mR-
 NA, complete cds.//0//1545bp//96%//AF152961
 C-Y79AA1002472//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7) //1.50E-136//472aa//
 49%//Q05481
 50 C-Y79AA1002482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7) //2.70E-137//340aa//
 51%//Q05481
 C-Y79AA1002487//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.//7.3e-311//
 1444bp//98%//AF129534

Claims

1. Use of an oligonucleotide as a primer for synthesizing the polynucleotide comprising the nucleotide sequence set

forth in any one of SEQ ID NOs: 1-5547 and SEQ ID NOs: 16111-16164, or the complementary strand thereof, wherein said oligonucleotide is complementary to said polynucleotide or the complementary strand thereof and comprises at least 15 nucleotides.

2. A primer set for synthesizing polynucleotides, the primer set comprising an oligo-dT primer and an oligonucleotide complementary to the complementary strand of the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-5547 and SEQ ID NOs: 16111-16164, wherein said oligonucleotide comprises at least 15 nucleotides.
3. A primer set for synthesizing polynucleotides, the primer set comprising a combination of an oligonucleotide comprising a nucleotide sequence complementary to the complementary strand of the polynucleotide comprising a 5'-end nucleotide sequence and an oligonucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising a 3'-end nucleotide sequence, wherein said oligonucleotides comprise at least 15 nucleotides and wherein said combination of 5'-end nucleotide sequence 3'-end nucleotide sequence is selected from the group consisting of:

SEQ ID NO: 1 / SEQ ID NO: 5548, SEQ ID NO: 4 / SEQ ID NO: 5549, SEQ ID NO: 5 / SEQ ID NO: 5550, SEQ ID NO: 6 / SEQ ID NO: 5551, SEQ ID NO: 7 / SEQ ID NO: 5552, SEQ ID NO: 8 / SEQ ID NO: 5553, SEQ ID NO: 9 / SEQ ID NO: 5554, SEQ ID NO: 10 / SEQ ID NO: 5555, SEQ ID NO: 11 / SEQ ID NO: 5556, SEQ ID NO: 12 / SEQ ID NO: 5557, SEQ ID NO: 13 / SEQ ID NO: 5558, SEQ ID NO: 14 / SEQ ID NO: 5559, SEQ ID NO: 15 / SEQ ID NO: 5560, SEQ ID NO: 16 / SEQ ID NO: 5561, SEQ ID NO: 17 / SEQ ID NO: 5562, SEQ ID NO: 18 / SEQ ID NO: 5563, SEQ ID NO: 19 / SEQ ID NO: 5564, SEQ ID NO: 20 / SEQ ID NO: 5565, SEQ ID NO: 21 / SEQ ID NO: 5566, SEQ ID NO: 22 / SEQ ID NO: 5567, SEQ ID NO: 23 / SEQ ID NO: 5568, SEQ ID NO: 24 / SEQ ID NO: 5569, SEQ ID NO: 25 / SEQ ID NO: 5570, SEQ ID NO: 26 / SEQ ID NO: 5571, SEQ ID NO: 27 / SEQ ID NO: 5572, SEQ ID NO: 28 / SEQ ID NO: 5573, SEQ ID NO: 29 / SEQ ID NO: 5574, SEQ ID NO: 30 / SEQ ID NO: 5575, SEQ ID NO: 31 / SEQ ID NO: 5576, SEQ ID NO: 32 / SEQ ID NO: 5577, SEQ ID NO: 33 / SEQ ID NO: 5578, SEQ ID NO: 34 / SEQ ID NO: 5579, SEQ ID NO: 35 / SEQ ID NO: 5580, SEQ ID NO: 37 / SEQ ID NO: 5581, SEQ ID NO: 38 / SEQ ID NO: 5582, SEQ ID NO: 39 / SEQ ID NO: 5583, SEQ ID NO: 40 / SEQ ID NO: 5584, SEQ ID NO: 42 / SEQ ID NO: 5585, SEQ ID NO: 43 / SEQ ID NO: 5586, SEQ ID NO: 44 / SEQ ID NO: 5587, SEQ ID NO: 45 / SEQ ID NO: 5588, SEQ ID NO: 46 / SEQ ID NO: 5589, SEQ ID NO: 47 / SEQ ID NO: 5590, SEQ ID NO: 48 / SEQ ID NO: 5591, SEQ ID NO: 49 / SEQ ID NO: 5592, SEQ ID NO: 50 / SEQ ID NO: 5593, SEQ ID NO: 51 / SEQ ID NO: 5594, SEQ ID NO: 52 / SEQ ID NO: 5595, SEQ ID NO: 53 / SEQ ID NO: 5596, SEQ ID NO: 54 / SEQ ID NO: 5597, SEQ ID NO: 55 / SEQ ID NO: 5598, SEQ ID NO: 56 / SEQ ID NO: 5599, SEQ ID NO: 57 / SEQ ID NO: 5600, SEQ ID NO: 58 / SEQ ID NO: 5601, SEQ ID NO: 59 / SEQ ID NO: 5602, SEQ ID NO: 60 / SEQ ID NO: 5603, SEQ ID NO: 61 / SEQ ID NO: 5604, SEQ ID NO: 62 / SEQ ID NO: 5605, SEQ ID NO: 63 / SEQ ID NO: 5606, SEQ ID NO: 65 / SEQ ID NO: 5607, SEQ ID NO: 66 / SEQ ID NO: 5608, SEQ ID NO: 67 / SEQ ID NO: 5609, SEQ ID NO: 68 / SEQ ID NO: 5610, SEQ ID NO: 69 / SEQ ID NO: 5611, SEQ ID NO: 70 / SEQ ID NO: 5612, SEQ ID NO: 71 / SEQ ID NO: 5613, SEQ ID NO: 72 / SEQ ID NO: 5614, SEQ ID NO: 74 / SEQ ID NO: 5615, SEQ ID NO: 76 / SEQ ID NO: 5616, SEQ ID NO: 77 / SEQ ID NO: 5617, SEQ ID NO: 78 / SEQ ID NO: 5618, SEQ ID NO: 79 / SEQ ID NO: 5619, SEQ ID NO: 80 / SEQ ID NO: 5620, SEQ ID NO: 81 / SEQ ID NO: 5621, SEQ ID NO: 82 / SEQ ID NO: 5622, SEQ ID NO: 83 / SEQ ID NO: 5623, SEQ ID NO: 84 / SEQ ID NO: 5624, SEQ ID NO: 85 / SEQ ID NO: 5625, SEQ ID NO: 86 / SEQ ID NO: 5626, SEQ ID NO: 87 / SEQ ID NO: 5627, SEQ ID NO: 88 / SEQ ID NO: 5628, SEQ ID NO: 89 / SEQ ID NO: 5629, SEQ ID NO: 90 / SEQ ID NO: 5630, SEQ ID NO: 91 / SEQ ID NO: 5631, SEQ ID NO: 92 / SEQ ID NO: 5632, SEQ ID NO:

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NO: 16216, SEQ ID NO: 16163 / SEQ ID NO: 16217, and SEQ ID NO: 16164 / SEQ ID NO: 16218

4. A polynucleotide which can be synthesized with the primer set of claim 2 or 3.
5. A polynucleotide comprising a coding region in the polynucleotide of claim 4.
6. A substantially pure protein encoded by polynucleotide of claim 4.
7. A partial peptide of the protein of claim 6.
8. An isolated polynucleotide selected from the group consisting of
 - (a) a polynucleotide comprising a coding region of the nucleotide sequence set forth in any one of the following SEQ ID NOs:

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[illegible]

[illegible]

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 SEQ ID NO: 18966, SEQ ID NO: 18968, SEQ ID NO: 18969, SEQ ID NO: 18970, SEQ ID
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 SEQ ID NO: 19002, SEQ ID NO: 19004, SEQ ID NO: 19006
 SEQ ID NO: 19007, SEQ ID NO: 19009, SEQ ID NO: 19011, SEQ ID NO: 19012, SEQ ID
 NO: 19013, SEQ ID NO: 19014, SEQ ID NO: 19016, SEQ ID NO: 19018, SEQ ID NO: 19020,
 SEQ ID NO: 19022, SEQ ID NO: 19024, and SEQ ID NO: 19025

(b) a polynucleotide comprising a nucleotide sequence encoding a protein comprising the amino acid sequence
 set forth in any one of the following SEQ ID NOs:

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(c) a polynucleotide comprising a nucleotide sequence encoding a protein comprising an amino acid sequence
 selected from the amino acid sequences of (b), in which one or more amino acids are substituted, deleted,
 inserted, and/or added, wherein said protein is functionally equivalent to the protein comprising said amino
 acid sequence selected from the amino acid sequences of (b);

(d) a polynucleotide that hybridizes with a polynucleotide comprising a nucleotide sequence selected from the
 nucleotide sequences of (a), and that comprises a nucleotide sequence encoding a protein functionally equivalent
 to the protein encoded by the nucleotide sequence selected from the nucleotide sequences of (a);

(e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a protein
 encoded by the polynucleotide of (a) to (d);

(f) a polynucleotide comprising a nucleotide sequence with at least 70% identity to the nucleotide sequence
 of (a).

9. A substantially pure protein encoded by the polynucleotide of claim 8.

10. An antibody against the protein or peptide of any one of claims 6, 7, and 9.

11. A vector comprising the polynucleotide of claim 5 or 8.
12. A transformant carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.
- 5 13. A transformant expressively carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.
14. A method for producing the protein or peptide of any one of claims 6, 7, and 9, comprising culturing the transformant of claim 13 and recovering the expression product.
- 10 15. An oligonucleotide comprising the nucleotide sequence of claim 8 (a) or the nucleotide sequence complementary to the complementary strand thereof, wherein said oligonucleotide comprises 15 nucleotides or more.
16. Use of the oligonucleotide of claim 15 as a primer for synthesizing a polynucleotide.
- 15 17. Use of the oligonucleotide of claim 15 as a probe for detecting a gene.
18. An antisense polynucleotide against the polynucleotide of claim 8, or the portion thereof.
19. A method for synthesizing a polynucleotide, the method comprising:
 - 20 a) synthesizing a complementary strand using a cDNA library as a template, and using the primer set of claim 2 or 3, or the primer of claim 16; and
 - b) recovering the synthesized product.
- 25 20. The method of claim 19, wherein the cDNA library is obtainable by oligo-capping method.
21. The method of claim 19, wherein the complementary strand is obtainable by PCR.
22. A method for detecting the polynucleotide of claim 8, the method comprising:
 - 30 a) incubating a target polynucleotide with the oligonucleotide of claim 15 under the conditions where hybridization occurs, and
 - b) detecting the hybridization of the target polynucleotide with the oligonucleotide of claim 15.
- 35 23. A database of polynucleotides and/or proteins, the database comprising information on at least one sequence selected from the nucleotide sequences of claim 8 (a) and/or the amino acid sequences of claim 8 (b), or a medium on which the database is stored.

Figure 1

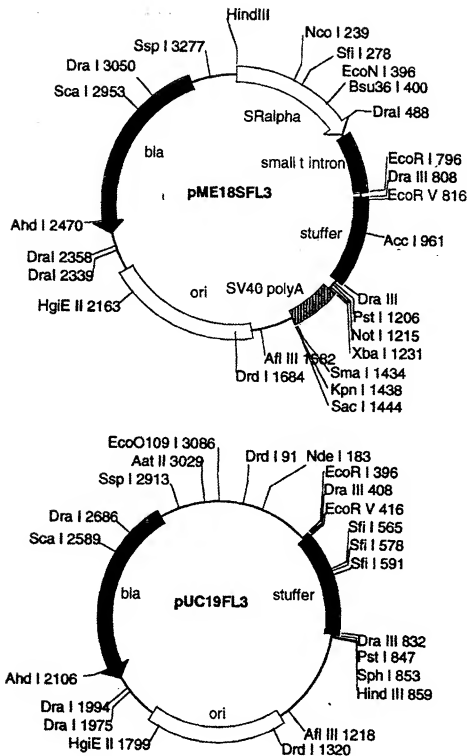


Figure 2

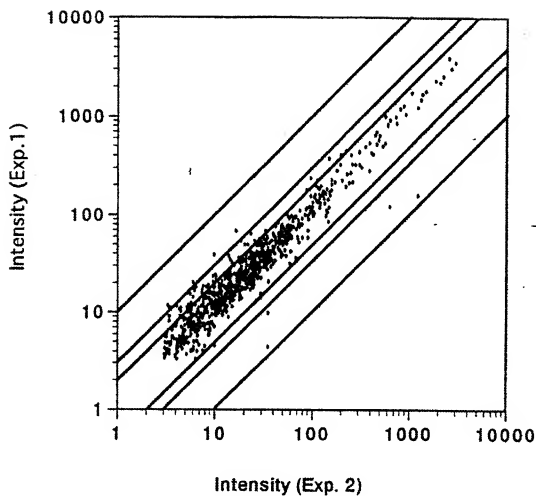


Figure 3

